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OM nucleic - nucleic search, using sw model

Run on: December 16, 2004, 19:01:48 ; Search time 996 Seconds  
(without alignments)  
6945.391 Million cell updates/sec

Title: US-09-806-277A-13

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Gapop 10.0, Gapext 1.0

Searched: 4093002 seqs, 276041825 residues

Total number of hits satisfying chosen parameters: 8186004

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications NA:\*

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- 20: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 21: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1230	98.2	1238	9	US-09-989-723-356 Sequence 356, App
3	1230	98.2	1238	9	US-09-989-729-356 Sequence 356, App
4	1230	98.2	1238	9	US-09-989-727-356 Sequence 356, App
5	1230	98.2	1238	9	US-09-989-731-356 Sequence 356, App
6	1230	98.2	1238	9	US-09-989-733-356 Sequence 356, App
7	1230	98.2	1238	9	US-09-991-073-356 Sequence 356, App
8	1230	98.2	1238	9	US-09-990-442-356 Sequence 356, App
9	1230	98.2	1238	9	US-09-991-163-356 Sequence 356, App
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17	1230	98.2	1238	9	US-09-991-161-356 Sequence 356, App
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25	1230	98.2	1238	10	US-09-990-441-356 Sequence 356, App
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36	1230	98.2	1238	10	US-09-997-514-356 Sequence 356, App
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43	1230	98.2	1238	10	US-09-991-854-356 Sequence 356, App
44	1230	98.2	1238	10	US-09-997-628-356 Sequence 356, App
45	1230	98.2	1238	10	US-09-997-683-356 Sequence 356, App

#### ALIGNMENTS

RESULT 1  
US-09-989-722-356  
; Sequence 356, Application US/09989722  
; Patent No. US20020072067A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerltzen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tamas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zenlin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C63  
CURRENT APPLICATION NUMBER: US/09/989, 722  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787

[illegible]

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; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Query Match 98.2%; Score 1230; DB 9; Length 1238;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1201 TAGTGCAAGTAAAGTCAAAAAA 1230

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RESULT 2  
US-09-989-723-356  
Sequence 356, Application US/09989723  
Patent No. US20020072092A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltzen, Mary B.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grunwald, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Napier, Mary A.  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C62  
CURRENT APPLICATION NUMBER: US/09/989, 723  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787

[illegible]



PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 98.2%; Score 1230; DB 9; Length 1238;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3  
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Sequence 356, Application US/09989279  
Patent No. US20020072496A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: KJavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730PIC56  
CURRENT APPLICATION NUMBER: US/09/989,279  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787

1	PRIOR APPLICATION NUMBER: 60/089440
2	PRIOR FILING DATE: 1998-06-16
3	PRIOR APPLICATION NUMBER: 60/089512
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5	PRIOR APPLICATION NUMBER: 60/089514
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18	PRIOR FILING DATE: 1998-06-17
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20	PRIOR FILING DATE: 1998-06-18
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22	PRIOR FILING DATE: 1998-06-18
23	PRIOR APPLICATION NUMBER: 60/089908
24	PRIOR FILING DATE: 1998-06-18
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 3 PRIOR FILING DATE: 1998-06-26  
 4 PRIOR APPLICATION NUMBER: 60/091360  
 5 PRIOR FILING DATE: 1998-07-01  
 6 PRIOR APPLICATION NUMBER: 60/091478  
 7 PRIOR FILING DATE: 1998-07-02  
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 11 PRIOR FILING DATE: 1998-07-02  
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 13 PRIOR FILING DATE: 1998-07-02  
 14 PRIOR APPLICATION NUMBER: 60/091633  
 15 PRIOR FILING DATE: 1998-07-02  
 16 PRIOR APPLICATION NUMBER: 60/091978  
 17 PRIOR FILING DATE: 1998-07-07  
 18 PRIOR APPLICATION NUMBER: 60/091982  
 19 PRIOR FILING DATE: 1998-07-07  
 20 PRIOR APPLICATION NUMBER: 60/092182  
 21 PRIOR FILING DATE: 1998-07-09

Query Match	98.2%	Score 1230;	DB 9;	Length 1238;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1230;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0

Oy	24	CGACGCGGCAGAGACGCCCGCTTGGCTGAGCGGTGCCTACAGAGTTGATGTCCTGGCTGGG	83
Db	1	GGACGGGCGAGACCCCGCTTGGCTTACGGGTGCCTACAGAGTTGATGTCCTGGCTGGG	60
Oy	84	CTCAGGATGAGGGGGAATCTGGCGCCCTGGTGGCGCTTCTTAATCAGCCTGGCTTCTCTGTCA	143
Db	61	CTCAGGATGAGGGGGAATCTGGCGCCCTGGTGGCGCTTCTTAATCAGCCTGGCTTCTCTGTCA	120
Oy	144	CTGCTGCGCATCTGGAACATCTTAAGCCGGCTGGCGAATGACGCTTGGCTTGTGCAGATCTCTC	203
Db	121	CTGCTGCGCATCTGGAACATCTTAAGCCGGCTGGCGAATGACGCTTGGCTTGTGTGAGATCTCTC	180
Oy	204	GTCCTCGGCTTCAAAAGGGGATCGGGAGAGAGACAAGAGCGCCCGCGAGCGCT	263
Db	181	GTCCTCGGCTTCAAAAGGGGATCGGGAGAGAGACAAGAGCGCCCGCGAGCGCT	240
Oy	264	GGAAGAGTCGCGCCCAACGGGAGAAAAAGGACATGAGGGGACAAAGACAGAAAGGCACT	323
Db	241	GGAAGAGTCGCGCCCAACGGGAGAAAAAGGACATGAGGGGACAAAGGACAGAAAGGCACT	300
Oy	324	GTCGGTCGTATGGAATAATGGTCCCATTTGGCTCTAAAGGTGAGAAAGGAAATTCGCGGT	383
Db	301	GTCGGTCGTATGGAATAATGGTCCCATTTGGCTCTAAAGGTGAGAAAGGAAATTCGCGGT	360
Oy	384	GACATATGAGACCCCGTGGTCTTAATGAGAAACGAGGCTTCCCATGTGAGTGCAGCCAGCTG	443
Db	361	GACATATGAGACCCCGTGGTCTTAATGAGAAACGAGGCTTCCCATGTGAGTGCAGCCAGCTG	420
Oy	444	CGCAAGGCGATCGGGGAGATGGAACAACAGGCTCTCAGGTCACACAGAGGCTCAAGTTC	503
Db	421	CGCAAGGCGATCGGGGAGATGGAACAACAGGCTCTCAGGTCACACAGAGGCTCAAGTTC	480
Oy	504	ATCAAGATGCTGTGGCGGTGTGGCGGAGACGAGAGCAGATCTACTGCTGTGAAG	563
Db	481	ATCAAGATGCTGTGGCGGTGTGGCGGAGACGAGAGCAGATCTACTGCTGTGAAG	540
Oy	564	GAGGAGAAAGCGTTACGCGGACGCCCAAGTGTCTCTGCAAGGCGCGGGGGGCAACGCTAGAC	623
Db	541	GAGGAGAAAGCGTTACGCGGACGCCCAAGTGTCTCTGCAAGGCGCGGGGGGCAACGCTAGAC	600
Oy	624	ATGCCCAAGACGAGGCTGCAATGAGCTGATGCGCGCATACCTGAGCGCAACCGGCGCTG	683
Db	601	ATGCCCAAGACGAGGCTGCAATGAGCTGATGCGCGCATACCTGAGCGCAACCGGCGCTG	660
Oy	684	GCCGCTGCTTCATGGGCATCAACGACCTGGAGAAAGAGGGCGCCTTGCTGTACTCTGAC	743
Db	661	GCCGCTGCTTCATGGGCATCAACGACCTGGAGAAAGAGGGCGCCTTGCTGTACTCTGAC	720

QY	744	CACCTCCCAATCGGGACCTTTAAACAAGTGGGGACCGGTGAGGCCCAACAATGCCCTAGAC	803
Db	721	CACCTCCCAATCGGGACCTTTAAACAAGTGGGGACCGGTGAGGCCCAACAATGCCCTAGAC	780
QY	804	GAGAGAGACTCGGTGAGAGATGGTGGCCCTCGGGCCGGTGGAAACGACGTGGCTGGCCACAC	863
Db	781	GAGAGAGACTCGGTGAGAGATGGTGGCCCTCGGGCCGGTGGAAACGACGTGGCTGGCCACAC	840
QY	864	ACCATGTACTTCATGTGTGAGTTTGACACAGGAGAAATGTGAGCCTCAGGCTGGGGCTGC	923
Db	841	ACCATGTACTTCATGTGTGAGTTTGACACAGGAGAAATGTGAGCCTCAGGCTGGGGCTGC	900
QY	924	CCATTTGGGGGGGGCCCAACATGTCCTCGACGGGTGGGCGAGGAGCCAGACATGAGTC	983
Db	901	CCATTTGGGGGGGGCCCAACATGTCCTCGACGGGTGGGCGAGGAGCCAGACATGAGTC	960
QY	984	CAGCCAGGAGACTGTCCTCTGTGTAAGGGGTGAGAGGCTCACTGAGTAGAGGGCTGTGTCT	1043
Db	961	CAGCCAGGAGACTGTCCTCTGTGTAAGGGGTGAGAGGCTCACTGAGTAGAGGGCTGTGTCT	1020
QY	1044	AAACTGAGAAATGGCCTTATGCTTAAAGAGAAATGAAAGTGTCTGGGGTGTGTCTC	1103
Db	1021	AAACTGAGAAATGGCCTTATGCTTAAAGAGAAATGAAAGTGTCTGGGGTGTGTCTC	1080
QY	1104	TGAAGAACACAGTTTCAATTACCTGTATGTAGGCCCAATGTCATTTATTAATTATACC	1163
Db	1081	TGAAGAACACAGTTTCAATTACCTGTATGTAGGCCCAATGTCATTTATTAATTATACC	1140
QY	1164	CAGAAATGCTCTTCATTAAGCTTGCGCTTGTGTCGAAGCTATACAATAAATCTTTAAG	1223
Db	1141	CAGAAATGCTCTTCATTAAGCTTGCGCTTGTGTCGAAGCTATACAATAAATCTTTAAG	1200
QY	1224	TAGTGCACTAGTTAAGTCCAAAAA	1253
Db	1201	TAGTGCACTAGTTAAGTCCAAAAA	1230

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1  RESULT 4
2  US-09-989-727-356
3  Sequence 356 Application US/09989727
4  Patent No. US20020072457A1
5  GENERAL INFORMATION:
6  APPLICANT: Ashkenazi, Avi J.
7  APPLICANT: Baker, Kevin P.
8  APPLICANT: Botstein, David
9  APPLICANT: Desnoyers, Luc
10 APPLICANT: Eaton, Dan L.
11 APPLICANT: Ferrara, Napoleone
12 APPLICANT: Fong, Sherman
13 APPLICANT: Gerber, Hanspeter
14 APPLICANT: Gerritsen, Mary E.
15 APPLICANT: Goddard, Audrey
16 APPLICANT: Godowski, Paul J.
17 APPLICANT: Grimaldi, J. Christopher
18 APPLICANT: Gurney, Austin L.
19 APPLICANT: Kljavin, Ivar J.
20 APPLICANT: Napier, Mary A.
21 APPLICANT: Pan, James
22 APPLICANT: Paoni, Nicholas F.
23 APPLICANT: Roy, Margaret Ann
24 APPLICANT: Stewart, Timothy A.
25 APPLICANT: Tumas, Daniel
26 APPLICANT: Watanabe, Colin K.
27 APPLICANT: Williams, P. Mickey
28 APPLICANT: Wood, William I.
29 APPLICANT: Zhang, Zhenli
30 TITLE OF INVENTION: Secreted and Transmembrane polypeptides and Nucleic
31 TITLE OF INVENTION: Acids Encoding the Same
32 FILE REFERENCE: P2730P1C65
33 CURRENT APPLICATION NUMBER: US/09/989,727
34 PRIOR FILING DATE: 2001-11-19
35 PRIOR APPLICATION NUMBER: 60/045787

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[illegible]

PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 98.2%; Score 1230; DB 9; Length 1238;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GCGAGGCGAGAGCCCGCTTGGCTAGCGGTCTCAGAGTGTGTCTCTGCTCG 83  
DB 1 GCGAGGCGAGAGCCCGCTTGGCTAGCGGTCTCAGAGTGTGTCTCTGCTCG 60  
QY 84 CTCAGATGAGGGGAGATCTGGCCCTGGTGGGCTTTCTAATCAGGCTGGCTTCTGCA 143  
DB 61 CTCAGATGAGGGGAGATCTGGCCCTGGTGGGCTTTCTAATCAGGCTGGCTTCTGCA 120  
QY 144 CTGCTGCATCTGACATCTTCAGCGGCTGGCGATGACGCGCTGCTGTGCAATCTC 203  
DB 121 CTGCTGCATCTGACATCTTCAGCGGCTGGCGATGACGCGCTGCTGTGCAATCTC 180  
QY 204 GTCCCTGGCTTCAAGGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 263  
DB 181 GTCCCTGGCTTCAAGGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
QY 264 GGAAGAGTCGGCCCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 323  
DB 241 GGAAGAGTCGGCCCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
QY 324 GTGGGTCTCATGAGAAAAATTGGTCCATTTGGCTTAAAGTGAGAGAGAGATTCCGGT 383  
DB 301 GTGGGTCTCATGAGAAAAATTGGTCCATTTGGCTTAAAGTGAGAGAGAGATTCCGGT 360  
QY 384 GACATAGAGACCCCTGGTCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 443  
DB 361 GACATAGAGACCCCTGGTCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
QY 444 CGCAAGGCGATGGGAG 503  
DB 421 CGCAAGGCGATGGGAG 480  
QY 504 ATCAAGATGTGTGCGCGGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 563  
DB 481 ATCAAGATGTGTGCGCGGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540  
QY 564 GAGAGAGAGCGCTTACGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 623  
DB 541 GAGAGAGAGCGCTTACGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600  
QY 624 ATGCCCAAG 683  
DB 601 ATGCCCAAG 660  
QY 684 GCCCGTGTCTTCTCATGCGCATCAACGACCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 743  
DB 661 GCCCGTGTCTTCTCATGCGCATCAACGACCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 720

QY 744 CACTCCCCCATGCGGAGCCTTCAACAGTGGCGGAGCGGTGAGCCCAATAGCTTACGAC 803  
DB 721 CACTCCCCCATGCGGAGCCTTCAACAGTGGCGGAGCGGTGAGCCCAATAGCTTACGAC 780  
QY 804 GAGAGAGAGCTGCGTGAAGATGTGGCTCGGCGGCTGGAAAGAGCTGGCTGCGACAC 863  
DB 781 GAGAGAGAGCTGCGTGAAGATGTGGCTCGGCGGCTGGAAAGAGCTGGCTGCGACAC 840  
QY 864 ACCATGATCTTCAATGTGTGAGATTGACAGAGAAACATGTGAGCTCAGGCTGGGGCTGC 923  
DB 841 ACCATGATCTTCAATGTGTGAGATTGACAGAGAAACATGTGAGCTCAGGCTGGGGCTGC 900  
QY 924 CCATTGGGGGGCCCCACATGTCTCCGACAGGCTTGGACAGAGAGAGAGAGAGAGAGAGAG 983  
DB 901 CCATTGGGGGGCCCCACATGTCTCCGACAGGCTTGGACAGAGAGAGAGAGAGAGAGAGAG 960  
QY 984 CAGCCAGGAGCTGTCCCTCTGTGAAGGTTGAGAGGCTTCACTGATGAGAGAGGCTGTGCT 1043  
DB 961 CAGCCAGGAGCTGTCCCTCTGTGAAGGTTGAGAGGCTTCACTGATGAGAGAGGCTGTGCT 1020  
QY 1044 AAATCTGAGAAATGAGCTTATGCTTAAAGAGAAATGAAAGTTCCTGGGGTGTGCTC 1103  
DB 1021 AAATCTGAGAAATGAGCTTATGCTTAAAGAGAAATGAAAGTTCCTGGGGTGTGCTC 1080  
QY 1104 TGAAGAGAGAGAGTTCACTTATGTAAGCCCAATGTCAATTAATTAATTAATTAATTA 1163  
DB 1081 TGAAGAGAGAGAGTTCACTTATGTAAGCCCAATGTCAATTAATTAATTAATTAATTA 1140  
QY 1164 CAGAAATGCTTCTTCATTAAGCTTGTGCTTGTCAAGCTATTAATTAATTAATTAATTA 1223  
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QY 1224 TAGTGCAGTACTTAAGTCAAAAAA 1253  
DB 1201 TAGTGCAGTACTTAAGTCAAAAAA 1230

RESULT 5  
US-09-989-731-356  
Sequence 356, Application US/09989731  
Patent No. US20020103125A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Falcon, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C70  
CURRENT APPLICATION NUMBER: US/09/989, 731  
CURRENT FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/049787

[illegible]

;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/090863  
;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/091360  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091478  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091544  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091626  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 98.2%; Score 1230; DB 9; Length 1238;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GCGACGGGAGAGACCCCGCTTCCCTTACGCGCTGCTCAGAGTTGTGTCTCTGCTGCG 83  
DB 1 GCGACGGGAGAGACCCCGCTTCCCTTACGCGCTGCTCAGAGTTGTGTCTCTGCTGCG 60  
QY 84 CTCAGATGAGGGGGAAATCTGGCCCTGGTGGGCGTTCTTAATAGGCTGGCCCTCTGCA 143  
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QY 144 CTGCTGCAATCTGCAATCTCTCAGCGGCTGGGAGTGAAGCGCTGCTGTGCAATCTCTC 203  
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QY 204 GTCCCTGGCTCAAAAGGGGATCGGGAGAGAAAGGAGCAAAAGCGCCCGGACGGCT 263  
DB 181 GTCCCTGGCTCAAAAGGGGATCGGGAGAGAAAGGAGCAAAAGCGCCCGGACGGCT 240  
QY 264 GGAAGAGTCGGCCCAAGGAGAGAAAGGAGCATGGGGGCAAAAGGACAGAAAGGACGT 323  
DB 241 GGAAGAGTCGGCCCAAGGAGAGAAAGGAGCATGGGGGCAAAAGGACAGAAAGGACGT 300  
QY 324 GTGGGTCTCATGAAAAATTGGTCCCATTTGGCTCTAAAGGTGAGAAAGAGATTCCGGT 383  
DB 301 GTGGGTCTCATGAAAAATTGGTCCCATTTGGCTCTAAAGGTGAGAAAGAGATTCCGGT 360  
QY 384 GACATAGAGACCCCTGGTCTTAATGAGAGAACAGGCTTCCATGTGAGTGACGACGCTG 443  
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DB 601 ATGCCCAAGAGAGAGGCTGCGCAATGGCTGATGGCGGATTAATCTGGCCCAAGCGGCTG 660  
QY 684 GCCCGTGTCTTCATCGGATCAACAGACCTGAGAGAGAGGCGCTTGTGTACTGTAC 743  
DB 661 GCCCGTGTCTTCATCGGATCAACAGACCTGAGAGAGAGGCGCTTGTGTACTGTAC 720

QY 744 CACTCCCCCATGCGGACCTTCAACAGAGGAGGAGCGGTGAGCCCAACATGCTTACGAC 803  
DB 721 CACTCCCCCATGCGGACCTTCAACAGAGGAGGAGCGGTGAGCCCAACATGCTTACGAC 780  
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DB 781 GAGAGAGACTGCTGAGAGATGAGGCTCGGGCGGCTGGAAGAGAGTGGCTGCGACACC 840  
QY 864 ACCATGTACTTCATGTGTGAGTTTGAACAGAGAAACATGTAGGCTCAGGCTGGGGCTGC 923  
DB 841 ACCATGTACTTCATGTGTGAGTTTGAACAGAGAAACATGTAGGCTCAGGCTGGGGCTGC 900  
QY 924 CCATTGGGGGGCCCAACATGTCCTTCGACAGGCTTGGCAGAGGAGACAGGCCCAACATGTCG 983  
DB 901 CCATTGGGGGGCCCAACATGTCCTTCGACAGGCTTGGCAGAGGAGACAGGCCCAACATGTCG 960  
QY 984 CAGCAGGAGACTGTCTCTGTGAGAGGGGTGAGGCTCACTGAGTGAAGGCTGTGTCT 1043  
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QY 1044 AAACAGAGAAATGCGCTTATGAGAGAAATGAAGGTTCCTGGGGCTGTCTC 1103  
DB 1021 AAACAGAGAAATGCGCTTATGAGAGAAATGAAGGTTCCTGGGGCTGTCTC 1080  
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DB 1201 TAGTGACAGTAAGTCAAAAAA 1230  
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US-09-989-732-356  
; Sequence 356, Application US/09989732  
; Patent No. US20020123463A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerltzen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gunney, Aubin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tsumab, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C57  
; CURRENT APPLICATION NUMBER: US/09/989,732  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049787

[illegible]



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; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      98.2%; Score 1230; DB 9; Length 1238;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      24 GCGACGGGAGAGACGCGCGCTTACGCGCTGCTCAGAGTTGTTCTGCTGCG 83
DB      1  GCGACGGGAGAGACGCGCGCTTACGCGCTGCTCAGAGTTGTTCTGCTGCG 60
QY      84 CTCAGAGTGGGGGAATCTGCGCGCTGCGCTTCTAATAGCGCTGCTTCTGCTCA 143
DB      61 CTCAGAGTGGGGGAATCTGCGCGCTGCGCTTCTAATAGCGCTGCTTCTGCTCA 120
QY      144 CTGCTGCGCATCTGACATCTCTGCGCGCTGCGCTGCTGCTGCTGCTGCTGCTG 203
DB      121 CTGCTGCGCATCTGACATCTCTGCGCGCTGCGCTGCTGCTGCTGCTGCTGCTG 180
QY      204 GTCCCTGGCTCAAAAGGGGATCGGGAGAGAGAGAGAGAGAGAGAGAGAGAG 263
DB      181 GTCCCTGGCTCAAAAGGGGATCGGGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY      264 GGAAGAGTGGGCGCCAGCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 323
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QY      384 GACATAGAGACCCCTGCTCTTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 443
DB      361 GACATAGAGACCCCTGCTCTTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY      444 CGCAAGGCGCATGGGGAGATGAGCAACAGAGTCTCTCAAGCTACAGAGAGTCA 503
DB      421 CGCAAGGCGCATGGGGAGATGAGCAACAGAGTCTCTCAAGCTACAGAGAGTCA 480
QY      504 ATCAAGAAATGCTGTGCGCGGTGTGCGCGAGAGAGAGAGAGAGAGAGAGAGAG 563
DB      481 ATCAAGAAATGCTGTGCGCGGTGTGCGCGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY      564 GAGAGAGAGCGCTACGCGGAGCGCCAGCTGTCTGCGAGGGCGCGGGGGGACGCTGAG 623
DB      541 GAGAGAGAGCGCTACGCGGAGCGCCAGCTGTCTGCGAGGGCGCGGGGGGACGCTGAG 600
QY      624 ATGCCCAAGAGAGAGAGCGCAATGAGCGCTGAGAGAGAGAGAGAGAGAGAGAGAG 683
DB      601 ATGCCCAAGAGAGAGAGCGCAATGAGCGCTGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY      684 GCCCGTGTCTTCTCATCGCATCAACGAGCTGAGAGAGAGAGAGAGAGAGAGAGAG 743
DB      661 GCCCGTGTCTTCTCATCGCATCAACGAGCTGAGAGAGAGAGAGAGAGAGAGAGAG 720
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QY      744 CACTCCCCCATGCGGACCTTCAACAGAGGCGGACCGGTGAGCCCAAGATGCCAGAG 803
DB      721 CACTCCCCCATGCGGACCTTCAACAGAGGCGGACCGGTGAGCCCAAGATGCCAGAG 780
QY      804 GAGAGAGACTCGTGTGAGATGATGAGCTCGGGGCGGCTGGAAGAGAGAGAGAGAGAG 863
DB      781 GAGAGAGACTCGTGTGAGATGATGAGCTCGGGGCGGCTGGAAGAGAGAGAGAGAG 840
QY      864 ACCATGTAATTCATGTGTGAGTTTGAACAAGAGAGAGAGAGAGAGAGAGAGAGAG 923
DB      841 ACCATGTAATTCATGTGTGAGTTTGAACAAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY      924 CCATTGGGGGGGCGGCAATGTCCTTCCAGAGGTTTGGAGAGAGAGAGAGAGAGAGAG 983
DB      901 CCATTGGGGGGGCGGCAATGTCCTTCCAGAGGTTTGGAGAGAGAGAGAGAGAGAGAG 960
QY      984 CAGCCAGGAGAGCTGTCCCTCTGTGAGAGGGTGAAGGCTCACTGAGTGAAGGCTGTGCT 1043
DB      961 CAGCCAGGAGAGCTGTCCCTCTGTGAGAGGGTGAAGGCTCACTGAGTGAAGGCTGTGCT 1020
QY      1044 AAACCTGAGAAAATGCGCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1103
DB      1021 AAACCTGAGAAAATGCGCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
QY      1104 TGAAGAGAGAGAGTTTCAATCTGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1163
DB      1081 TGAAGAGAGAGAGTTTCAATCTGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
QY      1164 CAGAAATGCTCTTCCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1223
DB      1141 CAGAAATGCTCTTCCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
QY      1224 TAGTGACAGTAAAGTCAAAAAA 1253
DB      1201 TAGTGACAGTAAAGTCAAAAAA 1230

RESULT 7
US-09-991-073-356
; Sequence 356, Application US/09991073
; Patent No. US2002012576A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlt, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guiney, Auecin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zhenli
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C15
; CURRENT APPLICATION NUMBER: US/09/991,073
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
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PRIOR FILING DATE:	1998-06-15
PRIOR APPLICATION NUMBER:	60/089440
PRIOR FILING DATE:	1998-06-16
PRIOR APPLICATION NUMBER:	60/089512
PRIOR FILING DATE:	1998-06-16
PRIOR APPLICATION NUMBER:	60/089514
PRIOR FILING DATE:	1998-06-16
PRIOR APPLICATION NUMBER:	60/089533
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089538
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089596
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089599
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089600
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089655
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089801
PRIOR FILING DATE:	1998-06-18
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PRIOR FILING DATE:	1998-06-18
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PRIOR FILING DATE:	1998-06-18
PRIOR APPLICATION NUMBER:	60/089947
PRIOR FILING DATE:	1998-06-19
PRIOR APPLICATION NUMBER:	60/089948
PRIOR FILING DATE:	1998-06-19
PRIOR APPLICATION NUMBER:	60/089952
PRIOR FILING DATE:	1998-06-19
PRIOR APPLICATION NUMBER:	60/090026
PRIOR FILING DATE:	1998-06-20
PRIOR APPLICATION NUMBER:	60/090025
PRIOR FILING DATE:	1998-06-22
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PRIOR FILING DATE:	1998-06-23
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PRIOR FILING DATE:	1998-06-23
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PRIOR FILING DATE:	1998-06-24
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PRIOR APPLICATION NUMBER:	60/090694
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PRIOR APPLICATION NUMBER:	60/090655
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PRIOR APPLICATION NUMBER:	60/090656
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090652
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090652



[illegible]



[illegible]

PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 98.2%; Score 1230; DB 9; Length 1238;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GCGAGGGGAGAGACCCCGCTTCCGCTAGCGGCTGCTCAGAGTTGTTGTTCTCTGCTGCG 83  
DB 1 GCGAGGGGAGAGACCCCGCTTCCGCTAGCGGCTGCTCAGAGTTGTTGTTCTCTGCTGCG 60  
QY 84 CTGAGAGTGGGGGAGATCTGCGCCCTGCTGCGGCTTCTAATCAGCCTGCGCTTCTCTGTA 143  
DB 61 CTCAGAGTGGGGGAGATCTGCGCCCTGCTGCGGCTTCTAATCAGCCTGCGCTTCTCTGTA 120  
QY 144 CTGCTGCATCTGACATCTTCAAGCGGCTGCGGATGACGCTGCTCTGTCAGATCTCTC 203  
DB 121 CTGCTGCATCTGACATCTTCAAGCGGCTGCGGATGACGCTGCTCTGTCAGATCTCTC 180  
QY 204 GTCCCTGCGCTCAAGGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 263  
DB 181 GTCCCTGCGCTCAAGGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
QY 264 GGAAGAGTGGCGCCCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 323  
DB 241 GGAAGAGTGGCGCCCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
QY 324 GTGGTCTGATGAGAAAAATGTTGCTCCATTTGCTCTAAAGTGAAGAGAGATTCCGGT 383  
DB 301 GTGGTCTGATGAGAAAAATGTTGCTCCATTTGCTCTAAAGTGAAGAGAGATTCCGGT 360  
QY 384 GACATAGAGACCCCTGCTTCTAATGAGAACAGGCTTCCATTTGATGTCAGCCAGCTG 443  
DB 361 GACATAGAGACCCCTGCTTCTAATGAGAACAGGCTTCCATTTGATGTCAGCCAGCTG 420  
QY 444 CGCAAGGCTGCGGAGATGAGAACAGGCTTCTAATGAGAACAGGCTTCCATTTGATGTCAG 503  
DB 421 CGCAAGGCTGCGGAGATGAGAACAGGCTTCTAATGAGAACAGGCTTCCATTTGATGTCAG 480  
QY 504 ATCAAGATGCTGTGCGCGGTGTCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 563  
DB 481 ATCAAGATGCTGTGCGCGGTGTCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540  
QY 564 GAGGAGAGCGCTAGCGGAG 623  
DB 541 GAGGAGAGCGCTAGCGGAG 600  
QY 624 ATGCCCAAG 683  
DB 601 ATGCCCAAG 660  
QY 664 GCCCGTCTTCTCATGCGCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 743  
DB 661 GCCCGTCTTCTCATGCGCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720

QY 744 CACTCCCCCAGCGGACCTTCAACAAGTGGCGCAGCGGAGAGAGAGAGAGAGAGAGAGAG 803  
DB 721 CACTCCCCCAGCGGACCTTCAACAAGTGGCGCAGCGGAGAGAGAGAGAGAGAGAGAGAG 780  
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DB 781 GAGAGAGACTGCGTGGAGATGCTGCGGCGGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAG 840  
QY 864 ACCATGACTTCTCATGCTGAGATTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 923  
DB 841 ACCATGACTTCTCATGCTGAGATTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900  
QY 924 CCATTGGGGGGCCCCCAGATGCTCCCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 983  
DB 901 CCATTGGGGGGCCCCCAGATGCTCCCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960  
QY 984 CAGCAGGAGAGCTGCTCCCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1043  
DB 961 CAGCAGGAGAGCTGCTCCCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020  
QY 1044 AAAGTGAAGAAATGCGCTTATGCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1103  
DB 1021 AAAGTGAAGAAATGCGCTTATGCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080  
QY 1104 TGAAGAGAGAGAGTTCATTAAGTGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1163  
DB 1081 TGAAGAGAGAGAGTTCATTAAGTGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140  
QY 1164 CAGAAATGCTCTTCCATTAAGTGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1223  
DB 1141 CAGAAATGCTCTTCCATTAAGTGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200  
QY 1224 TAGTGCAGTAGTTAAGTCAAAAAA 1253  
DB 1201 TAGTGCAGTAGTTAAGTCAAAAAA 1230

RESULT 10  
US-09-993-604-356  
Sequence 356, Application US/09993604  
Patent No. US20020137075A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Baton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Geider, Hanspeter  
APPLICANT: Gerlt, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavina, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tamas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zhen  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P27301P25  
CURRENT FILING DATE: 2001-11-14  
PRIOR FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787

[illegible]



PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 98.2%; Score 1230; DB 9; Length 1238;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GCGAGGCGGAGAGCCCGCTTCGCTAGCGCGTCTCAGAGTTGGTGTCTGCTGCG 83  
DB 1 GCGAGGCGGAGAGCCCGCTTCGCTAGCGCGTCTCAGAGTTGGTGTCTGCTGCG 60

QY 84 CTCAGAGTGGGGGAAATGCGCCCTGCGGGGCTTCTAATAGCTGGCTTCTCTGCA 143  
DB 61 CTCAGAGTGGGGGAAATGCGCCCTGCGGGGCTTCTAATAGCTGGCTTCTCTGCA 120

QY 144 CTGCTGCCATCTGACATCTCAGCGCGCTGCGATGAGCGCTGCTGTGTGCAATCTC 203  
DB 121 CTGCTGCCATCTGACATCTCAGCGCGCTGCGATGAGCGCTGCTGTGTGCAATCTC 180

QY 204 GTCCCTGCGCTCAAGGGGATGCGGGAGAGAGGAGAGAGGCGCCCGGAGGCGCT 263  
DB 181 GTCCCTGCGCTCAAGGGGATGCGGGAGAGAGGAGAGAGGCGCCCGGAGGCGCT 240

QY 264 GGAAGAGTGGGCGCCAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 323  
DB 241 GGAAGAGTGGGCGCCAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 300

QY 324 GTGGGTGCTGATGAGAGAAATTTGCTCCATTTGCTCTAAGGTGAGAGAGAGATTCGGT 383  
DB 301 GTGGGTGCTGATGAGAGAAATTTGCTCCATTTGCTCTAAGGTGAGAGAGAGATTCGGT 360

QY 384 GACATAGAGAGCCCTGCTCTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 443  
DB 361 GACATAGAGAGCCCTGCTCTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGT 420

QY 444 CGCAGAGCCATGGGGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTC 503  
DB 421 CGCAGAGCCATGGGGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTC 480

QY 504 ATCAAGATGCTGTGCGCGGTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGT 563  
DB 481 ATCAAGATGCTGTGCGCGGTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGT 540

QY 564 GAGAGAGAGCGTTAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 623  
DB 541 GAGAGAGAGCGTTAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 600

QY 624 ATGCCCAAGAGAGAGCGTCCATAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 683  
DB 601 ATGCCCAAGAGAGAGCGTCCATAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 660

QY 684 GCCCGTGTCTATCGGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 743  
DB 661 GCCCGTGTCTATCGGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 720

QY 744 CACTCCCCAGGAGAGAGCTTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 803  
DB 721 CACTCCCCAGGAGAGAGCTTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 780

QY 804 GAGAGAGAGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 863  
DB 781 GAGAGAGAGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 840

QY 864 ACCATGTAATCTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 923  
DB 841 ACCATGTAATCTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 900

QY 924 CCATTTGGGGGCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 983  
DB 901 CCATTTGGGGGCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 960

QY 984 CAGCAGAGAGAGCTGCTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 1043  
DB 961 CAGCAGAGAGAGCTGCTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 1020

QY 1044 AAATGAGT 1103  
DB 1021 AAATGAGT 1080

QY 1104 TGAAGT 1163  
DB 1081 TGAAGT 1140

QY 1164 CAGT 1223  
DB 1141 CAGT 1200

QY 1224 TAGTGCAGTGTAAAGTCAAAAAA 1253  
DB 1201 TAGTGCAGTGTAAAGTCAAAAAA 1230

RESULT 11  
US-09-990-456-356  
Sequence 356, Application US/09990456  
Patent No. US20020137890A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Geider, Hanspeter  
APPLICANT: Gerlt, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zhenli  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C22  
CURRENT APPLICATION NUMBER: US/09/990,456  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787

[illegible]



[illegible]

PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 98.2%; Score 1230; DB 9; Length 1238;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GCGAGGCGAGAGACCCCGCTTGGCTAGCGGCTCTCAGAGGTTGTCTCTGCTCG 83  
DB 1 GCGAGGCGAGAGACCCCGCTTGGCTAGCGGCTCTCAGAGGTTGTCTCTGCTCG 60

QY 84 CTCAGAGTGAAGGGGGAATCTGAGCCCTGAGGCGTTCTATACAGCCTGCTCTCTCA 143  
DB 61 CTCAGAGTGAAGGGGGAATCTGAGCCCTGAGGCGTTCTATACAGCCTGCTCTCTCA 120

QY 144 CTGCTGCAATCTGAGCATCTCAGCCGCTGCGATGAGCGCTGCTCTGTCAGATCTCT 203  
DB 121 CTGCTGCAATCTGAGCATCTCAGCCGCTGCGATGAGCGCTGCTCTGTCAGATCTCT 180

QY 204 GTTCCTGCTCTCAAAAGGGGATCGGGAGAGAAAGGAGAGGCGCCCGGAGCGCT 263  
DB 181 GTTCCTGCTCTCAAAAGGGGATCGGGAGAGAAAGGAGAGGCGCCCGGAGCGCT 240

QY 264 GGAAGAGTGGGCGCCAGCGGAGAGAAAGGAGCATGGGGGAGCAAGAGAGGAGCT 323  
DB 241 GGAAGAGTGGGCGCCAGCGGAGAGAAAGGAGCATGGGGGAGCAAGAGAGGAGCT 300

QY 324 GTGGGTCTGATGAGAAATTTGGTCCATTTGCTCTAAAGTGAAGAGAGATTTCCGT 383  
DB 301 GTGGGTCTGATGAGAAATTTGGTCCATTTGCTCTAAAGTGAAGAGAGATTTCCGT 360

QY 384 GACATAGAGACCCCTGCTCTTAATGAGAGAACAGGCTCTCCATGTGAGTGACGCACTG 443  
DB 361 GACATAGAGACCCCTGCTCTTAATGAGAGAACAGGCTCTCCATGTGAGTGACGCACTG 420

QY 444 CGCAAGGCGCATGGGGAGATGAGCAACAGGCTCTCAAGCTACAGAGAGCTCAAGTTC 503  
DB 421 CGCAAGGCGCATGGGGAGATGAGCAACAGGCTCTCAAGCTACAGAGAGCTCAAGTTC 480

QY 504 ATCAAGAAATGCTGCTGCGCGGTGCGCGAGAGAGAGAGAAATCTACTGCTGTGAAG 563  
DB 481 ATCAAGAAATGCTGCTGCGCGGTGCGCGAGAGAGAGAGAAATCTACTGCTGTGAAG 540

QY 564 GAGAGAAAGCGTACGCGGAGCGCCAGCTGTCTGCAAGGCGCGGGGAGCAAGCTGAGC 623  
DB 541 GAGAGAAAGCGTACGCGGAGCGCCAGCTGTCTGCAAGGCGCGGGGAGCAAGCTGAGC 600

QY 624 ATGCCCAAGAGAGAGGCTGCAATGAGCTGAGAGCGGCACTACTGGCGCAACCGGCTG 683  
DB 601 ATGCCCAAGAGAGAGGCTGCAATGAGCTGAGAGCGGCACTACTGGCGCAACCGGCTG 660

QY 684 GCGCGTCTTCTATCGGAGATCAACAGCTGAGAGAGAGGCGCTTCTGTAAGTCTGAC 743  
DB 661 GCGCGTCTTCTATCGGAGATCAACAGCTGAGAGAGAGGCGCTTCTGTAAGTCTGAC 720

QY 744 CACTCCCGATCGGAGCTTCAACAGTGGCGCAGCGGTGAGCCCAACATGCTTAGAC 803  
DB 721 CACTCCCGATCGGAGCTTCAACAGTGGCGCAGCGGTGAGCCCAACATGCTTAGAC 780

QY 804 GAGAGAGATGCTGAGAGATGGTGGCTCGGGCGGCTGGAACAGCTGGCTTCCACACC 863  
DB 781 GAGAGAGATGCTGAGAGATGGTGGCTCGGGCGGCTGGAACAGCTGGCTTCCACACC 840

QY 864 ACCATGTAATTCATGATGATTTGACAGAGAAACATGAGCTCAGAGCTGGGGCTGC 923  
DB 841 ACCATGTAATTCATGATGATTTGACAGAGAAACATGAGCTCAGAGCTGGGGCTGC 900

QY 924 CCATTGGGGGCGCCCAATGCTCTGAGAGGCTTGGACAGAGAGAGAGAGAGAGAGAGAG 983  
DB 901 CCATTGGGGGCGCCCAATGCTCTGAGAGGCTTGGACAGAGAGAGAGAGAGAGAGAGAG 960

QY 984 CAGCAGGAGAGCTGCTCTGTAAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1043  
DB 961 CAGCAGGAGAGCTGCTCTGTAAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020

QY 1044 AAATGAGAAATGAGCTTATGCTTAAAGAGAAATGAAAGTCTCTGGGGTGTCTCT 1103  
DB 1021 AAATGAGAAATGAGCTTATGCTTAAAGAGAAATGAAAGTCTCTGGGGTGTCTCT 1080

QY 1104 TGAAGAGCAGAGTTTCAATGATGATTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1163  
DB 1081 TGAAGAGCAGAGTTTCAATGATGATTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140

QY 1164 CAGAAATGCTCTTCAATGAGCTTGTGCTTGTCAAGCTATACATTAATTTAAAG 1223  
DB 1141 CAGAAATGCTCTTCAATGAGCTTGTGCTTGTCAAGCTATACATTAATTTAAAG 1200

QY 1224 TAGTCACTAGTTAAGTCAAAAAA 1253  
DB 1201 TAGTCACTAGTTAAGTCAAAAAA 1230

RESULT 13  
US-09-992-598-356  
Sequence 356, Application US/09992598  
Patent No. US20020160384A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: KJavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C20  
CURRENT APPLICATION NUMBER: US/09/992,598  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787

PRIOR APPLICATION NUMBER:	60/08944
PRIOR FILING DATE:	1998-06-16
PRIOR APPLICATION NUMBER:	60/089512
PRIOR FILING DATE:	1998-06-16
PRIOR APPLICATION NUMBER:	60/089514
PRIOR FILING DATE:	1998-06-16
PRIOR APPLICATION NUMBER:	60/089532
PRIOR FILING DATE:	1998-06-17
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PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089599
PRIOR FILING DATE:	1998-06-17
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Db	1	CGGACGGGCGAGGACCCCGCTTCGGCTAGCGGTGCTCAGAGATTGTCTCTGCTGGC	60
OY	84	CTCAGGATGAGGGGGAATCTGGCCCTGTGTGGCGTTCTAATCAGCCTGGCTTCTGTCA	143
Db	61	CTCAGGATGAGGGGGAATCTGGCCCTGTGTGGCGGTCTAATCAGCCTGGCTTCTGTCA	120
OY	144	CTGCGGCATCTGGACATCTCAGCGCGGTGGCGATGACGCGTCTGTGGAGATTCCTC	203
Db	121	CTGCTGCCATCTGGACATCTCAGCGCGGTGGCGATGACGCGTCTGTGGAGATTCCTC	180
OY	204	GTCCTCGCCTTCAAGGGGATGCGGGAGAAAGGAGCAAAAGCGCCCCCGAGCGCCT	263
Db	181	GTCCTCGCCTTCAAGGGGATGCGGGAGAAAGGAGCAAAAGCGCCCCCGAGCGCCT	240
OY	264	GGAAGAGTCGGCCCCCAGCGGAGAAAAAGAGCATGTGGGGACAAAGAGACAGAAAGCACT	323
Db	241	GGAAGAGTCGGCCCCCAGCGGAGAAAAAGAGCATGTGGGGACAAAGAGACAGAAAGCACT	300
OY	324	GTCGGTCGTCAATGAGAAAAATTGTCCTCATTTGACTCTAAAGGTGAGAAAGAGATTCCGGT	383
Db	301	GTCGGTCGTCAATGAGAAAAATTGTCCTCATTTGACTCTAAAGGTGAGAAAGAGATTCCGGT	360
OY	384	GACATAGGACCCCCCTGTGTCTAATGGAGAACAGGCTTCCATGTGATGTGCAGCCAGCTG	443
Db	361	GACATAGGACCCCCCTGTGTCTAATGGAGAACAGGCTTCCATGTGATGTGCAGCCAGCTG	420
OY	444	CGCAAGGCGCATGCGGGGAGATGGACAACCAAGTCTCTCAGCTAGCCAGAGCTCAAGTTTC	503
Db	421	CGCAAGGCGCATGCGGGGAGATGGACAACCAAGTCTCTCAGCTAGCCAGAGCTCAAGTTTC	480
OY	504	ATCAAGAAATGCTGTGCGCGGTGTGCGGAGACGAGAGCAGAAATCTAATCTGTGTGAAG	563
Db	481	ATCAAGAAATGCTGTGCGCGGTGTGCGGAGACGAGAGCAGAAATCTAATCTGTGTGAAG	540
OY	564	GAGGAGAAAGCGGTAGCGGAGCGCCAGCTGTCTCAGAGGCGCGGGGGACAGCGCTGAGC	623
Db	541	GAGGAGAAAGCGGTAGCGGAGCGCCAGCTGTCTCAGAGGCGCGGGGGACAGCGCTGAGC	600
OY	624	ATGCCCAAGAGCAGAGCTGCCAATGGCTGATGCGCAGATACCTGTGCGCAACCGGCTGTG	683
Db	601	ATGCCCAAGAGCAGAGCTGCCAATGGCTGATGCGCAGATACCTGTGCGCAACCGGCTGTG	660
OY	684	GCCCCGTCTTATATGGGCATCAACGACTCTGGAGAAAGAGGGCGCTTTCGTGTATCTCTGAC	743
Db	661	GCCCCGTCTTATATGGGCATCAACGACTCTGGAGAAAGAGGGCGCTTTCGTGTATCTCTGAC	720

OY	744	CACATCCCCCAATGCGGAACTCTTCAACAAGTGGGCGACGGTGAAGCCCAACATGCTTAAGAC	803
Db	721	CACATCCCCCAATGCGGAACTCTTCAACAAGTGGGCGACGGTGAAGCCCAACATGCTTAAGAC	780
OY	804	GAGAGAGACTGCGTGGAGAGATGTGGCCTCGGGCGGCTTGGAAAGACGTGGCTGCGACAC	863
Db	781	GAGAGAGACTGCGTGGAGAGATGTGGCCTCGGGCGGCTTGGAAAGACGTGGCTGCGACAC	840
OY	864	ACCATGTACTTCATGTGTGAATTGTGACAAAGGAGAAATGTGAGGCTCAAGCTTGAGGCTGC	923
Db	841	ACCATGTACTTCATGTGTGAATTGTGACAAAGGAGAAATGTGAGGCTCAAGCTTGAGGCTGC	900
OY	924	CCATTGGGGGCCCCACATGTCTCTTGCAAGGTTGGCAGGGACAGAGCCCAAGCCATGTGTGC	983
Db	901	CCATTGGGGGCCCCACATGTCTCTTGCAAGGTTGGCAGGGACAGAGCCCAAGCCATGTGTGC	960
OY	984	CAGCGAGGGAGACTGTCCCTCTGTGTGAAGGGTGAAGGCTCACTGAATTAGGGGCTGTGTCT	1043
Db	961	CAGCGAGGGAGACTGTCCCTCTGTGTGAAGGGTGAAGGCTCACTGAATTAGGGGCTGTGTCT	1020
OY	1044	AAACTGAGAAATGGCCTTATGCTTAAGAAGAAATGAAAGTTCCTTGGGGTGTGTCTC	1103
Db	1021	AAACTGAGAAATGGCCTTATGCTTAAGAAGAAATGAAAGTTCCTTGGGGTGTGTCTC	1080
OY	1104	TGAAGAGACAAAGTTCATTAACCTGTATGTGAAGGCCCAATGTCAATTATGTATTAATACC	1163
Db	1081	TGAAGAGACAAAGTTCATTAACCTGTATGTGAAGGCCCAATGTCAATTATGTATTAATACC	1140
OY	1164	CAGAAATGCTCTTCCATTAAGCTTGTGCTTGTCCAAAGCTATACAAATAAATCTTTAAG	1223
Db	1141	CAGAAATGCTCTTCCATTAAGCTTGTGCTTGTCCAAAGCTATACAAATAAATCTTTAAG	1200
OY	1224	TAGTGCAGTACTTAAGTCCAAAAA	1253
Db	1201	TAGTGCAGTACTTAAGTCCAAAAA	1230

Search completed: December 16, 2004, 23:11:16  
Job time : 1000 secs

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1      OPERATING SYSTEM:  PC-DOS/MS-DOS
2      SOFTWARE:  Patent In Release #1.0,  Version #1.25
3      CURRENT APPLICATION DATA:
4      APPLICATION NUMBER:  US/08/494,168
5      FILING DATE:
6      CLASSIFICATION:  435
7      PRIOR APPLICATION DATA:
8      APPLICATION NUMBER:  US 08/112,465
9      FILING DATE:  27-AUG-1993
10     ATTORNEY/AGENT INFORMATION:
11     NAME:  SAXE, Bernhard D.
12     REGISTRATION NUMBER:  28,665
13     REFERENCE/DOCKET NUMBER:  40397/104/BAHR
14     TELECOMMUNICATION INFORMATION:
15     TELEPHONE:  (202) 672-5300
16     TELEFAX:  (202) 672-5399
17     TELEX:  904136
18     INFORMATION FOR SEQ ID NO:  1:
19     SEQUENCE CHARACTERISTICS:
20     LENGTH:  5102 base pairs
21     TYPE:  nucleic acid
22     STRANDEDNESS:  double
23     TOPOLOGY:  linear
24     FEATURE:
25     NAME/KEY:  CDS
26     LOCATION:  join(2..82, 86..97, 101..4399, 4403..4420, 4424
27     LOCATION:  ..4465, 4469..4876, 4880..5101)
28     US-08-494-168-1

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Db 247 AGGTCAACAGAGCCCGGCGCTTCTGTGAGAGAGGAC 287

RESULT 7  
US-09-215-681-273  
; Sequence 273, Application US/09215681A  
; Patent No. 6528253  
; GENERAL INFORMATION:  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Frudakis, Tony N.  
; APPLICANT: King, Gordon E.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS  
; FILE REFERENCE: 210121.463  
; CURRENT APPLICATION NUMBER: US/09/215.681A  
; CURRENT FILING DATE: 1998-12-17  
; SOFTWARE: FastSeq for Windows Version 3.0  
; NUMBER OF SEQ ID NOS: 310  
; SEQ ID NO 273  
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; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(579)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-215-681-273

Query Match 5.3%; Score 66.8; DB 4; Length 579;  
Best Local Similarity 52.0%; Pred. No. 2.4e-08;  
Matches 146; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

Qy 140 GTCACCTGCTGCATCTGACATCTCTCCAGCCGCTGGCGCATGACCCCTGCTGTGCAGAT 199  
Db 7 GTCCGGCGCGAGGTCTGTGCGCTCTCTGCGCAAGCTGGTGAAGATGCTCACTCTGAAAAACC 66

Qy 200 CCTGCTCCCTGCGCTCAAGGGAGATGCGGAGAGAGAGAGACAAAGCGCCCGCGAGC 259  
Db 67 CGAGACACTGTGTAGAGAGAGATGTTGAGACACAGGGTCTCTGTTTCCCTGGAAC 126

Qy 260 GCTTGAAGAGTCCGCCCCCAGCGGAGAAAAAGAGACATGGGGGACAAAGACAGAAAG 319  
Db 127 TCCGTGACTTCTGCTTCAAGGATGAGGACACATGCTGTGATGATTTGAAGGG 186

Qy 320 CAGTGTGGGTGCTGATGAGAAAAATTGTCATGCGCTTAAAGTGAAGAGATTC 379  
Db 187 ACAGCCCGGTCTCTGTGTGAGAGGTGAACCTGAGNCCCTGTGTGAATGGAATCC 246

Qy 380 CGGTGACATAGACCCCTGTGTCTTAATGAGAACAGGCC 420  
Db 247 AGGTCAACAGAGCCCGGCGCTTCTGTGAGAGAGGAC 287

RESULT 8  
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; Sequence 273, Application US/09216003A  
; Patent No. 6670463  
; GENERAL INFORMATION:  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Frudakis, Tony N.  
; APPLICANT: King, Gordon E.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF OVARIAN CANCER  
; FILE REFERENCE: 210121.462  
; CURRENT APPLICATION NUMBER: US/09/216.003A  
; CURRENT FILING DATE: 1998-12-17  
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; LENGTH: 579  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base

LOCATION: (223)  
; OTHER INFORMATION: Where n is a, c, g or t  
; NAME/KEY: modified\_base  
; LOCATION: (265)  
; OTHER INFORMATION: Where n is a, c, g or t  
; NAME/KEY: modified\_base  
; LOCATION: (277)  
; OTHER INFORMATION: Where n is a, c, g or t  
; NAME/KEY: modified\_base  
; LOCATION: (308)  
; OTHER INFORMATION: Where n is a, c, g or t  
; NAME/KEY: modified\_base  
; LOCATION: (329)  
; OTHER INFORMATION: Where n is a, c, g or t  
; NAME/KEY: modified\_base  
; LOCATION: (346)  
; OTHER INFORMATION: Where n is a, c, g or t  
; NAME/KEY: modified\_base  
; LOCATION: (360)  
; OTHER INFORMATION: Where n is a, c, g or t  
; NAME/KEY: modified\_base  
; LOCATION: (366)  
; OTHER INFORMATION: Where n is a, c, g or t  
; NAME/KEY: modified\_base  
; LOCATION: (429)  
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; NAME/KEY: modified\_base  
; LOCATION: (448)  
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; NAME/KEY: modified\_base  
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; NAME/KEY: modified\_base  
; LOCATION: (524)  
; OTHER INFORMATION: Where n is a, c, g or t  
; NAME/KEY: modified\_base  
; LOCATION: (531)  
; OTHER INFORMATION: Where n is a, c, g or t  
; NAME/KEY: modified\_base  
; LOCATION: (578)  
; OTHER INFORMATION: Where n is a, c, g or t  
US-09-216-003A-273

Query Match 5.3%; Score 66.8; DB 4; Length 579;  
Best Local Similarity 52.0%; Pred. No. 2.4e-08;  
Matches 146; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

Qy 140 GTCACCTGCTGCATCTGACATCTCTCCAGCCGCTGGCGCATGACCCCTGCTGTGCAGAT 199  
Db 7 GTCCGGCGCGAGGTCTGTGCGCTCTCTGCGCAAGCTGGTGAAGATGCTCACTCTGAAAAACC 66

Qy 200 CCTGCTCCCTGCGCTCAAGGGAGATGCGGAGAGAGAGAGACAAAGCGCCCGCGAGC 259  
Db 67 CGAGACACTGTGTAGAGAGATGTTGAGACCAAGGTCTGTGTGTTCCCTGGAAC 126

Qy 260 GCTTGAAGAGTCCGCCCCCAGCGGAGAAAAAGAGACATGGGGGACAAAGAGAGAAAG 319  
Db 127 TCCGTGACTTCTGCTTCAAGGATGAGGACATGCTGTGATGATTTGAAGGG 186

Qy 320 CAGTGTGGGTGCTGATGAGAAAAATTGTCATGCGCTTAAAGTGAAGAGATTC 379  
Db 187 ACAGCCCGGTCTCTGTGTGAGAGGTGAACCTGAGNCCCTGTGTGAATGGAATCC 246

Qy 380 CGGTGACATAGACCCCTGTGTCTTAATGAGAACAGGCC 420  
Db 247 AGGTCAACAGAGCCCGGCGCTTCTGTGAGAGAGGAC 287

RESULT 9  
US-09-667-857-273  
; Sequence 273, Application US/09667857  
; Patent No. 669664  
; GENERAL INFORMATION:



APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
APPLICANT: Vedick, Thomas S.  
APPLICANT: Carter, Darick  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.462C5  
CURRENT APPLICATION NUMBER: US/09/667,857  
CURRENT FILING DATE: 2000-09-20  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FASTSeq for Windows Version 3.0  
SEQ ID NO: 273  
LENGTH: 579  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(579)  
OTHER INFORMATION: n = A,T,C or G  
US-09-667-857-273

Query Match 5.3%; Score 66.8; DB 4; Length 579;  
Best Local Similarity 52.0%; Pred. No. 2.4e-08;  
Matches 146; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

QY 140 GTCACTGTCGTCATCGAGCATCTCAGCCGCTGGCCATGAGCGCTCTGTGTCAGAT 199  
DB 7 GTCTGGCGCGAGAGTGTGCTCTCTGCGAGAGCTGTGAGTGTCTACCTCTGAAAAAC 66  
QY 200 CCTCTCTCTGCTCTCAAGGGAGATCGGAGAGAGAGGAGCAAAAGCGCCCGGAG 259  
DB 67 CGGAGACCTGTGTGAGAGAGAGTGTGACACAGAGGTCTCTGTGTTCTCTGGAAC 126  
QY 260 GCCTGGAAGATCGGCGCCCAAGGAGAGAGAGAGAGATGTTGGGAGCAAGAGAGAG 319  
DB 127 TCTGTGACTTCTGCTCTCAAGGAGATGAGGAGACATGTGTGATGATGAGAGG 186  
QY 320 CAGTGTGGTGTCTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTC 379  
DB 187 ACAGCCCGGTCTCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTC 246  
QY 380 CGGTGACATAG 420  
DB 247 AGGTCAACAG 287

RESULT 10  
US-08-392-367B-1  
Sequence 1, Application US/08392367B  
Patent No. 5691197  
GENERAL INFORMATION:  
APPLICANT: Trygvaeson, Karl  
APPLICANT: Elomaa, Outi  
APPLICANT: Kangas, Maarit  
TITLE OF INVENTION: An Inolated DNA Sequence For a  
Patent No. 5691197  
TITLE OF INVENTION: No. 5691197 Macrophage Receptor with  
TITLE OF INVENTION: A Collagenous Domain and the  
TITLE OF INVENTION: Polypeptide Chain Encoded by  
TITLE OF INVENTION: such a Sequence  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fay, Sharpe, Beall, Fagan,  
ADDRESSEE: Minnich & McKee  
STREET: 1100 Superior Avenue  
CITY: Cleveland  
STATE: Ohio

COUNTRY: U.S.A.  
ZIP: 44114-2518  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch,  
MEDIUM TYPE: 720 Kb securable  
COMPUTER: IBM PS/2, Model 35 SX  
OPERATING SYSTEM: DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/392,367B  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Minnich, Richard J.  
REGISTRATION NUMBER: 24,175  
REFERENCE/DOCKET NUMBER: TRV 2 009  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (216) 861-5582  
TELEFAX: (216) 241-1666  
TELEX: (216) 980162  
INFORMATION FOR SEQ ID NO. 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1868 base pairs  
TYPE: Nucleic acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: Nucleotide-genomic DNA  
HYPOTHEICAL: No. 5691197 relevant  
ANTI-SENSE: No. 5691197 relevant  
US-08-392-367B-1

Query Match 5.3%; Score 65.8; DB 1; Length 1868;  
Best Local Similarity 52.3%; Pred. No. 8e-08;  
Matches 145; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 151 CATCTGACATCTCTCAGCCGCTGAGATGAGCGCTGTGTGTCAGATCTCTGCTG 210  
DB 809 CACTGTGTCTCTCAGAGACTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 868  
QY 211 GCTCTAAAGGGAGATCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 270  
DB 869 GCCCAAGGGGAGACATGAGACCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 928  
QY 271 TCGGCCCCAGGAG 330  
DB 929 AAGGGAGATGGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 988  
QY 331 GTCATGAAAAATTGTCTCCATTGAGCTCTAAAGGTGAGAGAGAGATTCGGATAG 390  
DB 989 GTAAAGGTGATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1048  
QY 391 GACCCCTGTCTCTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 427  
DB 1049 GTGACCAAG 1085

RESULT 11  
US-08-893-467A-1  
Sequence 1, Application US/08893467A  
Patent No. 6063901  
GENERAL INFORMATION:  
APPLICANT: Trygvaeson, Karl  
APPLICANT: Elomaa, Outi  
APPLICANT: Kangas, Maarit  
TITLE OF INVENTION: An Inolated DNA Sequence For a  
Patent No. 6063901  
TITLE OF INVENTION: No. 6063901 Macrophage Receptor with  
TITLE OF INVENTION: A Collagenous Domain and the  
TITLE OF INVENTION: Polypeptide Chain Encoded by  
TITLE OF INVENTION: such a Sequence  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fay, Sharpe, Beall, Fagan,

ADDRESSEE: Minnich & McKee  
STREET: 1100 Superior Avenue  
STREET: Suite 700  
CITY: Cleveland  
STATE: Ohio  
COUNTRY: U.S.A.  
ZIP: 44114-2518  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch,  
COMPUTER: IBM PS/2, Model 35 SX  
OPERATING SYSTEM: DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/893,467A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Minnich, Richard J.  
REGISTRATION NUMBER: 24,175  
REFERENCE/DOCKET NUMBER: TRV 2 009  
TELEPHONE: (216) 861-5582  
TELEFAX: (216) 241-1666  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1868 base pairs  
TYPE: Nucleic acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: Nucleotide-genomic DNA  
HYPOTHETICAL: No. 6063901 relevant  
ANTI-SENSE: No. 6063901 relevant  
US-08-893-467A-1

Query Match 5.3%; Score 65.8; DB 3; Length 1868;  
Best Local Similarity 52.3%; Pred. No. 8e-08;  
Matches 145; Conservative 0; Mismatches 132; Indels 0; Gaps 0;  
QY 151 CATCTGACATCTTCAGCGCGCTGCGCATGACGCTGCTGTGCAAGTCTCTGCTCCTG 210  
DB 809 CAACTGGCTCTCCAGACCTCGAAGAGAGAGAGGCGACGAAAGGTGACATAGCTCACTG 868  
QY 211 GCCTCAAGGGGAGCGGGAG 270  
DB 869 GCCCAAGGGGAG 928  
QY 271 TCGGCCCCAGGAG 330  
DB 929 AAGGGAGACATGGGATGAG 988  
QY 331 GTCAATGAAAAATTGGTCCCTTGGCTTAAGGTGAGAGAGAGAGAGAGAGAGAGAGAG 390  
DB 989 GTAAAGGTGATGCTGAG 1048  
QY 391 GACCCCTGTGCTTAATGAG 427  
DB 1049 GTGACCAAG 1085

RESULT 12  
US-09-404-879A-274/c  
Sequence 274, Application US/09404879A  
Patent No. 6468546  
GENERAL INFORMATION:  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.462C2  
CURRENT APPLICATION NUMBER: US/09/404,879A

CURRENT FILING DATE: 1999-09-24  
NUMBER OF SEQ ID NOS: 393  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 274  
LENGTH: 330  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(330)  
OTHER INFORMATION: n = A,T,C or G  
US-09-404-879A-274

Query Match 5.2%; Score 65.6; DB 4; Length 330;  
Best Local Similarity 52.0%; Pred. No. 3.8e-08;  
Matches 146; Conservative 0; Mismatches 135; Indels 0; Gaps 0;  
QY 140 GTCACTGCTCCATCTGACATCTTCAGCGCGCTGCGCATGACGCTGCTGTGACAGAT 199  
DB 324 GTGGCGGCGAGGCTGTGGCTCTCTGCGCAAGGCTGTGAAGATGTCACTGAGAAACC 265  
QY 200 CTTGCTCTGCGCTCAAAGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 259  
DB 264 CGAGCACTGTGTGAG 205  
QY 260 GCGTGAAGAGTGGCGCCCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 319  
DB 204 TCTTGACCTTCTGCTTCAAGGACATTTAGGAGACATGCTGTGATGATTTAGAGG 145  
QY 320 CAGTGGGTCTGATGATTC 379  
DB 144 ACAGCCGGTGTCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 85  
QY 380 CGGTGACATGAG 420  
DB 84 AGGTCAAG 44

RESULT 13  
US-09-338-933-274/c  
Sequence 274, Application US/09338933  
Patent No. 6488931  
GENERAL INFORMATION:  
APPLICANT: Mitcham, Jennifer Lynn  
APPLICANT: King, Gordon E.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF  
FILE REFERENCE: 210121.462C1  
CURRENT APPLICATION NUMBER: US/09/338,933  
NUMBER OF SEQ ID NOS: 312  
CURRENT FILING DATE: 1999-06-23  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 274  
LENGTH: 330  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(330)  
OTHER INFORMATION: n = A,T,C or G  
US-09-338-933-274

Query Match 5.2%; Score 65.6; DB 4; Length 330;  
Best Local Similarity 52.0%; Pred. No. 3.8e-08;  
Matches 146; Conservative 0; Mismatches 135; Indels 0; Gaps 0;  
QY 140 GTCACTGCTCCATCTGACATCTTCAGCGCGCTGCGCATGACGCTGCTGTGACAGAT 199  
DB 324 GTGGCGGCGAGGCTGTGGCTCTCTGCGCAAGGCTGTGAAGATGTCACTGAGAAACC 265  
QY 200 CTTGCTCTGCGCTCAAAGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 259  
DB 264 CGAGCACTGTGTGAG 205

Mon Dec 20 08:22:12 2004

us-09-806-277a-13.rn1

Page 7

QY 260 GCTTGAGAGAGTCGGCCCCCAAGGAGAGAAAGAGACATGGGGGACAAAGGACAGAAAGG 319  
DB 204 TCTGGAGCTCTTGGCTTCAAGGATTAAGGAGGACATGCTGATGATTAAGGAG 145  
QY 320 CAGTGTGGTGTCTATGAGAAATTTGTCCTTGGCTTAAAGGTGAGAAAGAGATTC 379  
DB 144 ACAAGCCGGTGTCTCTGGTGTGAAGGTGAACCTGTGCCCCCTGTGAAATGAACTCC 85  
QY 380 CGGTGACATAGAACCCCTGTCTTAATGAGAACAGGCC 420  
DB 84 AGTCAAAACAGAGCCCGTGGCTTCTGTGTAGAGAGGAC 44

RESULT 14  
US-09-215-681-274/C  
; Sequence 274, Application US/09215681A  
; Patent No. 6528253  
; GENERAL INFORMATION:  
; APPLICANT: MITCHEM, Jennifer L.  
; APPLICANT: FRUDEKIS, Tony N.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS  
; FILE REFERENCE: 210121.463  
; CURRENT APPLICATION NUMBER: US/09/215,681A  
; NUMBER OF SEQ ID NOS: 310  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 274  
; LENGTH: 330  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(330)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-215-681-274

Query Match 5.2%; Score 65.6; DB 4; Length 330;  
Best Local Similarity 52.0%; Pred. No. 3.8e-08;  
Matches 146; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

QY 140 GTCACTGTGTCATCTGAGCATCTCCAGCCGCTGGCATGACGCTCTCTGTGCAGAT 199  
DB 324 GTCCGGCCGAGGTCTGGCTCTCTGGCAAGGCTGTGAAGTGTCACTCGAATAACC 265  
QY 200 CCTCGTCCCTGGCTCAAAAGGAGATGCGGAGAGAGAAAGGACAAAGCGCCCCGAGC 259  
DB 264 CGGACGACTGTGTGAGAGAGAGATTTGTGACCAAGGTGCTCGTGTTCCTCGAAC 205  
QY 260 GCTTGAAGAGTCGCCCCCAGGAGAGAAAGAGACATGGGGGACAAAGGACAGAAAG 319  
DB 204 TCTTGAGCTTCTCGGCTTCAAGGCATTAGGGGACCAATGGTCTGATGATGAAGG 145  
QY 320 CAGTGTGGTGTCTATGAGAAATTTGTCCTTGGCTTAAAGGTGAGAAAGAGATTC 379  
DB 144 ACAAGCCGGTGTCTCTGGTGTGAAGGTGAACCTGTGCCCCCTGTGAAATGAACTCC 85  
QY 380 CGGTGACATAGAACCCCTGTCTTAATGAGAACAGGCC 420  
DB 84 AGTCAAAACAGAGCCCGTGGCTTCTGTGTAGAGAGGAC 44

RESULT 15  
US-09-216-003A-274/C  
; Sequence 274, Application US/09216003A  
; Patent No. 6670463  
; GENERAL INFORMATION:  
; APPLICANT: MITCHEM, Jennifer L.  
; APPLICANT: FRUDEKIS, Tony N.  
; APPLICANT: KING, Gordon B.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF OVARIAN CANCER

; FILE REFERENCE: 210121.462  
; CURRENT APPLICATION NUMBER: US/09/216,003A  
; CURRENT FILING DATE: 1998-12-17  
; NUMBER OF SEQ ID NOS: 310  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 274  
; LENGTH: 330  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (171)  
; OTHER INFORMATION: Where n is a, c, g or t  
US-09-216-003A-274

Query Match 5.2%; Score 65.6; DB 4; Length 330;  
Best Local Similarity 52.0%; Pred. No. 3.8e-08;  
Matches 146; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

QY 140 GTCACTGTGTCATCTGAGCATCTCCAGCCGCTGGCATGACGCTCTCTGTGCAGAT 199  
DB 324 GTCCGGCCGAGGTCTGGCTCTCTGGCAAGGCTGTGAAGTGTCACTCGAATAACC 265  
QY 200 CCTCGTCCCTGGCTCAAAAGGAGATGCGGAGAGAGAGAAAGGACAAAGCGCCCCGAGC 259  
DB 264 CGGACGACTGTGTGAGAGAGAGATTTGTGACCAAGGTGCTCGTGTTCCTCGAAC 205  
QY 260 GCTTGAAGAGTCGCCCCCAGGAGAGAAAGAGACATGGGGGACAAAGGACAGAAAG 319  
DB 204 TCTTGAGCTTCTCGGCTTCAAGGCATTAGGGGACCAATGGTCTGATGATGAAGG 145  
QY 320 CAGTGTGGTGTCTATGAGAAATTTGTCCTTGGCTTAAAGGTGAGAAAGAGATTC 379  
DB 144 ACAAGCCGGTGTCTCTGGTGTGAAGGTGAACCTGTGCCCCCTGTGAAATGAACTCC 85  
QY 380 CGGTGACATAGAACCCCTGTCTTAATGAGAACAGGCC 420  
DB 84 AGTCAAAACAGAGCCCGTGGCTTCTGTGTAGAGAGGAC 44

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2359.853 Million cell updates/sec

Title: US-09-806-277A-6

Perfect score: 271

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	271	100.0	1238	9	US-09-989-722-356	Sequence 356, App
3	271	100.0	1238	9	US-09-989-723-356	Sequence 356, App
4	271	100.0	1238	9	US-09-989-279-356	Sequence 356, App
5	271	100.0	1238	9	US-09-989-777-356	Sequence 356, App
6	271	100.0	1238	9	US-09-989-731-356	Sequence 356, App
7	271	100.0	1238	9	US-09-989-732-356	Sequence 356, App
8	271	100.0	1238	9	US-09-991-073-356	Sequence 356, App
9	271	100.0	1238	9	US-09-990-442-356	Sequence 356, App
10	271	100.0	1238	9	US-09-991-153-356	Sequence 356, App
11	271	100.0	1238	9	US-09-993-604-356	Sequence 356, App
12	271	100.0	1238	9	US-09-990-456-356	Sequence 356, App
13	271	100.0	1238	9	US-09-989-721-356	Sequence 356, App
14	271	100.0	1238	9	US-09-992-558-356	Sequence 356, App
15	271	100.0	1238	9	US-09-989-293A-356	Sequence 356, App
16	271	100.0	1238	9	US-09-989-735-356	Sequence 356, App
17	271	100.0	1238	9	US-09-990-444-356	Sequence 356, App
18	271	100.0	1238	9	US-09-991-161-356	Sequence 356, App
19	271	100.0	1238	9	US-09-989-730-356	Sequence 356, App
20	271	100.0	1238	9	US-09-990-441-356	Sequence 356, App
21	271	100.0	1238	9	US-09-993-667-356	Sequence 356, App
22	271	100.0	1238	10	US-09-989-734-356	Sequence 356, App
23	271	100.0	1238	10	US-09-997-653-356	Sequence 356, App
24	271	100.0	1238	10	US-09-989-724-356	Sequence 356, App
25	271	100.0	1238	10	US-09-989-728-356	Sequence 356, App
26	271	100.0	1238	10	US-09-990-441-356	Sequence 356, App
27	271	100.0	1238	10	US-09-993-667-356	Sequence 356, App
28	271	100.0	1238	10	US-09-997-628-356	Sequence 356, App
29	271	100.0	1238	10	US-09-997-666-356	Sequence 356, App
30	271	100.0	1238	10	US-09-990-438-356	Sequence 356, App
31	271	100.0	1238	10	US-09-990-562-356	Sequence 356, App
32	271	100.0	1238	10	US-09-990-711-356	Sequence 356, App
33	271	100.0	1238	10	US-09-989-726-356	Sequence 356, App
34	271	100.0	1238	10	US-09-989-156-356	Sequence 356, App
35	271	100.0	1238	10	US-09-990-437-356	Sequence 356, App
36	271	100.0	1238	10	US-09-991-157-356	Sequence 356, App
37	271	100.0	1238	10	US-09-997-514-356	Sequence 356, App
38	271	100.0	1238	10	US-09-997-573-356	Sequence 356, App
39	271	100.0	1238	10	US-09-991-172-356	Sequence 356, App
40	271	100.0	1238	10	US-09-990-726-356	Sequence 356, App
41	271	100.0	1238	10	US-09-997-559-356	Sequence 356, App
42	271	100.0	1238	10	US-09-997-601-356	Sequence 356, App
43	271	100.0	1238	10	US-09-990-443-356	Sequence 356, App
44	271	100.0	1238	10	US-09-991-654-356	Sequence 356, App
45	271	100.0	1238	10	US-09-997-628-356	Sequence 356, App

#### ALIGNMENTS

RESULT 1  
US-10-258-105-45  
; Sequence 45, Application US/10258105  
; Publication No. US20030158382A1  
; GENERAL INFORMATION:  
; APPLICANT: Wakamiya et al.  
; TITLE OF INVENTION: NO. US20030158382A1 Collectin  
; FILE REFERENCE: 19036/38785  
; CURRENT APPLICATION NUMBER: US/10/258,105  
; CURRENT FILING DATE: 2002-10-21  
; PRIOR APPLICATION NUMBER: PCT/JP01/03468  
; PRIOR FILING DATE: 2001-04-23  
; PRIOR APPLICATION NUMBER: JP 2000-120358  
; PRIOR FILING DATE: 2000-04-21  
; NUMBER OF SEQ ID NOS: 61  
; SEQ ID NO 45  
; LENGTH: 813  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-10-258-105-45

## Alignment Scores:

Pred. No.:	2,03e-269	Length:	813
Score:	271.00	Matches:	271
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	15	Gaps:	0

US-09-806-277a-6 (1-271) x US-10-258-105-45 (1-813)

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QY 1 MetArgGlyAenLeuAlaLeuValGlyValLeuLeuSerLeuAlaPheLeuSerLeuLeu 20
Db 1 ATGAGGGGGAATCTGGCCCTGCTGGCTTATTCAGCCCTGCTCTCTCTCTGCTG 60
QY 21 ProSerGlyHisProGlnProAlaGlyAAspAAlaCysSerValGlnIleLeuValPro 40
Db 61 CCATCTGGACATCTCTCAGCCGCTGGCGATGACCGCTGCTGCTGAGATCTGCTCCCT 120
QY 41 GlyLeuLysGlyAAspAAlaGlyValLysGlyAAspLysGlyAAspProGlyArg 60
Db 121 GGCTCAAGGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 61 ValGlyProThrGlyValLysGlyAAspMetGlyAAspLysGlyGlnLysGlySerValGly 80
Db 181 GTGGGCCCCACGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 81 ArgHisGlyLysIleGlyProIleGlySerLysGlyValLysGlyAAspSerGlyAAspIle 100
Db 241 CGTATGGAGAAATTTGGTCCCATTTGGCTTAAGGTGAGAAAGAGATTCGGGTGACATA 300
QY 101 GlyProProGlyProAenGlyValProGlyLeuProCysGlyLysGlnLysGlnLys 120
Db 301 GGACCCCTCTGTCTTAATGAGAACAGAGCCCTCCCATGTGTGTGACAGCCAGCTCGCAG 360
QY 121 AlaIleGlyLysMetCAspAenGlnValSerGlnLeuThrSerGlnLeuLysPheIleLys 140
Db 361 GCCATCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 141 AsnAlaValAlaGlyValArgGlyThrGlnSerLysIleIleIleLeuValLysGlnLys 160
Db 421 AATCTGTGCGCGGTGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 161 LysArgTyrAlaAspAAlaGlnLeuSerCysGlnGlyArgGlyIleThrLeuSerMetPro 180
Db 481 AAGGCTTACGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 181 LysAspGlnAlaAlaAsnGlyLeuMetAlaAlaTyrIleuAlaGlnAlaGlyLeuAlaArg 200
Db 541 AAGGACGAGGCTGCCAATGGCTGATGGCCGATATCTGGCGCAAGCGGCTGGCCCGT 600
QY 201 ValIleIleGlyIleAsnAspLeuGlnLysGlnGlyAlaPheValIleThrSerAspHisSer 220
Db 601 GTCTTCATCGGACATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 221 ProMetArgThrPheAsnLysIleTrpAspSerGlyGlnProAenAlaAlaTyrAspGlnLys 240
Db 661 CCATGCGGAGACTTCAACAATGGGCGAGCGGTGAGCCCAACAATGCTTACAGAGAGAGAG 720
QY 241 AspCysValGlnMetValAlaSerGlyValIleThrAsnAspValAlaCysHisThrMet 260
Db 721 GACTGCGTGGAGATGTGTGCTGGGCGGCTGGAGAACGACGTGGCTGCACACCAACATG 780
QY 261 TyrPheMetCysGlnPheAspLysGlnAsnMet 271
Db 781 TACTTCATGTGTGAGTTTGACAAAGAGAAACATG 813

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## RESULT 2

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US-09-989-722-356
; Sequence 356: Application US/09989722
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.

```

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APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
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APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
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APPLICANT: Williams, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
APPLICANT: Zemin, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C63
CURRENT APPLICATION NUMBER: US/09/989, 722
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
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PRIOR FILING DATE: 1998-06-05

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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

Pred. No.: 2,98e-269 Length: 1238  
Score: 271.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-09-806-277A-6 (1-271) x US-09-989-722-356 (1-1238)

QY 1 MetArgGlyAenLauAAlaLeuValGlyValLeuLLeSerLeuAlaPheLeuSerLeu 20  
Db 67 ATGAGGGGAATCTGGCCCTGTGCTGCTTAATCAAGCCCTGCTTCTCACTGCTG 126  
QY 21 ProSerGlyHISProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
Db 127 CCAATCTGACATCTCTACAGCCGCTGGCGATACCCCTCTCTGTGCAATCTCTGCTCCT 186  
QY 41 GlyLeuLysGlyAspAlaGlyGlyLysGlyAspLysGlyAlaProGlyArgProGlyArg 60  
Db 187 GGCCTCAAAAGGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246  
QY 61 ValGlyProThrGlyGlyLysGlyAspMetCysAspLysGlyGlyLysGlySerValGly 80

Db 247 GTCCGCCCCACGGAGAAAAAGAGACATGGGGGACAAAGACAGAAAGGAGTGGGT 306  
Qy 81 Arghisgilylsilleglyproilleglyserlysglyglyaspserglyaspille 100  
Db 307 CGTATGGAAAAATGGTCCCATGGCTCTAAAGGTGAGAAAGAGATTCCGGTGAACATA 366  
Qy 101 GTPROPVPGIYPRPANGIYGLUPROGIYLEUPROCYSGIYCYSESGLINLEUARGLYS 120  
Db 367 GGACCCCTGGTCTCTAATGAGAACCAAGCCCTCCCATGTGAGTGAAGCAGCAGCTGGCAG 426  
Qy 121 A1a1leglylmetaspanglnvalserglneuThrsrsglylueuylphe1leys 140  
Db 427 GCCATCGGGAGATGAGACACAGGTCTCTACAGCTGACGACGAGCTCAATTCTACAG 486  
Qy 141 AsnAlaValAlaGlyValArgGluThrGluSerlysllyeYrleuLeuVallyglu 160  
Db 487 AATGCTGTGCGCGGTGTGCGGAGACGAGAGCAAGATCTACCTGTGTGAGAGAGAG 546  
Qy 161 LysArgTyrAlaAspAlaGlnLeuSerCyglnglylYargglyYglYThrLeuSerMetPro 180  
Db 547 AAGCGCTHCGCGAGCGCCAGCTGTCTGCAAGGCGCGGGGCGACGCTGAGCATGCC 606  
Qy 181 LysaspGluAlaAlaAsnglyleuMetAlaAlaTyrleuAlaGlnAlaGlyleuAlaArg 200  
Db 607 AAGACGAGGCTGCGCAATGGCTGATGGCGCATACCTGGCGCAGCGCGCTGGCCCT 666  
Qy 201 ValhellleglyleuAsnAspLeuGluYlsglygluYalpheValYrSerAspHisSer 220  
Db 667 GTCTTCATCGGCATCAACGAGCTGAGAAAGAGGCGGCTTCGTGTCTGTGACCACTCC 726  
Qy 221 PrometArgThrPheAsnLysTrpArgserGlygluProAsnAlaTyrAspGluGlu 240  
Db 727 CCCATGGGAGCTTCAACAGATGGCGGAGCGGTAGGCCCAACATGCTTACGAGAGAGAG 786  
Qy 241 AspCyValGluMetValAlaSerGlyGlyTyrAsnAspValAlaCySHIsthThrMet 260  
Db 787 GACTGCGGAGATGATGGCTCGGGCGGCTGAAACGCGTGGCTGCACACCACTCATG 846  
Qy 261 TyrPheMetCySGluPheAspLyGluAsnMet 271  
Db 847 TACTTCATGTGTGATTGACAAAGAAACATG 879

RESULT 3  
US-09-989-723-356  
Sequence 356, Application US/09989723  
Patent No. US20020072092A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltzen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Pao, Nicholas P.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumes, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P27301C62  
CURRENT APPLICATION NUMBER: US/09/989,723  
PRIOR FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
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PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

Score: 2.98e-269 Length: 1238  
Percent Similarity: 271.00 Matches: 271  
Best Local Similarity: 100.00% Conservative: 0  
Query Match: 100.00% Mismatches: 0  
DB: 9 Indels: 0  
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US-09-806-277A-6 (1-271) x US-09-989-723-356 (1-1238)

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QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
DB 127 CCACTGTGACATCTCTCAAGCGGCTGGGATACCGCTCTGTGACATCTCTGCTT 186  
QY 41 GlyLeuYsgIyAspAlaGlyGlyLeuYsgIyAspIyGlyAlaProGlyYargProGlyYarg 60  
DB 187 GGCCTCAAAAGGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246  
QY 61 ValGlyProThrGlyGlyLeuYsgIyAspMetGlyAspIyGlyGlyLeuYsgIySerValGly 80  
DB 247 GTCCGCCCAAGGAG 306  
QY 81 ArgHisGlyIySileGlyProIleGlySerIyGlyGlyLeuYsgIyAspSerGlyAspIle 100  
DB 307 CGTCAATGAAAAAATTGGTCCATTGGCTTAAGGTGAAGAAAGAGATTCCGGTGAACATA 366  
QY 101 GlyProProGlyProAsnGlyGlyLeuProGlyLeuProCysGlyCysSerGlnLeuYargIys 120  
DB 367 GACCCCTGTGCTCAATAG 426  
QY 121 AlaIleGlyGlyMetAspAsnGlnValSerIleuThrSerGlyLeuLeuYsPheIleIys 140  
DB 427 GCCATCGGGAG 486  
QY 141 AsnAlaValAlaGlyValArgGlyThrGlySerIySileYrIleuLeuValIyGlyGly 160  
DB 487 AATGCTGTCCCGGTGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546  
QY 161 LysArgYrYrAlaAspAlaGlnLeuSerCysGlnGlyYargIyGlyYrThrLeuSerMetPro 180  
DB 547 AAGGCTACGGGAG 606

Qy	181	LYAASPQIULIALLAENGLYLEUWETALIAIATYLEUALLAGIALLAAGIYLEUALLAARG	200
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Qy	201	VALPHEIIEGLIYLEAENAPLEUGLIULYVGLUGIYALAPHEVALTYRSEAPHSER	220
Db	667	GCTTCATCGGCATCAACAGCACTGGAGGAAGGGCGGCTTCGTGTACTCGAACACTCC	726
Qy	221	PROMECATGRHAPHEANLYSTTPAAGSERGIYGIUPROAENAPALATYRASPGLUGLU	240
Db	727	CCCATGGGACCTTCAACAGTGGCGCAGCGGTAGCCCAACATGCTTACGACGAGAG	786
Qy	241	ASPQYVALGLUNEVALAASERGIYGIYTPAENAPVALALACYNHISTHThMet	260
Db	787	GACTGCGTGGAGATGCTGGCGCTGGGCGGCTGGAACGACAGTGGCTGCAACACCATG	846
Qy	261	TYRPHMETCYEGLUPHEAPLYSGIUAENMET	271
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RESULT 4			
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Sequence 356, Application US/09989279			
Patent No. US20020072496A1			
GENERAL INFORMATION:			
APPLICANT: Ashkenazi, Avi J.			
APPLICANT: Baker, Kevin P.			
APPLICANT: Botstein, David			
APPLICANT: Desnoyers, Luc			
APPLICANT: Eaton, Dan L.			
APPLICANT: Ferrara, Napoleone			
APPLICANT: Fong, Sherman			
APPLICANT: Gerber, Hanspeter			
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APPLICANT: Tumas, Daniel			
APPLICANT: Watanabe, Colin K.			
APPLICANT: Williams, P. Mickey			
APPLICANT: Wood, William I.			
APPLICANT: Zhang, Zemin			
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic			
TITLE OF INVENTION: Acids Encoding the Same			
FILE REFERENCE: P2730PIC56			
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982

PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09  
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Score: 271.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
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Db 67 ATGAGGGGGGAATCTGGCCCTGGTGGGCTTCTATTCAGCCCTGCTCTCTGCTCACTCTG 126  
QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
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Db 187 GGCCTCAAGGGGATGGGGGAG 246  
QY 61 ValGlyProThrGlyGlyLeuGlyAspMetGlyAspIleGlyGlyIleGlySerValGly 80  
Db 247 GTCGGCCCAACGGAG 306  
QY 81 ArgHisGlyIleIleGlyProIleGlySerIleGlyIleGlyAspSerGlyAspIle 100  
Db 307 CGTATGAGAAAATGTGCTCCATTTGCTCTTAAGGTGAGAAAGAGATTCCGGTACATA 366  
QY 101 GlyProProGlyProAsnGlyGlyLeuProGlyLeuProGlyCysSerGlnLeuArgIle 120  
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QY 141 AsnAlaValAlaGlyValArgGlyThrGlySerIleIleIleLeuValIleGlyGly 160  
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Db 547 AAGGCTTAGCGGAG 606  
QY 181 LysAspGlnAlaAlaAsnGlyLeuMetAlaAlaTyrLeuAlaGlnIleGlyLeuAlaArg 200  
Db 607 AAGAGCAGGCTGCAATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 666  
QY 201 ValPheIleGlyIleLeuAspLeuGlyIleGlyIleValPheValTyrSerAspHisSer 220  
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Sequence 356, Application US/09989727

Patent No. US20020072497A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gutney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Collin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C65  
CURRENT APPLICATION NUMBER: US/09/989,727  
CURRENT FILING DATE: 2001-11-19  
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 2,986-269 Length: 1238
Score: 271.00 Matches: 271
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-806-277a-6 (1-271) x US-09-989-727-356 (1-1238)

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Db 67 ATGAGGGGGAATCTGGCCCTGGTGGCGCTTCAATCAAGCTGCTTCTCTGCTGCTG 126

QY 21 ProSeRgIyHsIProGInProAlagIyAspAPAlaCySeSeValGInIleleuValPro 40
Db 127 CCATCTGGAGCATCTCCAGCGCGCTGCGCATGACGCGCTGCTGCTGCTGCTGCTGCT 186

QY 41 GtYleuLyBgIyAspAlagIyGtYleuLyBgIyAspLyBgIyAlaProGlyArgProGlyArg 60
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Db 187 GGCCTCAAGGGGATCGGGAGAGAGAGACAAAGCGCCCGCGAGCGGCTGGANGA 246
QY 61 ValgIyProthrgIyglYyBgIyAspMetGlyAspLyBgIyglYyBgIySeValGly 80
Db 247 GTCGGCCCCACGGGAGAAAAGAGACATGGGGGACAAAGACAGAAAGGACATGTGGGT 306
QY 81 ArgHsGlyLyBgIleGlyProIleGlySeIyBgIyglYyBgIyAspSeGlyAspIle 100
Db 307 CGTCATGGAAAAATGGCCCATTTGGCTTAAAGGTGAGAAAGAGATTCGGGAGACATA 366
QY 101 GLYProProGlyProAsnGlyglYProGlyleuProCyBgIyGlyCySeSerGlnleuArglys 120
Db 367 GGAACCCCTGGTCTTATGAGAAACAGGCTCCCAATGAGTGAGTACAGCCAGCTCGCANG 426
QY 121 AlaIleGlyIuMetAspAsnGlnValSerGlnleuThrSerGlnleuValysPheIlelys 140
Db 427 GCATCGGGAGAGATGAGACAAACAGGTCTCTCAGCTGACACAGAGCTCAAGTTCATCAAG 486
QY 141 AsnAlaValAlaGlyValArgGluThrgIuSerIySileYrleuVallyBgIuGlu 160
Db 487 AATGCTGCGCGGTGTGTGCGAGAGAGAGCAAGATCTACCTGTGTGAAGAGAGAG 546
QY 161 LysArgTYrAlaAspAlaGlnleuSerCyBgIingIyArgIyglYThrleuSerMetPro 180
Db 547 AAGGCTTACGGGAGAGCGCCAGCTGTCTGCCAGGCGCGGGGACCGCTAGACATGCC 606
QY 181 LysAspGluAlaAlaAsnGlyleuMetAlaAlaTYrleuAlaGlnAlaGlyleuAlaArg 200
Db 607 AAGGCGTACGGGAGAGCGCCAGCTGTGTGCCAGCATACCTGGGCAAGCGGCTGCGCCGT 666
QY 201 ValPheIleGlyIleAsnAspLeuGluLyBgIuGlyAlaPheValTYrSeAspHisSer 220
Db 667 GTCTTCATCGGCATCAAGAGCCTGAGAGAGAGGCGGCTTCGTACTCTGACCACTCC 726
QY 221 ProMetArgThrPheAsnLyseTrpArgSerGlyglYProAsnAlaAlaTYrAspGluGlu 240
Db 727 CCATCGGAGCTTCAACAAATGGCGGAGCGGTGAGGCCCAATGCTTACAGAGAGAG 786
QY 241 AspCyValGluMetValAlaSerGlyglYrTrpAsnAspValAlaCyHisThrThrMet 260
Db 787 GACTGCGTGGAGATGTGTGGCTCGGGCGGCTGGAGACGATGGCTGACACCACTCATG 846
QY 261 TyrPheMetCyBgIuPheAspLyBgIuAsnMet 271
Db 847 TACTTCATGTGTGATTTGACAAAGAGAACTAG 879

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; Sequence 356, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deemoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Wetanabe, Colin K.
```

APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C70  
CURRENT FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: US/09/989,731  
PRIOR FILING DATE: 1997-06-16  
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PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

Pred. No.: 2,986-269 Length: 1238  
Score: 271.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-806-277a-6 (1-271) x US-09-989-731-356 (1-1238)

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127 CCATCTGACATCTCAAGCGGCTGGCATGACGCTGCTGTGCAATCTGCTCCCT 186  
41 GlyLeuLeuGlyAspAlaGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60  
187 GGCCTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 246  
61 ValGlyProThGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 80  
247 GTCCGCCCCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 306  
81 ArgHLeuGlyLeuIleGlyProIleGlySerIleGlyGlyGlyGlyGlyGlyGly 100  
307 COTCATGGAATAATGTGCTCCATGCTCTTAAGGTGAGAAAGGAGGAGGAGGAGG 366  
101 GlyProProGlyProAsnGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 120  
367 GACCCCTGTGCTCTTAATGAGAAACAGGCTCCCATGATGACGACGACGACGAC 426  
121 AlaIleGlyGlyMetAspAsnGlnValSerGlnLeuThrSerGlnLeuLeuPheIle 140  
427 GCCATCGGGAGATGACACCAAGATCTCTCAAGCTGACGACGACGACGACGACG 486  
141 AsnAlaValAlaGlyValArgGlyThrGlySerIleGlyLeuLeuValGlyGly 160  
487 AATGCTGTGCGCGGTGTGTGCGAGACGAGGAGCAAGATCTAAGTCTGTGTGAAG 546

161 LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyArgGlyTyrThrLeuSerMetPro 180  
547 AAGGCTACGCGAGCGCCAGCTGTCTGCCAGGCGCGGAGGAGGAGGAGGAGGAGG 606  
181 LysAspGlyAlaAlaAsnGlyLeuMetAlaAlaTyrLeuAlaGlnAlaGlyLeuAlaArg 200  
607 AAGGACGAGGCTGCGCAATGGCTGATGGCGCATACCTGGGCGCAAGCGGCTGGCCCT 666  
201 ValPheIleGlyIleAsnAspLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 220  
667 GCTTCATCGGACATCAACGACTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 726  
221 ProMetArgThrPheAsnLeuTyrArgSerGlyGlyProAsnAlaTyrAspGlyGly 240  
727 CCATGCGGACCTTCACAGATGGGCGCGGCTGAGGCCAATGCTTACAGAGAGAG 786  
241 AspCysValGlyMetValAlaSerGlyGlyTyrAsnAspAlaAlaCysHleThrMet 260  
787 GACTGCGGAGAGATGATGCTCGGCGGCTGGAACGACGATGCTGACCAACCATG 846  
261 TyrPheMetCysGlyPheAspLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 271  
847 TACTTCATGTGTGAGTTTGACAGAGAGACATG 879

RESULT 7  
US-09-989-732-356  
Sequence 356, Application US/09989732  
Patent No. US20020123463A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gottlieb, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Thomas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C57  
CURRENT APPLICATION NUMBER: US/09/989, 732  
PRIOR FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
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PRIOR APPLICATION NUMBER: 60/065311  
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PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322

[illegible]



;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Alignment Scores:  
Pred. No.: 2,986-269 Length: 1238  
Score: 271.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-806-277A-6 (1-271) x US-09-989-732-356 (1-1238)

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DB 67 ATGAGGGGAAATCTGACCTGGTGGGCGCTTCAATCAAGCTGCTCTGCTGCTGCTG 126

QY 21 ProSerGlyHLeProGlnProAlaGlyAspAspAlaCySerValGlnIleLeuValPro 40  
DB 127 CCATCTGGACATCTCAAGCCGGCTGGCATGACGCTGCTCTGTCAGATCTCTGCTCCCT 186

QY 41 GlyLeuValGlyAspAlaGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 60  
DB 187 GGCCTCAAAAGGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246

QY 61 ValGlyProThGlyGlnValGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 80  
DB 247 GTCCGCCCCACGGAG 306

QY 81 ArgHLeGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 100  
DB 307 CGTCAATGGAGAAATTTGGTCCATTTGGCTCTAAAGGTGAGAGAGAGAGAGAGAGAG 366

QY 101 GlyProProGlyProAsnGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 120  
DB 367 GGAACCCCTGGTCTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 426

QY 121 AlaIleGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 140  
DB 427 GCCATCGGGAGATGACACCAAGGCTCTCAAGCTGACAGAGAGAGAGAGAGAGAGAG 486

QY 141 AsnAlaValAlaGlyValAlaGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 160  
DB 487 AATGCTGTGCGCGGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546

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DB 547 AAGCCCTACGCGAG 606

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DB 607 AAGGAG 666

QY 201 ValPheIleGlyValAlaAsnAspLeuGlyValGlyValGlyValGlyValGlyValGlyVal 220  
DB 667 GTCTTCATCGGATCAAG 726

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DB 727 CCCATCGGAG 786

QY 241 AspCyValAlaGlyValAlaSerGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 260  
DB 787 GACTCTCGGAG 846

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DB 847 TACTTCATGTGTGAG 879

RESULT 8  
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GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Geider, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
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APPLICANT: Stewart, Timothy A.  
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APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zhenli  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
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PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

Pred. No.: 2,98e-269 Length: 1238  
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Percent Similarity: 100.00% Conservative: 0  
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US-09-806-277a-6 (1-271) x US-09-991-073-356 (1-1238)

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Qy 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleuValPro 40

Db	127	CCATCTGGAGCATCTCTCAGCCGGCTGGCGATGACGCGTCTGTGTGAGAGATCTCTGTCTCT	186
Oy	41	GlyLeuLysGlyValAspAlaGlyGlyLysGlyValAspLysGlyValAlaProGlyValAspProGlyValArg	60
Db	187	GCCCTCAAAAGGAGATGCGGAGAGAAAGGAGAGACAAAGGCGCCCCCGGACGGCTTGAGAA	246
Oy	61	ValGlyProThrGlyGlyLysGlyAspMetGlyAspLysGlyGlyLysLysGlySerValGly	80
Db	247	GTCCGCCCCCAACGGAGAAAGAAAGACATCGGGGACAAAGAGACAAAGGACATGTGGCT	306
Oy	81	ArgHisGlyLysIleGlyProIleGlySerLysGlyGlyLysGlyValAspSerGlyAspIle	100
Db	307	CCTCATGTGAAAAATTGGTCCCATTTGGCTCTAAAGGTGAGAAAGAGATTCCGGTGCATATA	366
Oy	101	GlyProProGlyProAsnGlyGlyProGlyLysProGlyLysLysSerGlyLysLysLys	120
Db	367	GGAACCCCTGTGTCTATATGAGAACAGGCTCCATGTGATGAGACAGCCAGCTGGCGAAG	428
Oy	121	AlaIleGlyGlyLysMetAspAsnGlyValSerGlyLysLysLysLysLysLysLysLys	140
Db	427	GCCATCGGGAGATGAGCAACACGCTCTCTCAGCTGACGAGCGAGCTCAAGTTTCATCAAG	486
Oy	141	AsnAlaValAlaGlyValArgGlyLysLysLysLysLysLysLysLysLysLysLysLys	160
Db	487	AATGCTGTGCGCGGTGTGGCGAGACGAGACGAAATCTACCTGCTGTGTGAAGAGAGAG	546
Oy	161	LysArgTyrAlaAspAlaGlyLysSerCysGlyGlyValArgGlyGlyLysLysLysLysLys	180
Db	547	AAGCCTACGCGGACGCCACCCAGCTGTCTCTCCAGGGCCCGGGGGCAAGCTGAGACATGCC	606
Oy	181	LysAspGlyAlaAlaAsnGlyLysMetValAlaIleLysLysLysLysLysLysLysLys	200
Db	607	AAGACGAGGCTGCCAATGGCTGATGGCGCATACCTGGCGCAAGCGCGCTGGCGCCCT	666
Oy	201	ValPheIleGlyIleAsnAspLeuGlyLysGlyValAlaPheValTyrSerAspHisSer	220
Db	667	GTTCTCATCGGCATCAACACCTCGAGAAAGAGAGGGCGCTTGTGTGTACTTGACCACTCC	726
Oy	221	ProMetArgThrPheAsnLysIleTyrArgSerGlyGlyProAsnAsnAlaTyrAspGlyGly	240
Db	727	CCCATGCGGACCTTCAACAAGATGGCCGACGGGTGAGCCCAACATGGCTTCGACGAGAG	786
Oy	241	AspCysValGlyMetValAlaSerGlyGlyTyrAsnAspValAlaCysHisThrTrpMet	260
Db	767	GACTCGGTGAAATGTGTGGCTTCGGCGGCTGGAAAGACGTGGCTGCCACACACCATG	846
Oy	261	TyrPheMetCysGlyLysPheAspLysGlyLysMet	271
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APPLICANT: Ashkenazi, Avi J.			
APPLICANT: Baker, Kevin P.			
APPLICANT: Botstein, David			
APPLICANT: Desnoyers, Luc			
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1 APPLICANT: Roy, Margaret Ann  
2 APPLICANT: Stewart, Timothy A.  
3 APPLICANT: Tumas, Daniel  
4 APPLICANT: Matanabe, Colin K.  
5 APPLICANT: Williams, P. Mickey  
6 APPLICANT: Wood, William I.  
7 APPLICANT: Zhang, Zemin  
8 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
9 FILE REFERENCE: P2730PIC8  
10 CURRENT APPLICATION NUMBER: US/09/990,442  
11 CURRENT FILING DATE: 2001-11-14  
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 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.: 2,986-269 Length: 1238  
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 Query Match: 100.00% Indels: 0  
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US-09-806-277a-6 (1-271) x US-09-990-442-356 (1-1238)

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 DB 127 CCATCTGGACATCTCTAGCGGCTGGCGGAGAGCGCTGCTGTGAGATGCTGTCCT 186  
 QY 41 GlyLeuLeuGlyAspAlaGlyGlnGlyAspGlyValAlaProGlyArgProGlyArg 60  
 DB 187 GGCCTCAAGGGGATCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246  
 QY 61 ValGlyProThrGlyGlnGlyAspMetGlyAspGlyGlnGlySerValGly 80  
 DB 247 GTGGGCCCCACGGGAG 306  
 QY 81 ArgHisGlyLeuIleGlyProIleGlySerLeuGlyValGlyAspSerGlyAspIle 100  
 DB 307 GGTATGAG 366  
 QY 101 GlyProProGlyProAsnGlyGlnProGlyLeuProCysGlyCysSerGlnLeuArg 120  
 DB 367 GAGCCCCCTGGTCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 426  
 QY 121 AlaIleGlyLeuMetAspAsnGlnValSerGlnLeuThrSerGlnLeuValPheIle 140  
 DB 427 GGCATCGGGGAGATGAG 486

QY 141 AsnAlaValAlaGlyValArgGluThrGlySerIleTyrLeuLeuValIlyGluGlu 160  
Db 487 AATGCTGTGCGCGGTGTGCGAGACGAGACCAAGATCTACTCTGTGTAAGAGAG 546  
QY 161 LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyArgGlyTyrLeuSerMetPro 180  
Db 547 AAGCGCTACGGGAGAGCCAGCTGTCTCTCCAGGGCCGGGGGAGACGCTGAGCATGCC 606  
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Db 607 AAGGACGAGGCTGCCAATGGCTGTATGGCCGATCTGGCCCAAGCCGGCTGGCCCGT 666  
QY 201 ValPheIleGlyIleAsnAspLeuGlyuysGluGlyAlaPheValTyrSerAspHisSer 220  
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QY 221 PrometArgTyrPheAsnIleTyrArgSerGlyGluProAsnAsnAlaTyrAspGluGlu 240  
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QY 241 AspCysValGluMetValAlaSerGlyGlyTyrPasnAspValAlaCysHisThrThrMet 260  
Db 787 GACTCGTGGAGATGTGTGGCTCTGGGCGGCTGGAACGACGTGGCTGCACACCATG 846  
QY 261 TyrPheMetCysGluPheAspIlyGluAsnMet 271  
Db 847 TACTTCATGTGTGAGTTTGACAAGAGAACATG 879

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Sequence 356, Application US/09991163  
Patent No. US20020132253A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, V. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acide Encoding the Same  
FILE REFERENCE: P2730P1C17  
CURRENT APPLICATION NUMBER: US/09/991,163  
CURRENT FILING DATE: 2001-11-14  
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PRIOR FILING DATE: 1997-06-16  
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PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.:	2,98e-269	length:	1238
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US-09-806-277a-6 (1-271) x US-09-991-163-356 (1-1238)

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QY 21 ProSerGlyHisProGlnProAlaGlyAenAenAlaCysSerValGlnIleLeuAlaPro 40  
Db CCTCTGGACATCTCAGCCGCTGGCGATGAGCGCTGCTGTGACATCTGTCCT 186

QY 41 GlyLeuLeuGlyAenAenAenAenAenAenAenAenAenAenAenAenAenAenAen 60  
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QY 61 ValGlyProThrGlyGlyLeuGlyAenMetGlyAenGlyGlyLeuGlySerValGly 80  
Db GTGGGCCCCACGGAG 306

QY 81 ArgHisGlyValLeuIleGlyProIleGlySerLeuGlyValLeuGlyAenAenAen 100  
Db CGTCATGAG 366

QY 101 GlyProProGlyProAenGlyGlyProGlyLeuProCysGlyGlyCysSerGlnLeuArg 120  
Db GAGACCCCTGCTCTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 426

QY 121 AlaIleGlyGlyLeuAenAenAenAenAenAenAenAenAenAenAenAenAen 140  
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QY 141 AenAlaValAlaGlyValArgGlyValLeuGlySerLeuIleValLeuLeuValLeu 160  
Db AATGCTGTCGCGGTGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546

QY 161 LysArgTyrAlaAenAenAenAenAenAenAenAenAenAenAenAenAenAen 180  
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QY 181 LysAenGlyAlaAlaAenGlyLeuMetAlaAlaTyrLeuAlaGlnAlaGlyLeuAla 200  
Db AAGGACGAGGCTCCATGCTGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 666

QY 201 ValPheIleGlyIleAenAenAenAenAenAenAenAenAenAenAenAenAen 220  
Db GTTTCATGCGAGATCAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 726

QY 221 ProMetArgThrAenAenAenAenAenAenAenAenAenAenAenAenAenAen 240  
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 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
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 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2730P1C25  
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 PRIOR FILING DATE: 1998-07-09

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US-09-806-277a-6 (1-271) x US-09-993-604-356 (1-1238)

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 Db 187 GGCCTCAAGGAGATGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246  
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 Db 247 GTGGCCCAAGGAG 306  
 Qy 81 ArgHisGlyLysIleGlyProIleGlySerLysGlyValLysGlyAspSerGlyAspIle 100  
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 Qy 101 GlyProProGlyProAsnGlyLysProGlyLysProGlyLysSerGlnLeuValGly 120  
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 Qy 181 LysAspGlyValAlaAsnGlyLeuMetAlaAlaTyLeuAlaGlnAlaGlyLeuAlaArg 200  
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 Qy 221 ProMetArgThrPheAsnLysTyrPArgSerGlyGlyProAsnAsnAlaTyrAspGlyGln 240  
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 Qy 241 AspCysValGlyLeuValAlaSerGlyGlyTyrAsnAspValAlaCysHisThrMet 260  
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 Qy 261 TyrPheMetCysGlyLysPheAspLysGlyLysMet 271  
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RESULT 12

US-09-990-456-356  
 Sequence 356, Application US/09990456  
 Patent No. US20020137890A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Baton, Dan L.  
 APPLICANT: Retirara, Napoleone  
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 APPLICANT: Gerber, Hanspeter  
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 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.



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 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumes, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2730P1C22  
 CURRENT FILING DATE: 2001-11-14  
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PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

Pred. No.: 2,98e-269 Length: 1238  
Score: 271.00 Matches: 271  
Percent Similarity: 100.00% Conserved: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-806-277a-6 (1-271) x US-09-990-456-356 (1-1238)

1 MetArgIAsnLeuAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeuLeu 20  
67 ATGAGGGGGAATCTGGCCCTGCTGAGGCGCTTAACTAGCCCTGCGCTCTGCTGCTG 126  
21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
127 CCATCTGGACATCTCTGACCGCGCTGGGATGACCGCTGCTGTGACGATCTGCTGCT 186  
41 GlyLeuIleuysGlyAspAlaGlyGlyValGlyAspIleuysGlyValProGlyAspProGlyArg 60  
187 GGCCTCAAGGGGATGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246  
61 ValGlyProThrArgIleGlyValGlyAspMetGlyAspIleuysGlyValGlySerValGly 80  
247 GTCCGCCCGCCAG 306  
81 ArgHisGlyIleGlyIleGlyProIleGlySerIleGlyValGlyAspSerGlyAspIle 100  
307 CGATATGAGAAAAATTGGCTCATTTGGCTCTAAAGGTGAGAAAGAGATTCCGCTGAGATA 366  
101 GlyProProGlyProAsnGlyValProGlyIleuProCysGlyCysSerGlnLeuArgIle 120  
367 GGACCCCTGTCTTAATGAG 426

Qy 121 AlaIleGlyIleuMetAspAsnGlnValSerGlnLeuThrSerGlnLeuIleuysPheIleIys 140  
Db 427 GCCATCGGGAGATGAGCAACAGAGCTCTCAGCTGACCGAGCGAGCTCAAGTTTCATCAG 486  
Qy 141 AsnAlaValAlaGlyValArgGlyIleuThrGlySerIleuValIleuysGlyValGly 160  
Db 487 AATGCTGTCCCGGCTGTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546  
Qy 161 LysArgTyrAlaAspAlaGlnLeuSerCysGlnIleuysGlyValIleuSerMetPro 180  
Db 547 AAGGCTACCGGAGAGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 606  
Qy 181 LysAspGlnAlaAlaAsnGlyIleuMetAlaIleuValAlaGlnIleuysGlyValArg 200  
Db 607 AAGAGAGAGGCTCCATAGGCTGATGGCGGATACCTGGAGAGAGAGAGAGAGAGAGAG 666  
Qy 201 ValPheIleGlyIleuAsnAspLeuGlyValGlyValAlaPheValTyrSerAspHisSer 220  
Db 667 GTCTTATCGGATCAACAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 726  
Qy 221 ProMetArgThrPheAsnIleuSerGlyIleuProAsnAlaIleuysGlyValArg 240  
Db 727 CCATGCGGACCTTCAACAG 786  
Qy 241 AspCysValGlnIleuValAlaSerGlyIleuProAsnAlaIleuysGlyValArg 260  
Db 787 GACTGCTGAGATGAGTGGCTGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 846  
Qy 261 TyrPheMetCysGlnIleuAspIleuysGlyValGlyVal 271  
Db 847 TACTTATGCTGATGATTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 879

## RESULT 13

US-09-989-721-356  
Sequence 356, Application US/09989721  
Patent No. US20020142961A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlt, Audrey  
APPLICANT: Goddard, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavich, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Thomas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCES: F2730P1C55  
CURRENT APPLICATION NUMBER: US/09/989,721  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311

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PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
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PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Alignment Scores:  
Pred. No.: 2,986-269 Length: 1238  
Score: 271.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-806-277a-6 (1-271) x US-09-989-721-356 (1-1238)

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QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
DB 127 CCATCTGGACATCTCTCAACCCGCTGGCGATACGCTGCTGCTGCGAGATCTGCTGCT 186

QY 41 GlyLeuysGlyAspAlaGlyGlyLeuysGlyAspLeuysGlyAlaProGlyArgProGlyArg 60  
DB 187 GGCCCTCAAGGGGATGGCGGAG 246

QY 61 ValGlyProThrGlyGlyLeuysGlyAspMetCysAspLeuysGlyGlyLeuysGlySerValGly 80  
DB 247 GTCGGCCCGGAG 306

QY 81 ArgHisGlyLeuysGlyProIleGlySerLeuysGlyLeuysGlyAspSerGlyAspIle 100  
DB 307 CGTATGGAGAAATTTGCTCCATTTGCTTAAAGTGAAGAGAGAGAGAGAGAGAGAGAG 366

QY 101 GlyProProGlyProAsnGlyGlyLeuysGlyProGlyLeuysGlyCysSerGlnLeuysGly 120  
DB 367 GGAACCCCTGGTCTTAATGAG 426

QY 121 AlaIleGlyGlyMetCysAspAsnGlyValSerGlnLeuysGlyLeuysGlyPheIleGly 140  
DB 427 GCGATCGGGGAG 486

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DB 487 AATGCTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 546

QY 161 LysArgGlyAlaAspAlaGlnLeuysGlyGlnIleArgGlyGlyLeuysGlySerMetPro 180  
DB 547 AAGCGCTAAGCGGAG 606

QY 181 LysArgGlyAlaAspAlaGlnLeuysGlyMetAlaAlaGlyLeuysGlnIleArgGlyValGly 200  
DB 607 AAGAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 666

QY 201 ValPheIleGlyLeuysGlyLeuysGlyLeuysGlyLeuysGlyLeuysGlyLeuysGlySer 220  
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QY 221 ProMetArgThrPheAsnLeuysGlyArgSerGlyGlyLeuysGlnIleArgGlyGlyValGly 240  
DB 727 CCATGCGGAG 786

QY 241 AspCysValGlyMetValAlaSerGlyGlyTyrAspAspValAlaCysHisThrThrMet 260  
DB 787 GACTGCTGGAGATGGTGGCTGCGGGGCTGGAGACAGCTGGCTGCCACACACCATG 846

QY 261 TyrPheMetCysGlyPheAspLeuysGlyAspMet 271  
DB 847 TACTTCATGTGTAGATTGACAGAGAGACATG 879

RESULT 14  
US-09-992-598-356  
Sequence 356, Application US/09992598  
Patent No. US20020160384A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Matanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Acids Encoded and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PLC20  
CURRENT APPLICATION NUMBER: US/09/992,598  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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PRIOR APPLICATION NUMBER: 60/087827  
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PRIOR APPLICATION NUMBER: 60/088021  
PRIOR FILING DATE: 1998-06-04

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PRIOR APPLICATION NUMBER: 60/088876	PRIOR FILING DATE: 1998-06-25
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PRIOR FILING DATE: 1998-06-17	PRIOR APPLICATION NUMBER: 60/091978
PRIOR APPLICATION NUMBER: 60/089653	PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-06-17	PRIOR APPLICATION NUMBER: 60/091982
PRIOR APPLICATION NUMBER: 60/089801	PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-06-18	PRIOR APPLICATION NUMBER: 60/092182
PRIOR APPLICATION NUMBER: 60/089907	PRIOR FILING DATE: 1998-07-09
PRIOR FILING DATE: 1998-06-18	
PRIOR APPLICATION NUMBER: 60/089908	
PRIOR FILING DATE: 1998-06-18	
PRIOR APPLICATION NUMBER: 60/089947	
PRIOR FILING DATE: 1998-06-19	
PRIOR APPLICATION NUMBER: 60/089948	
PRIOR FILING DATE: 1998-06-19	
PRIOR APPLICATION NUMBER: 60/089952	

Alignment Scores:

Pred. No.:	2.98e-269	Length:	1238
Score:	271.00	Matches:	271
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-806-277a-6 (1-271) x US-09-992-598-356 (1-1238)

Qy 1 MetArgGlyAenLeuAlaLeuValGlyValLeuLeuSerLeuAlaPheLeuSerLeuLeu 20  
Db 67 ATGAGGGGAGATCTGGCCCTGCTGGGCTTAACTAGCCCTGGCTTCTGCTGCTG 126  
Qy 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCySerValGlnIleLeuValPro 40  
Db 127 CCATCTGGACATCTCTAGCCCGCTGGCGATGACCCCTGCTCTGTCAGATCTCTGCTCC 186  
Qy 41 GlyLeuLeuValGlyAspAlaGlyValGlyValGlyValGlyValGlyValGlyValGly 60  
Db 187 GGCCTCAAGAGGAGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246  
Qy 61 ValGlyProThrGlyGlyValGlyGlyValGlyValGlyValGlyValGlyValGlyVal 80  
Db 247 GTCCGGCCCAAGGAG 306  
Qy 81 ArgHisGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 100  
Db 307 CGTATGAGAAAATTTGGTCCCATTTGGCTCTAAAGGTGAGAAAGAGATTCGGTGACATA 366  
Qy 101 GlyProProGlyProAsnGlyGlyProGlyLeuProGlyGlyGlyGlyGlyGlyGlyGly 120  
Db 367 GGAACCCCTGCTCTAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 426  
Qy 121 AlaIleGlyGlyMetAspAsnGlnValSerGlnLeuThrSerGlyLeuValGlyValGly 140  
Db 427 GCCATCGGAGAGATGACCAACAGGTCTCTCAGCTGACCAACAGGTCTCAGCTGACCAAG 486  
Qy 141 AsnAlaValAlaGlyValArgGlyValGlyValGlyValGlyValGlyValGlyValGly 160  
Db 487 AATGTGTGCGCGGTGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546  
Qy 161 LysArgTyrAlaAspAlaGlnLeuSerCySerGlnGlyArgGlyValGlyValGlyValGly 180  
Db 547 AAGCCCTAGCGGAG 606  
Qy 181 LysAspGlyAlaAlaAsnGlyLeuMetAlaAlaTyrLeuAlaGlnAlaGlyValGlyVal 200  
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Qy 201 ValPheIleGlyValLeuAspLeuGlnGlyValGlyValGlyValGlyValGlyValGly 220  
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Qy 221 ProMetArgThrPheAsnAlaGlyTyrArgSerGlyGlyProAsnAlaAlaTyrAspGlyVal 240  
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Qy 241 AspCyValAlaGlyMetValAlaSerGlyValGlyValGlyValGlyValGlyValGly 260  
Db 787 GACTCGGTGAGATGCTGCGCTCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 846  
Qy 261 TyrPheMetCySerGlnPheAspGlyValGlyValGlyValGlyValGlyValGlyVal 271  
Db 847 TACTTCATGTGTGAGTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 879

RESULT 15  
US-09-989-293A-356

Sequence 356, Application US/0989293A

Patent No. US20020177164A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltzen, Mary E.

APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Nadler, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tuma, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C66  
CURRENT APPLICATION NUMBER: US/09/989,293A  
CURRENT FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
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PRIOR FILING DATE: 1998-07-09

Alignment Scores:  
Pred. No.: 2,98e-269 Length: 1238  
Score: 271.00 Matches: 271  
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US-09-806-277A-6 (1-271) x US-09-989-293A-356 (1-1238)

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Search completed: December 17, 2004, 15:51:35  
Job time : 640 secs



GenCore version 5.1.6  
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# OM protein - nucleic search, using frame\_plus.p2n model

Run on: December 17, 2004, 08:55:20 ; Search time 632 Seconds

(without alignments)  
2367.321 Million cell updates/sec

Title: US-09-806-277A-6

Sequence: 1 MRGNALVGVLIISLAFSL.....NDVACHTTMYFMCSEPKENM 271

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Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

## Command line parameters:

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## Database :

Published Applications NA: \*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1441	100.0	813	15 US-10-258-105-45	Sequence 45, Appl
2	1441	100.0	1238	9 US-09-989-722-356	Sequence 356, App
3	1441	100.0	1238	9 US-09-989-723-356	Sequence 356, App
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7	1441	100.0	1238	9 US-09-989-732-356	Sequence 356, App
8	1441	100.0	1238	9 US-09-991-073-356	Sequence 356, App
9	1441	100.0	1238	9 US-09-990-442-356	Sequence 356, App
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17	1441	100.0	1238	9 US-09-990-444-356	Sequence 356, App
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22	1441	100.0	1238	10 US-09-989-734-356	Sequence 356, App
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24	1441	100.0	1238	10 US-09-989-724-356	Sequence 356, App
25	1441	100.0	1238	10 US-09-989-728-356	Sequence 356, App
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44	1441	100.0	1238	10 US-09-991-854-356	Sequence 356, App
45	1441	100.0	1238	10 US-09-997-628-356	Sequence 356, App

## ALIGNMENTS

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; Publication No. US20030158382A1  
; GENERAL INFORMATION:  
; APPLICANT: Wakamiya et al.  
; TITLE OF INVENTION: No. US20030158382A1 Collectin  
; FILE REFERENCE: 19036/38785  
; CURRENT APPLICATION NUMBER: US/10/258, 105  
; CURRENT FILING DATE: 2002-10-21  
; PRIOR APPLICATION NUMBER: PCT/JP01/03468  
; PRIOR FILING DATE: 2001-04-23  
; PRIOR APPLICATION NUMBER: JP 2000-120358  
; PRIOR FILING DATE: 2000-04-21  
; NUMBER OF SEQ ID NOS: 61  
; SEQ ID NO 45  
; LENGTH: 813  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-10-258-105-45

## Alignment Scores:

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US-09-806-277a-6 (1-271) x US-10-258-105-45 (1-813)

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## RESULT 2

US-09-989-722-356

; Sequence 356, Application US/09989722

; Patent No. US20020072067A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Garber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730PIC63  
CURRENT APPLICATION NUMBER: US/09/989,722  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
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 PRIOR FILING DATE: 1998-07-09

Alignment Scores:  
 Pred. No.: 6,23e-157 Length: 1238  
 Score: 1441.00 Matches: 271  
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 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-09-806-277A-6 (1-271) x US-09-989-722-356 (1-1238)  
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 QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
 DB 127 CCATCTGGAACATCTCTCAAGCCGCTGGCGATACCGCTGCTGTGCAAGATCTGTCCCT 186  
 QY 41 GlyLeuIlysgIlyAspAlaGlyGlyIlysgIlyAspIlysgIlyAlaProGlyArgProGlyArg 60  
 DB 187 GGCTCAAGGAGGATGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246  
 QY 61 ValGlyProThrArgIlyGlyIlysgIlyAspMetClyAspIlysgIlyGlyIlysgIlySerValGly 80

TITLE OF INVENTION: Acid Encoding the Same  
FILE REFERENCE: P2730P1C62  
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PRIOR FILING DATE: 1998-07-07  
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PRIOR FILING DATE: 1998-07-07  
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PRIOR FILING DATE: 1998-07-09

Alignment Scores:  
Score: 6.23e-157 Length: 1238  
Percent Similarity: 144.00 Matches: 271  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-09-806-277a-6 (1-271) x US-09-989-723-356 (1-1238)

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Db 127 CCATCTGACATCTCTCAAGCCGCTGGCGATGACCGCTGCTGTGCGATCTCTGCTCT 186

QY 41 GlyleuysGlyAspAlaGlyGlyAspMetGlyAspMetGlyAspMetGlyAspMetGly 60  
Db 187 GGCCTCAAGGGGATCTGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246

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Db 247 GTCGGCCCAAGGGGAG 306

QY 81 ArgHisGlyValIleGlyProIleGlySertleuGlyGlyGlyAspMetGlyAspMetGly 100  
Db 307 GGTATGGAAAAATGTGCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 366

QY 101 GlyProProGlyProAlaGlyGlyProGlyLeuProGlyGlyGlyGlyGlyGlyGly 120  
Db 367 GGACCCCTGCTCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 426

QY 121 AlaIleGlyIleMetAspMetGlyValSerGlnleuThrSerGlnleuValSerGlnleu 140  
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QY 141 AsnAlaValAlaGlyValArgGlyThrGlySertleuGlyGlyGlyGlyGlyGlyGly 160  
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QY 161 LysArgTyrAlaAspAlaGlnLeuSerCysserGlnGlyGlyGlyGlyGlyGlyGly 180  
Db 547 AAGCGCTACGGAG 606

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Db 607 AAGACGAGGCTGCTCAATGCTGCTGATGCGCATACCTGGCGCAAGCGGCTGCGCTG 666  
Qy 201 ValHeiIleGlyIleAsnAspLeuGlyIleGlyIleAlaPheValTyrSerAspHisSer 220  
Db 667 GTCTTCATCGGCATCAACGACGCTGAGAGAGAGGCGCTTCGTCTACTCTGACCATCTCC 726  
Qy 221 ProMetArgThrPheAsnLysTyrPArgSerGlyIleProAsnAlaTyrAspGlyIle 240  
Db 727 CCCATGCGGAGCCTTCAACAAATGGCGCGCGTGTAGCCCAATGCTTACGACGAGAG 786  
Qy 241 AspCysValGlyMetValAlaSerGlyGlyTyrPheAspValAlaCysHisThrThMet 260  
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Qy 261 TyrPheMetCysGlyPheAspLysGlyIleAsnMet 271  
Db 847 TACTTCATGTGTGATGCTTTGACAGAGAACATG 879  
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Sequence 356, Application US/09989279  
Patent No. US20020072496A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gottlieb, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kjaer, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2730P1C56  
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CURRENT FILING DATE: 2001-11-19  
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PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

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Query Match:	100.00%	Indels:	0
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US-09-806-277a-6 (1-271) x US-09-989-279-356 (1-1238)

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DB 127 CCATCTGGACATCCTCAAGCCGCGTGGCGATACGCTGCTGTGCAAGATCCTGTCCT 186  
QY 41 G1LeuIlySG1YAAPAlaG1YGlulYleG1YAspIlySG1YAlaProG1YArgProG1YArg 60  
DB 187 GGCCTCAAGGGGATGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246  
QY 61 ValG1YProThrG1YGlulYleG1YAspMetG1YAspIlySG1YAlaProG1YArgValG1Y 80  
DB 247 GTCCGGCCCAAGGAG 306  
QY 81 ArgHisG1YIlySG1YleG1YProIleG1YSerIlySG1YGlulYleG1YAspSerG1YAspIle 100  
DB 307 CGTCATGGAAAAATGGTCCATGGCTTAAAGGTGAGAAAGAGAGAGAGAGAGAGAGAG 366  
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DB 367 GGACCCCTGGTCTTAATGAG 426  
QY 121 AlaIleG1YIleMetAspAsnGlnValSerGlnLeuThrSerGlnLeuYAspIleIly 140  
DB 427 GCATCGGGGAG 486  
QY 141 AsnAlaValAlaG1YValArgIleThrGlnSerIlyIleIleValLeuValG1YGlulY 160  
DB 487 AATCTGTGCGCGGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546  
QY 161 LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyArgG1YIlyThrLeuSerMetPro 180  
DB 547 AAGGCTTACGCGAG 606  
QY 181 LysAspG1YAlaAlaAsnG1YleuMetAlaAlaTyrLeuAlaGlnIleG1YleuAlaArg 200  
DB 607 AAGGACGAGGCTGCAATAGGCTGTAGTGGCGCATACCTGGCGAGAGAGAGAGAGAG 666  
QY 201 ValPheIleG1YIleAsnAspLeuGlnYleGlnIlyAlaPheValIlyThrLeuSerMet 220  
DB 667 GTCTTCATCGGCATCAACGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 726  
QY 221 ProMetArgThrPheAsnIlyeTyrArgSerG1YGlulYProAsnAlaAlaTyrAspG1Y 240  
DB 727 CCATGCGGACCTTCAACAGATGGCGAGCGGTGAGGCCCAATGCTTACGAGAGAGAG 786  
QY 241 AspCysValGlnMetValAlaSerG1YIlyTyrAsnAspValAlaCysHisThrThrMet 260  
DB 787 GACTGCGGAGAGATGTGTGGCTCGGGCGGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 846  
QY 261 TyrPheMetCysGlnPheAspIlyGlnAsnMet 271  
DB 847 TACTTCATGTGTGAGTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 879

RESULT 5  
US-09-989-727-356  
Sequence 356, Application US/09989727

Patent No. US20020072497A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
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APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J Christopher  
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APPLICANT: Kijavik, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zenlin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C65  
CURRENT FILING DATE: 2001-11-19  
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PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

Pred. No.: 6,236-157 Length: 1238  
Score: 1441.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-806-277A-6 (1-271) x US-09-989-727-356 (1-1238)

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Db 67 ATGAGGGGGAATCTGCGCTGTGCGCTTCTAATCAAGCTGCGCTTCTGCTGCTGCTG 126  
Qy 21 ProSerGlyAIPProGlnFroAlaGlyAAsPaPaLaCySerValGlnIleLeuValPro 40  
Db 127 CCATCTGGAGCATCTCAAGCGGCTGGCGATGACGCTGCTGTGTCAGATCTCTGCTCCT 186  
Qy 41 GlyLeuYegLyAsPaLaGlyGlyLeuYegLyAsPlyGlyAlaProGlyArgProGlyArg 60

Db 187 GGCCTCAAGGGAGATCGCGAGAGAGAGACAAAGCGCCCGCGACGCGCTGGAAGA 246  
Qy 61 ValGlyProThrGlyGlyLeuYegLyAsPmetGlyAsPlyGlyGlyLeuYegLySerValGly 80  
Db 247 GTCGGCCCAAGGAGAGAAAAGAGACATGGGGGAGACAAAGAGACAGAAAGGACGATGGGGT 306  
Qy 81 ArgHisGlyYegLyIleGlyProIleGlySerYegLyGlyLeuYegLyAsPmetGlyAsPly 100  
Db 307 GGTATGGAGAAAATGGTCCATTGGCTTAAAGGTGAGAAAGAGATTCGGGTGACATA 366  
Qy 101 GlyProProGlyProAsnGlyGlyProGlyLeuProGlyProGlyGlyGlySerGlnLeuArgYls 120  
Db 367 GGACCCCTGCTCTTATGAGAAACAGGCTCCCATGTGATGTGACGACGCTGCGCAG 426  
Qy 121 AlaIleGlyLeuMetAsPaSnGlnValSerGlnLeuThrSerGlnLeuYegLyPheIleYls 140  
Db 427 GCCATCGGGAGATGAGCAACCAAGTCTCTCAGCTGACAGCAGAGCTCAAGTTCATCAG 486  
Qy 141 AsnAlaValAlaGlyValArgGlyThrGlySerYegLyIleYrLeuLeuValYegLyGlu 160  
Db 487 AATGCTGTGCGCGGTGTGCGGAGACGAGAGCAAGATCTAAGTGTGTGAAGAGAGAG 546  
Qy 161 LysArgTYrAlaAsPaLaGlnLeuSerCySgInGlyArgGlyGlyThrLeuSerMetPro 180  
Db 547 AAGGCTTAGCGGAGACGCCAGCTGTCTGCCAGGGCCGGGGGACCGCTAGCATGCCC 606  
Qy 181 LysAsPaGlyAlaAlaAsnGlyLeuMetAlaAlaTYrLeuAlaGlnAlaGlyLeuAlaArg 200  
Db 607 AAGACGAGGCTGCAATAGGCTGATGGCCGATACCTGAGGAGCGGCGCTGAGCCGT 666  
Qy 201 ValPheIleGlyIleAsnAsPLeuGlyLeuGlyValAlaPheValTYrSerAsPHisSer 220  
Db 667 GCTTCATCGGACATCAACGACTGAGAGAGAGGGCGCTTCGTGACTGTGACCATCC 726  
Qy 221 ProMetArgThrPheAsnLYrTrpArgSerGlyGlyProAsnAlaAlaTYrAsPlyGlu 240  
Db 727 CCATGCGGACCTTCAACMAATGGCGGAGCGGTAGCCCAACATGCTTACAGCAGAGAG 786  
Qy 241 AspCyValGlyMetValAlaSerGlyGlyTYrPasnAsPaLaLaCySerHisThrThrMet 260  
Db 787 GACTGCGTGAAGATGTGTGCTCGGGGGGCTGGAACGATGCGCTGACACACCATG 846  
Qy 261 TYrPheMetCySgInPheAsPlyGlyLeuMet 271  
Db 847 TACTTCATGTGTGATTTGACAGAGAACATG 879

RESULT 6  
US-09-989-731-356  
Sequence 356, Application US/09989731  
Patent No. US20020103125A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gottlieb, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: KJ Javlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C70  
CURRENT APPLICATION NUMBER: US/09/389,731  
CURRENT FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
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PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
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 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.: 6,23e-157 Length: 1238  
 Score: 1441.00 Matches: 271  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-09-806-277A-6 (1-271) x US-09-991-073-356 (1-1238)

QY 1 MetaTgGlyAenLeuAlaValGlyValLeuIleSerLeuAlaPheLeuSerLeuLeu 20  
 Db 67 ATGAGGGGAATCTGGCCCTGTGGCGCTTCAATCAGCGCTTCTGTCACTGCTG 126  
 QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40

Db 127 CCATCTGCACATCTCTCAGCCGCGCATATACCGCTCTCTGTGCAGATCTGTCTCCT 186  
Qy 41 G1LeuYsg1YaSp1aG1Yg1uLysG1YaSp1Yg1a1aProG1YarProG1YarG 60  
Db 187 GGCCTCAAAAGGGGATGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246  
Qy 61 ValG1YProThrG1Yg1uLysG1YaSpMetG1YaSp1Yg1Yg1uLysG1YsValG1Y 80  
Db 247 GTCCGCCCCACGGGAG 306  
Qy 81 ARGH1aG1Ys11eG1YPro11eG1YSer1YsG1Yg1uLysG1YaSpSerG1YaSp11e 100  
Db 307 CCGTATGAG 366  
Qy 101 G1YProProG1YProAsnG1Yg1uLysProG1YLeuProG1YsSerG1YLeuArg1Ys 120  
Db 367 GAGCCCCCTGGTCTTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 426  
Qy 121 A1a11eG1Yg1uLysMetAsnG1YValSerG1YLeuThrSerG1YLeuLysPhe11eLys 140  
Db 427 GCCATCGGGAGATGAGACACAGAGTCTCTCAGCTGACGACGAGCTCAAGTTCATCAAG 486  
Qy 141 Aa1a1aVal1aG1YValArgG1YThrG1YSer1Ys11eYr1YLeuLysVal1Yg1uLys 160  
Db 487 AATGCTGTGCGCGGATGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546  
Qy 161 LysArg1Yr1aAsp1aG1YLeuSerCyserG1YArg1Yg1YThrLeuSerMetPro 180  
Db 547 AAGGCTACGGGAG 606  
Qy 181 LysArgG1U1a1aAsnG1YLeuMet1a1a1Yr1YLeu1aG1YLeu1aArg 200  
Db 607 AAGGCGAGGCTGCGCAATGCGCTGTATGCGCGATCTCTGCGCGAGCCGCGCTGCGCGT 666  
Qy 201 ValPhe11eG1YLeuAsnAspLeuG1Yg1uLysG1YVal1aPheVal1Yr1YSerAsp11eSer 220  
Db 667 GTCTTCACTGCGCATACAG 726  
Qy 221 ProMetArg1YThrPheAsn1Yr1YArgSerG1Yg1uProAsnAsn1a1Yr1YAsp1u 240  
Db 727 CCCATCGGAG 786  
Qy 241 AspCyVal1G1uMetVal1a1aSerG1Yg1Yr1YAsnAspVal1a1aCyHis1Yr1YMet 260  
Db 787 GACTCGCGAGATGATGCGCTCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 846  
Qy 261 TyrPheMetCyG1uPheAsp1Yg1uLysMet 271  
Db 847 TACTTCATGTGTGAGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 879

RESULT 9  
US-09-990-442-356  
Sequence 356, Application US/09990442  
Patent No. US20020132252A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Ferrara, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tamas, Daniel  
APPLICANT: Watanabe, Collin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C8  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
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 PRIOR FILING DATE: 1998-07-09

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 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-09-806-277a-6 (1-271) x US-09-990-442-356 (1-1238)

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 QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
 Db 127 CCACTCGACATCTCTAGCGGCTGGCGATGAGCGCTGCTGTGCAAGATCCCTGCTCC 186  
 QY 41 GlyLeuIleGlyAspAlaGlyGlyGlyGlyAspLeuGlyValAspLeuGlySerValGly 60  
 Db 187 GGCCTCAAGGGGATCGGGAG 246  
 QY 61 ValGlyProThrGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 80  
 Db 247 GTCGGCCCCACGGGAG 306  
 QY 81 ArgHisGlyLeuValLeuIleProIleGlySerIleGlyValGlyValAspSerGlyAsp 100  
 Db 307 GTCATGAGAAAATTGCTCCATGCTGCTTAAAGTGAGAGAGAGAGAGAGAGAGAGAG 366  
 QY 101 GlyProProGlyProAsnGlyGlyProGlyLeuProCysGlySerGlyLeuAspGly 120  
 Db 367 GAGCCCCCTGGTCTTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 426  
 QY 121 AlaIleGlyLeuMetAspAsnGlnValSerGlnLeuThrSerGlyLeuIleValys 140  
 Db 427 GCCATCGGGAGATGAGAACAGAGTCTCAGCTGACAGAGAGAGAGAGAGAGAGAGAG 486



141 AapAlaValAlaGlyValArgLunThrGlySerLysIleTyrLeuLeuValIleGlyLun 160  
Db AATGCTGTCGCGCGGTGTCGCGAGCGAGCAAGATCTACTGCTGTGAAGAGAG 546  
Oy LysAGTyrAlaAapAlaGlyLunSerCysGlnGlyTyrGlyTyrThrLeuSerMetPro 180  
547 AAGCCCTACGCGGAGCCCAAGCTGTCTGCTCCAGGGGCCCGGGGGGACCGCTAGCATGCC 606  
Oy LysAapGlyAlaAlaAaGlyLunLeuValAlaTyrLeuAlaGlnAlaGlyLeuAlaArg 200  
Db AAGGACGAGGCTGCGCAATGCTGTATGGCCGCACTGCGGCAAGCCGCGCTGCGCCCT 666  
Oy ValPheIleGlyTyrLeuAaAapLeuGlyLunGlyLunGlyAlaPheValTyrSerAaPheSer 220  
Db GCTTCATCGCGCATCAAGCACTGAGAGAGGGGCGGCTGTCTACTGTGACCATCC 726  
Oy PromelaGlyTrpPheAaLysTyrPargSerGlyLunProAaAaAlaTyrAaPGLun 240  
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Oy AapCysValAlaGlyMetValAlaSerGlyTyrPaaAaPvalAlaCysHisThrThrMet 260  
Db GACTCGTGAGATGTGTGCTCGGCGGCTGGAACAGCTGTGCTGCGCACACCATG 846  
Oy TyrPheMetCysGlyPheAaPlyGlyLunMet 271  
Db 847 TACTTCATGTGTGAGTTTGAACAGGAACATG 879

RESULT 10  
US-09-991-163-356  
Sequence 356, Application US/09991163  
Patent No. US20020132253A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C17  
CURRENT APPLICATION NUMBER: US/09/991,163  
CURRENT FILING DATE: 2001-11-14  
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PRIOR FILING DATE: 1997-11-24  
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PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089514  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089532  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089538  
PRIOR FILING DATE: 1998-06-17



OY 261 TyPhemecCyGgIupheAspLyGtUbanMet 271  
Db 847 TACTTCATGTGTGAGTTTGACAGAGAACATG 879  
RESULT 11  
US-09-993-604-356  
Sequence 356, Application US/09993604  
Patent No. US20020137075A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyer, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
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APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
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APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C25  
CURRENT APPLICATION NUMBER: US/09/993,604  
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 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091978  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

Alignment Scores:  
 Pred. No.: 6.23e-157 Length: 1238  
 Score: 1441.00 Matches: 271  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-09-806-277a-6 (1-271) x US-09-993-604-356 (1-1238)

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 QY 21 ProSerGIyHISProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
 Db 127 CCATCTGACATCTCTACGCGGCTGGCGATGACGCTGCTCTGACGATCTCTGCTCC 186  
 QY 41 GILyLeuLyGIyAspAlaGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60  
 Db 187 GSCCTCAAGGGGATCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 246  
 QY 61 ValGlyProThrGIyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 80  
 Db 247 GTGGGCCCGCCAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 306  
 QY 81 ArgHISGIyLySISleGIyProIISleGIySerLySISleGIyGlyGlyGlyGlyGly 100  
 Db 307 CGTCATGGAAGAAATTTGGCTCCATTTGGCTCTAAAGGTGAGAGGAGGAGGAGGAG 366  
 QY 101 GILyProGlyProGlnGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 120  
 Db 367 GGAACCCCTGGCTCTATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 426  
 QY 121 AlaIISleGIyLysSerAspAspGlnValSerGlnLeuThrSerGlyLeuIleValys 140  
 Db 427 GCCATCGGGGAGATGAGCAACAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 486  
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 Db 547 AAGCGCTACGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 606  
 QY 181 LysAspGlyAlaAlaAspGlyLeuMetAlaAlaTyrLeuAlaGlnAlaGlyLeuAlaArg 200  
 Db 607 AAGGACGAGGCTGCGCAATGCGCTGATGGCGGATACCTGCGGAGGAGGAGGAGGAG 666  
 QY 201 ValPheIISleGIyLysAspLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 220  
 Db 667 GTCTTCATCGGATCAACACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 726  
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 QY 261 TyrPheMetCysGluPheAspLysGluAsnMet 271  
 Db 847 TACTTCATGTGTGAGTTTGACAAAGGAGAACATG 879

RESULT 12

US-09-990-456-356 Application US/09990456

Patent No. US20020137890A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

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APPLICANT: Godowski, Paul J.

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APPLICANT: Gurney, Austin L.

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APPLICANT: Paoni,Nicholas F.  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumes, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C22  
CURRENT APPLICATION NUMBER: US/09/990,456  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
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PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

Pred. No: 6.23e-157 Length: 1238  
Score: 1441.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-09-806-277a-6 (1-271) x US-09-990-456-356 (1-1238)

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21 ProSerGIyHisProGInProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
127 CCATCTGGAATCTCTCAAGCGGCTGGGATGACGCTGCTGCTGCTGCTGCTGCTGCTGCT 186  
41 GlyLeuIyGlyAspAlaGlyIyGlyIyAspIyGlyIyAspIyGlyIyAspIyGlyIyAsp 60  
187 GGCTCTCAAGGGGATGCGGAGAGAAAGGAGACAAAGGCGCCCGGAGCGCTGGAAGA 246  
61 ValGlyProThrGlyGlyIyGlyIyAspMetGlyAspIyGlyIyGlyIyGlyIyGlyIy 80  
247 GTGGGCGCCCAAGGAGAAAGAGACATGGGGACAAAGAGCAAGAGCATGTGGGT 306  
81 ArgHisGlyIy 100  
307 CGTCATGAAATAATGGTCCATGGCTTAAGAGTGAAGAGAGATTCGGGTGACATA 366  
101 GlyProProGlyProAlaGlyIyGlyIyProGlyIyLeuProGlyIyGlyIyGlyIyGlyIy 120  
367 GGACCCCTGCTCTAATGAGAACGAGGCTCCCATGTGATGACAGCCAGCTGGCAG 426

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Db 427 GCCATCGGGAGATGAGCAACAGGTCTCTCACTGACCTGACCAAGCTCAAGTTCATCAAG 486  
Qy 141 AsnAlaValAlaGlyIy 160  
Db 487 AATGCTGTGCGCGGTGTGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546  
Qy 161 LysArgIy 180  
Db 547 AAGCGCTACCGCGGAGCCCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 606  
Qy 181 LysAspGlyIy 200  
Db 607 AAGGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 666  
Qy 201 ValPheIleGlyIy 220  
Db 667 GTCTTCATGCGCATCAACGACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 726  
Qy 221 ProMetArgThrPheAsnIy 240  
Db 727 CCCATCGGACCTTCAACAAAGTGGCCGAGCGGTGAGCCCAACATGCTTACGAGAGAGAG 786  
Qy 241 AspCysValGlyIy 260  
Db 787 GACTGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 846  
Qy 261 TyrPheMetCysGlyIy 271  
Db 847 TACTTCATGTGTGATGTTGACAAAGAGAACATG 879

## RESULT 13

US-09-989-721.356

Sequence 356, Application US/09989721

Patent No. US20020142961A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

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APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730PIC55

CURRENT APPLICATION NUMBER: US/09/989,721

PRIOR FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

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[illegible]

PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
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PRIOR FILING DATE: 1998-07-09

Alignment Scores:  
Pred. No.: 6,23e-157 Length: 1238  
Score: 1441.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-09-806-277a-6 (1-271) x US-09-989-721-356 (1-1238)

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QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
Db 127 CCATCTGGACATCTCTACGCGGCTGGCGATACCCCTGCTTGCGAGATCTCTGCTCT 186

QY 41 GlyLeuLeuGlyAspAlaGlyGluLeuGlyAspLeuGlyAlaProGlyAspProGlyArg 60  
Db 187 GGCCTCAAGGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246

QY 61 ValGlyProThrGlyGluLeuGlyAspMetClyAspLeuGlyGlnLeuGlySerValGly 80  
Db 247 GTCGGCCCCCGAG 306

QY 81 ArgHisGlyLeuIleGlyProIleGlySerLeuGlyGluLeuGlyAspSerGlyAspIle 100  
Db 307 CGTATGGAGAAATTTGCTCCATTTGCTCTAAAGGTAGAGAGAGAGAGAGAGAGAG 366

QY 101 GlyProProGlyProAsnGlyGluProGlyLeuProCysGlyCysSerGlnLeuArgLys 120  
Db 367 GAGCCCCCTGGTCTTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 426

QY 121 AlaIleGlyGluMetAspAsnGlnValSerGlnLeuThrSerGlnLeuLeuPheIleLys 140  
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Db 487 AATGCTCTCGCGGTGTCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546

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QY 201 ValPheIleGlyIleAsnAspLeuGluLysGluGlyValaPheValTyrSerAspHisSer 220  
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Db 727 CCATGCGAGAGCTTCAAG 786

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QY 261 TyrPheMetCysGluPheAspLysGluAsnMet 271  
Db 847 TACTCATGTGTGATGTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 879

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Sequence 356, Application US/09992598  
Patent No. US20020160384A1

GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
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APPLICANT: Williams, P. Mickey  
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APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C20  
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;; PRIOR FILING DATE: 1998-07-09

Alignment Scores:  
Pred. No.: 6,23e-157 Length: 1238  
Score: 1441.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-806-277a-6 (1-271) x US-09-992-598-356 (1-1238)

QY 1 MetArgGlyAsnLeuAlaLeuValGlyValLeuLeuSerLeuAlaPheLeuSerLeuLeu 20  
Db 67 ATGAGGGGGAATCTGGCCCTGCTGGCTTATCTACGCTGGCTTCTCTCTCTCTG 126  
QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnLeuValPro 40  
Db 127 CCATCTGGACATCTCTACGCTGGGAGTACCCCTCTCTGTCAGATCTCTGCTCT 186  
QY 41 GlyLeuYsgGlyAspAlaGlyGlyLeuYsgGlyAspYsgGlyAlaProGlyArgProGlyArg 60  
Db 187 GGCCTCAAGGGGATGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246  
QY 61 ValGlyProThrGlyGlyLeuYsgGlyAspMetGlyAspYsgGlyGlnYsgGlySerValGly 80  
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Db 307 CGTATGAG 366  
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RESULT 15  
US-09-989-293A-356

; Sequence 356, Application US/09989293A

; Patent No. US20020177164A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
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; APPLICANT: Goddard, Audrey  
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; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
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 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

Alignment Scores:  
 Pred. No.: 6,23e-157 Length: 1238  
 Score: 1441.00 Matches: 271  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-09-806-277A-6 (1-271) x US-09-989-293A-356 (1-1238)

QY 1 MetAArgGlyAenLeuAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeu 20  
 DB 67 ATGAGGGGGAATCTGGCCCTGTGCGGTCTTAATTCAGCCCTGCTCTCTCTGCTG 126  
 QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
 DB 127 CCATCTGGACATCTCTCAGCCGGCTGGCGATGACCGCTCTGTGACAGATCTGTCCT 186  
 QY 41 GlyLeuLysGlyAspAlaGlyGlyLysGlyAspLysGlyValAspProGlyValArg 60  
 DB 187 GGCCTCAAGGAGATGCGGAGAGAAAGGAGACAAAGCGCCCGAGCGGCTGGAAGA 246  
 QY 61 ValGlyProThrGlyGlyLysGlyAspMetGlyAspLysGlyGlnLysGlySerValGly 80  
 DB 247 GTCCGCCACCGAGAGAAAGAGACATGGGGAGCAAAAGACGAAAGAGAGTGTGGT 306  
 QY 81 ArgHisGlyLysIleGlyProIleGlySerLysGlyGlyLysGlyAspSerGlyAspIle 100  
 DB 307 CGTCATGGAAAAATTGGTCCATTTGGCTCTAAAGGTGAGAAAGAGATTCCGGTGACATA 366

Qy 101 GlyProFroglyProaenglyGluProglyLeuProCysgluCysSerGlnLeuArglys 120  
Db 367 GGACCCCTGGTCTTAATGAGAACCAAGGCTCCCATGTGAGTGACAGCAGCTGGCAAG 426  
Qy 121 AAlaIleGlyGluMetAspAsnGlnValSerGlnLeuThrSerGluLeuLysPheIleLys 140  
pb 427 GCCATCGGGAGAGAACCAAGGCTCTCTGACCGACGAGCTCAAGTTTCATCAAG 486  
Qy 141 AsnAlaValAlaGlyValArgGluThrGluSerLysIleTyrLeuLeuValLysGluGlu 160  
Db 487 AATGCTGCGCGGTGTGCGGAGAGAGCAAGATCTACCTGCTGCTGTAAGAGAGAG 546  
Qy 161 LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyArgGlyGlyThrLeuSerMetPro 180  
Db 547 AAGCGCTACGCGGACGCGCCAGCTGTCTCTGCAAGGGCGCGGAGGAGCATGCCC 606  
Qy 181 LysAspGluAlaAlaAsnGlyLeuMetAlaAlaTyrLeuAlaGlnAlaGlyLeuAlaArg 200  
Db 607 AAGAGCGAGGCTGCCAATGCGCTGATGCGCCATTCCTGCGCGCAAGCGCGCTGCGC 666  
Qy 201 ValPheIleGlyIleAsnAspLeuGluLysGluGlyAlaPheValTyrSerAspHisSer 220  
Db 667 GTCTTCATCGGCAATCAACGACCTGAGAGAGAGGCGCGCTTCGTGTACTGTGACCACTCC 726  
Qy 221 ProMetArgThrPheAsnLysTyrArgSerGlyGluProAsnAspAlaTyrAspGluGlu 240  
Db 727 CCCATGCGGACCTTCMAACAGTGGCGAGCGGTGAGCCCAACATGCTTACGACGAGGAG 786  
Qy 241 AspCysValGluMetValAlaSerGlyGlyTyrPheAspValAlaCysHisThrThrMet 260  
Db 787 GACTGCGTGGAGATGTGGCTTCGGGCGGCTGGAAAGACGTGGCTGCGCACACCACTG 846  
Qy 261 TyrPheMetCysGluPheAspLysGluAsnMet 271  
Db 847 TACTTCATGTGTGAGTTGACACAGAGAAACATG 879

Search completed: December 17, 2004, 11:34:15  
Job time : 639 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

# OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 17, 2004, 05:42:01 ; Search time 3865 Seconds  
(without alignments)  
2355.024 Million cell updates/sec

Title: US-09-806-277a-6

Perfect score: 1441  
Sequence: 1 MRGNLALGVGLISLFLSL.....NDVACHTMYMCEFDKENM 271

## Scoring table:

BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Command line parameters:

-MODEL=frame+g2n.model -DEV=xlp  
-Q=/cgn2.1/USPTO\_spool\_p/US09806277/runcat\_15122004\_101628\_29262/app\_query.fasta\_1.455  
-DB=EST -QFMT=fastap -SUFFIX=est -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45  
-DOCLIN=200 -THR SCORE=pcr -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTMT=ptco -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09806277@cgn\_1.1.6425@runcat\_15122004\_101628\_29262 -NCPU=6 -ICPU=3  
-NO MMAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6  
-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database :

EST:  
1: gb\_est1:  
2: gb\_est2:  
3: gb\_hic:  
4: gb\_est3:  
5: gb\_est4:  
6: gb\_est5:  
7: gb\_est6:  
8: gb\_est1:  
9: gb\_g982:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1441	100.0	1252	3	CR604552 full-length
2	1441	100.0	1397	3	CR612268 full-length
3	1397	96.9	894	5	BU147034 AGENCOURT
4	1384	96.0	1083	5	BK427124 BX427124
5	1353	93.9	1078	5	BK333394 BX333394
6	1331	92.4	1383	5	AK003121 Mus muscu
7	1306	89.6	962	5	BQ927000 AGENCOURT
8	1286	89.2	1150	3	CR599770 full-length
9	1124	78.0	834	7	CO398423 AGENCOURT

c	10	1102	76.5	1095	5	BX394893	BX394893
	11	1100	76.3	1015	5	BX394625	BX394625
	12	1098	76.2	823	4	BX198782	BX198782
c	13	1072	74.4	1071	5	BX394624	BX394624
	14	1067	74.0	788	4	BF311981	BF311981
	15	1032	71.6	1094	4	BW547424	BW547424
	16	1030	71.5	723	3	BE382845	BE382845
	17	1021	70.9	1012	2	BE260904	BE260904
	18	1013	70.3	640	2	BE383325	BE383325
	19	1000	69.4	672	2	BE206254	BE206254
	20	987.5	68.5	683	2	BE382433	BE382433
	21	980	68.0	702	2	BF311185	BF311185
	22	962	66.8	715	2	BE313199	BE313199
	23	955.5	66.3	737	2	BE313410	BE313410
	24	955	66.3	644	2	BE262656	BE262656
	25	944	65.5	1000	4	BE198831	BE198831
	26	937	65.0	613	2	BF312666	BF312666
	27	933	64.7	767	2	BE260355	BE260355
	28	930	64.5	893	3	BF314316	BF314316
	29	930	64.5	916	2	BF316717	BF316717
	30	928	64.4	654	2	BE312923	BE312923
	31	913	63.4	769	2	BE312920	BE312920
	32	903.5	62.7	892	2	BF314275	BF314275
	33	902.5	62.6	728	2	BE260359	BE260359
	34	884	61.3	619	4	BE199068	BE199068
	35	881	61.1	626	2	BF316496	BF316496
	36	869	60.3	962	5	BE069775	BE069775
	37	862.5	59.9	878	4	BE197505	BE197505
	38	859	59.6	828	7	CK602638	CK602638
	39	858	59.5	697	2	BF317087	BF317087
	40	848	58.8	542	2	BE313758	BE313758
	41	836.5	58.0	851	6	CB993054	CB993054
	42	836	58.0	537	2	BE261686	BE261686
	43	834	57.9	538	2	BE312003	BE312003
	44	824	57.2	665	2	BF317432	BF317432
	45	823	57.1	525	2	BE261369	BE261369

## ALIGNMENTS

RESULT 1  
LOCUS CR604552  
DEFINITION full-length cDNA clone CSDDC024Y19 of Neuroblastoma Cot  
25-normalized of Homo sapiens (human).  
ACCESSION CR604552  
VERSION CR604552.1 GI:50485359  
KEYWORDS HTC; CNSLT CDNA.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE Li W.B., Gruber C., Jesssee J. and Polayes D.  
Full-length cDNA libraries and normalization  
Unpublished  
Contact: Feng Liang Email: fliang@life.techn.com URL:  
http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Faraday Avenue  
2 (bases 1 to 1252)  
Genoscope.  
Direct Submission  
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 Evry cedex - FRANCE (E-mail: seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
1st strand cDNA was primed with a Noci-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Nci I and cloned  
into the Nci I and Bcl I sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
Location/Qualifiers  
1..1252  
/organism="Homo sapiens"

ORIGIN

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DM08YL18"
/tissue_type="Neuroblastoma Cot 25-normalized"
/plasmid="pCMVSPORT_6"

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Alignment Scores:

Pred. No.:	1.4e-124	Length:	1252
Score:	1441.00	Matches:	271
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
	3	Gaps:	0

US-09-806-277a-6 (1-271) x CR604552 (1-1252)

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QY 1 MetArgGlyAsnLeuAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeu 20
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QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40
Db 164 CCATCTGGACATCTCTCAAGCCGCTGCGCATGACGCTGCTGCTGCTGCTGCTGCTGCT 223
QY 41 GlyLeuIleYsgIYAspAlaGlyGlyIleYsgIYAspIleYsgIYAlaProGlyArgProGlyArg 60
Db 224 GGCTCTCAAGAGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 283
QY 61 ValGlyProThrGlyGlyIleYsgIYAspMetGlyAspIleYsgIYAlaIleYsgIYSerValGly 80
Db 284 GTCCGGCCCAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 343
QY 81 ArgHisGlyIleYsgIYProIleGlySerIleYsgIYValYsgIYAspSerGlyAspIle 100
Db 344 CGTATGGAGAAATTTGGTCCATTTGGCTCTAAGGTGAGAAAGAGATTCGGTGACATA 403
QY 101 GlyProProGlyProAsnGlyGlyIleProGlyLeuProCysGlyCysSerGlnLeuArgIle 120
Db 404 GGACCCCTGCTCTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 463
QY 121 AlaIleGlyIleMetAspAsnGlnValSerGlnLeuThrSerGlnLeuYsPheIleYs 140
Db 464 GCCATCGGGAGATGAGACACAGGCTCTCTCAGCTGACACGAGCTCAAGTTCATCAAG 523
QY 141 AsnAlaValAlaGlyValArgGlyIleThrGlySerIleIleYrLeuLeuValIleGlyIle 160
Db 524 AATGCTGTGCGCGGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 583
QY 161 LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyArgGlyIleThrLeuSerMetPro 180
Db 584 AAGGCTACGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 643
QY 181 LysAspGlnAlaAlaAsnGlyLeuMetAlaAlaTyrLeuAlaGlnIleGlyLeuAlaArg 200
Db 644 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 703
QY 201 ValPheIleGlyIleAsnAspLeuGlnIleYsgIYAlaPheValIleYrSerAspHisSer 220
Db 704 GTCTTCATCGGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 763
QY 221 PrometArgThrPheAsnIleYrPheSerGlyGlyIleProAsnAlaAlaTyrAspGlyIle 240
Db 764 CCCTACGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 823
QY 241 AspCysValGlnMetValAlaSerGlyIleYrPheAspValAlaCysHisThrThrMet 260
Db 824 GACTGCGGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 883
QY 261 TyrPheMetCysGlyIlePheAspIleGlyLeuMet 271
Db 884 TACTTCATGTTGAGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 916

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RESULT 2  
CR612268  
LOCUS 1397 bp mRNA linear HTC 21-JUL-2004  
DEFINITION full-length cDNA clone CS0DM08YL18 of Fetal liver of Homo sapiens (human).

ACCESSION  
CR612268  
VERSION  
HTC: CNS/LT cDNA.  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REMARK  
Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Faraday Avenue  
2 (bases 1 to 1397)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REMARK  
Genoscope.  
Direct Submission  
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)

COMMENT  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
Location/Qualifiers  
1. 1397

FEATURES  
source  
1. 1397  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DM08YL18"  
/tissue\_type="Fetal liver"  
/plasmid="pCMVSPORT\_6"

## ORIGIN

Alignment Scores:

Pred. No.:	1.6e-124	Length:	1397
Score:	1441.00 <td>Matches:</td> <td>271 </td>	Matches:	271
Percent Similarity:	100.00% <td>Conservative:</td> <td>0 </td>	Conservative:	0
Best Local Similarity:	100.00% <td>Mismatches:</td> <td>0 </td>	Mismatches:	0
Query Match:	100.00% <td>Indels:</td> <td>0 </td>	Indels:	0
	3	Gaps:	0

US-09-806-277a-6 (1-271) x CR612268 (1-1397)

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Db 92 ATGAGGGGGAATCTGGCCCTGCTGAGGCTTCTAATCACTCGCCCTTCTCACTGCTG 151
QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40
Db 152 CCATCTGGACATCTCTCAAGCCGCTGCGCATGACGCTGCTGCTGCTGCTGCTGCTGCT 211
QY 41 GlyLeuIleYsgIYAspAlaGlyGlyIleYsgIYAspIleYsgIYAlaProGlyArgProGlyArg 60
Db 212 GGCTCTCAAGAGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 271
QY 61 ValGlyProThrGlyGlyIleYsgIYAspMetGlyAspIleYsgIYAlaIleYsgIYSerValGly 80
Db 272 GTCCGGCCCAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 331
QY 81 ArgHisGlyIleYsgIYProIleGlySerIleYsgIYValYsgIYAspSerGlyAspIle 100
Db 332 CGTATGGAGAAATTTGGTCCATTTGGCTCTAAGGTGAGAAAGAGATTCGGTGACATA 391
QY 101 GlyProProGlyProAsnGlyGlyIleProGlyLeuProCysGlyCysSerGlnLeuArgIle 120
Db 392 GGACCCCTGCTCTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 451

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QY 121 AAlaIleGIyGluMetAspAsnGluValSerGluLeuThrSerGluLeuLeuPheIleIys 140  
DB 452 GCCATCGGGAGATGACCAACAGGTCTCTCAAGCTGACGACGAGCTCAAGTTCAATCAAG 511  
QY 141 AsnAlaValAlaGlyValArgGluThrGluSerIleTyrLeuLeuValIleGluGlu 160  
DB 512 AATGCTGTCCCGGTCTCGCGAGACGAGACCAAGATCTACCTGCTGTGTAAGAGAGAG 571  
QY 161 LysArgTyrAlaAspAlaGluLeuSerCysGlnGlyArgGlyTyrThrLeuSerMetPro 180  
DB 572 AAGCGCTACGCGGAGCGCCAGCTGTCTGCCAGCGCGCGGAGCACCTGAGCATGCC 631  
QY 181 LysAspGluAlaAlaAsnGlyLeuMetAlaAlaTyrLeuAlaGlnAlaGlyLeuAlaArg 200  
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QY 201 ValPheIleGlyIleAsnAspLeuGluIlyArgGluGlyAlaPheValTyrSerAspIleSer 220  
DB 692 GTCTTCATCGGCATACGACCTGAGAGAGAGAGGCGCTTGTGTACTGTGACCATCTCC 751  
QY 221 ProMetArgThrPheAsnIleTyrArgSerGlyGluProAsnAsnAlaTyrAspGluGlu 240  
DB 752 CCCATGCGGACCTTCAACAAAGTGGCGGACGCGGTGAGCCCAACATGCTTACGACAGAGAG 811  
QY 241 AspCysValGluMetValAlaSerGlyTyrTrpAsnAspValAlaCysHisThrThrMet 260  
DB 812 GACTGCGTGGAGATGTGGCTCGGCGCGCTGGAAACGACGTGGCTGCACACCACTATG 871  
QY 261 TyrPheMetCysGluPheAspIlyArgIleAsnMet 271  
DB 872 TACTTCATGTGTGAGTTTGAACAAGAGAACATG 904

RESULT 3  
LOCUS BUI47034 894 bp mRNA linear EST 03-SEP-2002  
DEFINITION AGENCOURT 8736281 NIH\_MGC\_47 Homo sapiens cDNA clone IMAGE:6338772  
5', mRNA sequence.  
ACCESSION BUI47034  
VERSION BUI47034.1 GI:22660566  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 894)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@bcr-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LHCW2532 row: 1 column: 13  
High quality sequence stop: 621.  
Location/Qualifiers  
1..894  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/clone="IMAGE:6338772"  
/cfeature\_type="neuroblastoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_47"  
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average

Insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

## ORIGIN

## Alignment Scores:

Pred. No.:	1,22e-120	Length:	894
Score:	1397.00	Matches:	266
Percent Similarity:	98.16%	Conservative:	1
Best Local Similarity:	97.79%	Mismatches:	4
Query Match:	96.95%	Indels:	1
DB:	5	Gaps:	0

US-09-806-277a-6 (1-271) x BUI47034 (1-894)

QY 1 MetArgGlyAsnLeuAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeu 20  
DB 72 ATGAGGGGGAATCTGGCTGTGGCTTCTATACCTGCTGCTTCTGCTGCTG 131  
QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
DB 132 CCATCTGGACATCTCTCAAGCCGCTGGCGATGACCGCTGCTGTGCAATCTCGTCCCT 191  
QY 41 GlyLeuIlySerGlyAspAlaGlyValGluIlyAspIlyArgGlyAlaProGlyValArg 60  
DB 192 GGCCTCAAAAGGAGATGCGGAGAGAAAGGAGAAAGGCGCCCGGAGCGCTGGAAAG 251  
QY 61 ValGlyProThrGlyValIlyGlyValAspMetGlyAspIlyGlyGlnIlyGlySerValGly 80  
DB 252 GTCCGCCCAAGGAGAAAGAGACATGGCGGACAAAGACAGAAAGCATGTGGGT 311  
QY 81 ArgHisGlyIlyIleGlyProIleGlySerIlyGlyGluIlyGlyAspSerGlyAspIle 100  
DB 312 CGTATGAGAAATTTGGTCCCATTTGCTTAAAGGTGAGAAAGAGATTCGGTGACATA 371  
QY 101 GlyProProGlyProAsnGlyGluProGlyLeuProCysGlyCysSerGlnLeuArgIys 120  
DB 372 GGAACCCCTGTGTCTTAAAGAGAAACAGGCTCCCATGTGATGAGCCAGCTGCGCAAG 431  
QY 121 AAlaIleGIyGluMetAspAsnGluValSerGluLeuThrSerGluLeuLeuPheIleIys 140  
DB 432 GCCATCGGGAGATGACCAACAGGTCTCTCAAGCTGACGACGAGCTCAAGTTCAATCAAG 491  
QY 141 AsnAlaValAlaGlyValArgGluThrGluSerIleTyrLeuLeuValIleGluGlu 160  
DB 492 AATGCTGTCCCGGTCTCGCGAGACGAGACCAAGATCTACCTGCTGTGAGAGAGAG 551  
QY 161 LysArgTyrAlaAspAlaGluLeuSerCysGlnGlyArgGlyTyrThrLeuSerMetPro 180  
DB 552 AAGCGCTACGCGGAGCGCCACAGCTGTCTGCCAGGCGCGGAGGACCTGACATGAGCC 611  
QY 181 LysAspGluAlaAlaAsnGlyLeuMetAlaAlaTyrLeuAlaGlnAlaGlyLeuAlaArg 200  
DB 612 AAGACGAGGCTGCGCAATGCGCTGATGGCCGATACCTGGGCAAGCGCGCTGCGCT 671  
QY 201 ValPheIleGlyIleAsnAspLeuGluIlyArgGluGlyAlaPheValTyrSerAspIleSer 220  
DB 672 GTCTTCATCGGCATACGACCTGAGAGAGAGGCGCTTGTGTACTGTGACCATCTCC 731  
QY 221 ProMetArgThrPheAsnIleTyrArgSerGlyGluProAsnAsnAlaTyrAspGluGlu 240  
DB 732 CCCATGCGGACCTTCAACAAAGTGGCGGACGCGGTGAGCCCAACATGCTTACGACAGAGAG 791  
QY 241 AspCysValGluMetValAlaSerGlyTyrTrpAsnAspValAlaCysHisThrThrMet 260  
DB 792 GACTGCGTGGAGATGTGGCTCGGAGCGCTGGAAACGACGTGGCTGCACACCACTATG 851  
QY 261 Tyr-PheMetCysGluPheAspIlyArgIleAsnMet 271  
DB 852 TACTTCATGTGTGAGTTTGAACAAGAGAACATG 885

RESULT 4  
 BX427124 1083 bp mRNA linear EST 04-MAY-2004  
 LOCUS BX427124 Homo sapiens FETAL LIVER Homo sapiens cDNA clone  
 DEFINITION CS0DM08Y118 5-PRIME, mRNA sequence.  
 ACCESSION BX427124  
 VERSION BX427124.2 GI:47002248  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 1083)  
 AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT On May 15, 2003 this sequence version replaced gi:30774621.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 Evry cedex - France  
 Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library  
 was not normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen.  
 This sequence belongs to sequence cluster 1719.f  
 For more information about this cluster, see  
 http://www.genoscope.cns.fr/cdna?b=CS0AM08D090P1&c=1719.f.  
 Location/Qualifiers  
 1. 1083  
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 /clone="CS0DM08Y118"  
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 /dev\_stage="fetal"  
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 was primed with a NotI-oligo(dT) primer. Five prime end  
 enriched, double-strand cDNA was digested with Not I and  
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6  
 vector. Library was not normalized."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 2.57e-119 Length: 1083  
 Score: 1384.00 Matches: 266  
 Percent Similarity: 98.15% Conservative: 0  
 Best Local Similarity: 98.15% Mismatches: 5  
 Query Match: 96.04% Indels: 1  
 DB: 5 Gaps: 0

US-09-806-277a-6 (1-271) x BX427124 (1-1083)  
 QY 1 MetArgGlyAenLeuAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeuLeu 20  
 Db 92 ATGAGGGGGAGATCTGGCCCTGTGGGCGTTCTTAATCAAGCCCTGCTCTCTCACTGCTG 151  
 QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCySerValGlnIleLeuValPro 40  
 Db 152 CCATCTGGACATCTCTCAAGCCGCTGGCGCATACCGCTCTGTGCAGATCTCTGTCCT 211  
 QY 41 G1yleuLySg1yAaPaLaG1yG1uLySg1yAaPlySg1yAlaProG1yAaRgProG1yAaRg 60  
 Db 212 GGCTCTCAAAAGGAGATCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 271  
 QY 61 ValG1yProThrG1yG1uLySg1yAaPwMetG1yAaPlySg1yG1uLySg1ySerValG1y 80  
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 QY 81 ArgHisG1yValIleG1yProIleG1ySerIySg1yG1uLySg1yAaPserG1yAaPile 100

Db 332 CGTCATGAGAAATGTCCTCCATTTGGCTTAAGAGTGAGAGAGAGATTCGGTGACATA 391  
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 Db 392 GAGACCCCTGTCTTAATGAG 451  
 QY 121 AlaIleG1yLumeAaPaenGlnValSerG1yLeuThrSerG1yLeuLySg1yPheIleLyS 140  
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 Db 572 AAGGCTACCGGAG 631  
 QY 181 LyAaPAlaValaAaenG1yLumeAaPAlaA1aThrLeuAlaG1yLeuAlaAaRg 200  
 Db 632 AAGGAGAGAGCTCCATATGAGCTGATGCGCGCATACCTGCGGAGAG-6GCTGCGCCGT 690  
 QY 201 ValPheIleG1yIleAaPaPLeuG1yG1uLySg1yAlaPheValIySerAaPHisSer 220  
 Db 691 GTCCTCATCGGATCAACGAG 750  
 QY 221 ProMetArgThrPheAenIySg1yTrpAaRserG1yG1uProAaPAlaIyAaPAlaG1u 240  
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 QY 241 AspCySerValG1uMetValaAaSerG1yG1yTrpAaPAlaValaCyHisIsthThMet 260  
 Db 811 GACTGCGTGAGATGAGTGGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 870  
 QY 261 TyrPheMetCySg1yPheAaPlySg1yAaMet 271  
 Db 871 TACTTCATGTGTAGTTKACAG 903

RESULT 5  
 BX333394 1078 bp mRNA linear EST 07-APR-2004  
 LOCUS BX333394 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens  
 DEFINITION CS0DC024Y19 5-PRIME, mRNA sequence.  
 ACCESSION BX333394  
 VERSION BX333394.2 GI:46262347  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 1078)  
 AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT On May 1, 2003 this sequence version replaced gi:30308204.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 Evry cedex - France  
 Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library  
 was not normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 1719.f  
 For more information about this cluster, see  
 http://www.genoscope.cns.fr/cdna?b=CS0DC024Y19P1&c=1719.f.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CS0DC024Y19"

FEATURES  
 source





## COMMENT

Please visit our web site (<http://genome.gsc.riken.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5'-GAGAGAGAGAGCGCCGCACTCGAGTTTCTTTTCTTTT 3']. cDNA was prepared by using Crealase thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to R0 = 5.0. Second strand cDNA was prepared with the primer adapter of sequence [5'-GAGAGAGAGAGCGCCGCACTCGAGTTTCTTTTCTTTT 3']. cDNA was cleaved with XhoI and SclI. Cloning sites, 5' end: SclI; 3' end: XhoI. Host: SOLR.

## FEATURES

## source

Location/Qualifiers  
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/tissue\_type="heart"  
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/dev\_stage="adult"  
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/db\_xref="GI:12833584"  
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## CDS

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/note="putative"  
1362..1367  
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polya\_site  
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ORIGIN

## Alignment Scores:

Pred. No.: 3.24e-114 Length: 1383  
Score: 1331.00 Matches: 249  
Percent Similarity: 96.31% Conservative: 12  
Best Local Similarity: 91.88% Mismatches: 10  
Query Match: 92.37% Indels: 0  
Gaps: 0

US-09-806-277A-6 (1-271) x AK003121 (1-1383)

QY 1 MetcrgtgaenleuAlaleuValGlyValleulleterleuAlapheleuSerleu 20  
Db ATGATGAGGACCGGCTCTTGACGAGCATGCTGATTGACCTGCTCTCTCTCTG 143  
QY 21 ProserglYHsPProglInProAlagLYAspAspAlaCyseerValGlnleleuValPro 40  
Db 144 CCACTTGATGATCTCTTCAGCAGACCAACAGGACCGCTGCTGTGCAATTCCTGCTCCT 203  
QY 41 G1yleuysgLYAspAlagLYGlyLyslysgLYAspLYsLYAlaProglYArgProglYArg 60  
Db 204 GGCTCTAAAGGCGATGACAGAGAAAGGAGACAAAGAGCCCAAGAGCGCCAGAGAA 263  
QY 61 ValAlYProthrgLYGlyLysLYAspMetLYAspLYsLYGlyLYsLYsLYsLYsLYsLY 80  
Db 264 GTCGGCCCTACAGAGAAAGAGACATGCGGAGCAAGAGACAGAAAGGACATGCGGC 323  
QY 81 ArghieglYsLYleglYProleglYserLYsLYGlyLYsLYsLYsLYsLYsLYsLYsLYs 100

Db 324 CGCCATGAGAAAATTGGTCCCATTTGGCGCAAAAGGTGAAAAGAGATTCTGGGATATC 383

QY 101 G1YProFrogLYProAngLYGlyProGLYLeuProCYsGLYsLYsLYsLYsLYsLYsLYs 120

Db 384 GAGACCCCTGGCCCGGAGGAGAACTGGATTCATGATGATGATGATGATGATGATGATG 443

QY 121 AlAlleglYleuMetAspAngLYsLYsLYsLYsLYsLYsLYsLYsLYsLYsLYsLYsLYs 140

Db 444 GCTATTGGGAGATGAGCAACAGGTCTCACTGACCTGACCTGACCTGACCTGACCTGAC 503

QY 141 AsAlaValAlagLYValArgLYsLYsLYsLYsLYsLYsLYsLYsLYsLYsLYsLYsLYs 160

Db 504 AATGCTCTTCTGGCGCGCGCGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 563

QY 161 LysArgTYrAlaAspAlagLYsLYsLYsLYsLYsLYsLYsLYsLYsLYsLYsLYsLYs 180

Db 564 AAGCGTACCGAGATGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 623

QY 181 LysAspGLYAlaAlaAngLYLeuMetAlaAlaTYrleuAlaGlnAlaGlyLeuAlaArg 200

Db 624 AAAGACAGAGCAGCAGATGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 683

QY 201 ValPhe1leglY1leAspAspLeuGlyLYsLYsLYsLYsLYsLYsLYsLYsLYsLYsLYs 220

Db 684 GTCTTCATCGGTATCAATGACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 743

QY 221 ProMetArgThrPheAspLYsLYsLYsLYsLYsLYsLYsLYsLYsLYsLYsLYsLYs 240

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QY 241 AspCYsValGlnMetValAlaSerGLYLYsLYsLYsLYsLYsLYsLYsLYsLYsLYsLYs 260

Db 804 GACTGTGAGATGAGTGGCTGAGGCTGAGAAATGATGCTGCTCCCATTTACATG 863

QY 261 TyrPheMetCYsGLYsLYsLYsLYsLYsLYsLYsLYsLYsLYsLYsLYsLYsLYsLYs 271

Db 864 TACTTCATGTCGAGATTGACAAAGAGAACTTG 896

RESULT 7  
LOCUS B0927000 962 bp mRNA linear EST 20-AUG-2002

DEFINITION AGENCOURT\_8804355 NIH\_MGC\_47 Homo sapiens cDNA clone IMAGE:6377965

ACCESSION B0927000 BQ927000.1 GI:22342031

VERSION BQ927000.1 GI:22342031

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [egads@femail.nih.gov](mailto:egads@femail.nih.gov)  
Tissue Procurement: ATCC  
cDNA Library Preparation: Rubin Laboratory  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: LICM2562 row: j column: 14  
High quality sequence stop: 616.

## FEATURES

## source

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 /note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
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 adaptor: GGCACGAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
 Score: 4.53e-112 Length: 962  
 1306.00 Matches: 262  
 Percent Similarity: 96.03% Conservative: 4  
 Best Local Similarity: 94.58% Mismatches: 5  
 Query Match: 90.63% Indels: 6  
 DB: 5 Gaps: 0

US-09-806-277a-6 (1-271) x BQ927000 (1-962)

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 DB 72 ATGAGGGGGAATCTGCGCTGCTGAGCGCTTCAATCAGCTGCGCTTCTGCTGCTG 131  
 QY 21 ProSerGlyAHPProGlnProAlaGlyAHPAAspAlaCysSerValGlnIleLeuValPro 40  
 DB 132 CCATCTGGACATCTTCAGCGCGCTGCGCATGACGCTGCTGTGTCAGATCTCTGCTCCT 191  
 QY 41 GYLeuLYGlyAAspAlaGlyGlyLeuLYGlyAAspLYGlyAAspProGlyArg 60  
 DB 192 GGCCTCAAGGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 251  
 QY 61 ValGlyProThrGlyGlyLeuLYGlyAAspMetGlyAAspLYGlyGlyGlySerValGly 80  
 DB 252 GTCCGCCCCACCGGAG 311  
 QY 81 ATGAGTAAATLeuValAGTValLeuLeuSerLeuAlaPheLeuSerLeu 100  
 DB 312 CGTCAATGAGAAATTCGCTCCATTCGCTCAATGAGAGAGAGAGAGAGAGAGAGAG 371  
 QY 101 GYLeuProGlyProAAspGlyGlyLeuProGlyGlyLeuProGlyGlyLeuArg 120  
 DB 372 GAGACCCCTGCTCTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 431  
 QY 121 ATGAGTAAATLeuValAGTValLeuLeuSerLeuAlaPheLeuSerLeu 140  
 DB 432 GGCATCGGGGAGATGAG 491  
 QY 141 AAspAlaValAlaGlyValArgGlyLeuArgGlyLeuArgGlyLeuValArg 160  
 DB 492 AATGCTGCTGCGCGGTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 551  
 QY 161 LYAAspGlyValAlaAspAlaGlyLeuSerGlyGlyGlyGlyGlyGlyGlyGlyGly 180  
 DB 552 AAGCGCTAGCGGAG 611  
 QY 181 LYAAspGlyValAlaAspAlaGlyLeuSerGlyGlyGlyGlyGlyGlyGlyGlyGly 200  
 DB 612 AAGGAG 671  
 QY 201 ValI-PheIleGlyIleAspAlaGlyLeuValArgGlyLeuValArgGlyLeuVal 219  
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 QY 220 SerProMetArgThrPheLeuValArgGlyGlyLeuProAAspAlaGlyArgGly 239  
 DB 732 TCCCCCATCGGAGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 791  
 QY 240 GUAAspCys-ValGlyMetValAlaSerGlyGlyTrpAAspValAlaCysHisThr 259

DB 792 GANAGACTGCTTGGAAATGATGCTGCGGCGCTGGAGAGACATGCTGCCACACCAC 851

QY 259 rMetTYrPhe-MetCysGlu-PheAspLYGlyLeuMet 271

DB 852 ATGTACTTCATATGAGGAGAGATTGACAGAGAGAGATG 890

## RESULT 8

CR599770

LOCUS CR599770 1150 bp mRNA linear HTC 21-JUL-2004

## DEFINITION

Full-length cDNA clone CSDDC018Y07 of Neuroblastoma Cot

## ACCESSION

CR599770.1 GI:50480577

## VERSION

CR599770.1

## KEYWORDS

HTC; CNSLT; cDNA.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

## REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## AUTHORS

Li W.B., Gruber C., Jesssee J. and Polayes D.

## TITLE

Full-length cDNA libraries and normalization

## JOURNAL

Unpublished

## REMARK

Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/InvitrogenCorporation1600

## REFERENCE

Genoscope. 2 (bases 1 to 1150)

## AUTHORS

Direct Submission

## TITLE

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)

## JOURNAL

- Web : www.genoscope.cns.fr

## COMMENT

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

## FEATURES

Location/Qualifiers

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1. 1150

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## FEATURES

/tissue\_type="Neuroblastoma Cot 25-normalized"

## FEATURES

/plasmid="pCMVSPORT\_6"

## ORIGIN

Alignment Scores:

## ORIGIN

Score: 4.25e-110 Length: 1150

## ORIGIN

1286.00 Matches: 247

## ORIGIN

Percent Similarity: 91.14% Conservative: 0

## ORIGIN

Best Local Similarity: 91.14% Mismatches: 0

## ORIGIN

Query Match: 89.24% Indels: 24

## ORIGIN

DB: 3 Gaps: 1

## ORIGIN

US-09-806-277a-6 (1-271) x CR599770 (1-1150)

QY 1 MetATGAGTAAATLeuValAGTValLeuLeuSerLeuAlaPheLeuSerLeu 20  
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 QY 21 ProSerGlyAHPProGlnProAlaGlyAHPAAspAlaCysSerValGlnIleLeuValPro 40  
 DB 157 CCATCTGGACATCTTCAGCGCGCTGCGCATGACGCTGCTGTGTCAGATCTCTGCTCCT 216  
 QY 41 GYLeuLYGlyAAspAlaGlyGlyLeuLYGlyAAspLYGlyAAspProGlyArg 60  
 DB 217 GGCCTC----- 222  
 QY 61 ValGlyProThrGlyGlyLeuLYGlyAAspMetGlyAAspLYGlyGlyGlySerValGly 80  
 DB 223 -----AAGAGAGACATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 264  
 QY 81 ATGAGTAAATLeuValAGTValLeuLeuSerLeuAlaPheLeuSerLeu 100

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Db      265  COTGATGAAAAATGTGTCATTCATTCGCTTAAGGTGAGAAAGAGATTCCGGTGACTA 324
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Qy      121  AATAGTGTGCGGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 140
Db      385  GCGATCGGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAG 444
Qy      141  AenAlaValAlaGlyValArgGluThrgLuserGlyLeuValLeuValGluGlu 160
Db      445  AATGCTGTGCGGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 504
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Db      505  AAGCGCTACGGGAGAGCCGACCTGTCTGCGAGGCGCCGCGGAGGAGCCTGAGC 564
Qy      181  LysAenGlyAlaAlaAenGlyLeuMetAlaAlaTyrLeuAlaGlnAlaGlyLeu 200
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Qy      221  ProMetArgThrPheAenLysTyrArgSerGlyGluProAenAenAlaTyrAen 240
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Qy      241  AspCysValGluMetValAlaSerGlyTyrTyrAenAenValAlaCysHisThr 260
Db      745  GACTGCGTGAAGTGTGCTCGGCGGCTGGAACAGAGTGGCTGCAACACCATG 804
Qy      261  TyrPheMetCysGluPheAenAenAenAenAenAenAenAenAenAenAenAen 271
Db      805  TACTTCATGTGTGATTTGACAGAGAAACATG 837
RESULT 9      834 bp      mRNA      linear      EST 01-JUL-2004
LOCUS      CO398423      834 bp      mRNA      linear      EST 01-JUL-2004
DEFINITION  AGNCOURT 27822626 NIH MGC 252 Rattus norvegicus cDNA clone
VERSION     CO398423
ACCESSION  CO398423
KEYWORDS   EST.
SOURCE     Rattus norvegicus (Norway rat)
ORGANISM   Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE  1 (bases 1 to 834)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: gsdbs-remail.nih.gov
            Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical
            College of Wisconsin
            cDNA Library Preparation: Express Genomics
            DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://image.llnl.gov
            Plate: LLM15348 row: d column: 17
            High quality sequence stop: 666.
            Location/Qualifiers
            1. 834
FEATURES
SOURCE

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Tissue was snap-frozen adn transferred in -70C. RNAse free
for the entire procedure"
/lab_host="DH10B TONa"
/clone_1lb="NIH_MGC_252"
/notes="Organ: ovary; Vector: pDONR 201, Site1: NotI,
Site2: NotI; RNA obtained from female ovaries animals at
8 wk old. Tissues were snap-frozen and kept at -80C for
two days before RNA extraction and purification
(Tri-reagent method). cDNA was primed using oligo-dt
primer: 5'-pGACTGATCTTCTGATCGGAGCGGCGCCCTT-3' and
cloned into the EcoRV/NotI sites of pEXpress-1.
Size-selection >1.25kb resulted in an average insert size
of 1.7kb. This primary library is not normalized
(normalized library is NIH MGC 252) and was constructed by
Express Genomics (Frederick, MD). Note: this is a NIH_MGC
library"

ORIGIN
Alignment Scores:
Pred. No.:      4,35e-95      Length:      834
Score:          1124.00      Matches:      220
Percent Similarity: 91.86%      Conservative: 17
Best Local Similarity: 85.27%      Mismatches: 17
Query Match:      78.00%      Indels:      6
DB:              Gaps:      2

US-09-806-277a-6 (1-271) x CO398423 (1-834)
Qy      18  SerLeuLeuProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIle 37
Db      1  TCCTCTGTCATCTGATGATGTCCTCCAGAGAGCCAGAGAGAGCCCTGCTCGTGCAGATT 60
Qy      38  LeuValProGlyLeuLysGlyAspAlaGlyGluLysGlyGlyGlyGlyGlyGlyGly 57
Db      61  CTGTGCTCCCGGCTTCAAGAGGAGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
Qy      58  ProGlyArgValGlyProThrgLysGlyLysGlyAspMetGlyAspLysGlyGlnLys 77
Db      121  CCAAGAGAGTGTGCGCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 180
Qy      78  SerValGlyArgHisGlyLysIleGlyProIleGlySerLysGlyGlyGlyAspSer 97
Db      181  ACTGTGGGCGCCATGAGAAATTTGCTCCATTGGCGCAAAAGGTGAAAGAGAGATTCT 240
Qy      98  GlyAspIleGlyProProGlyProAenGlyGluProGlyLeuProGlyCysSerGln 117
Db      241  GGTGACATCGAGACCCCTGTGCTCCAGTGAAGAACTGTGATTCATGTGATGACAGC 300
Qy      118  LeuArgLysAlaIleGlyGluMetAenAenValSerGlnLeuThrsGlnLeuLys 137
Db      301  CTGAGAGAGGCTATTGTGGAGATGATTAACAGAGTCACTCACTGACCACTGAGATAAA 360
Qy      138  PheIleLysAsnAlaValAlaGlyValArgGluThrgLuserGlyLeuValLeuVal 157
Db      361  TTCTATAAAAATGCTTGTCTGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Qy      158  LysGluGlyLysArgTyrAlaAenAlaGlnLuserCysGlnGlyArgGlyGlyThrLeu 177
Db      421  AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Qy      178  SerMetProLysAenGlyAlaAlaAenGlyLeuMetAlaAlaTyrLeuAlaGlnAla 197
Db      481  AGCATGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Qy      198  LeuAlaArgValPheIleGlyTyrLeuAenAenAenGlyGlyGlyGlyGlyGlyGly 217
Db      541  CTGGCTCGGCTCTTCACTTGTGATGACCTGAGAGAGAGAGAGAGAGAGAGAGAG 600

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QY 218 Asph1SerPromeArGThrPheasnlySTrPaSerglyGluPProAsnAlaYr 237  
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 QY 238 Aspg1uAspCyseValGluMetValAlaSerGlyGlyTrpAsn-----AspVal 254  
 Db 660 GATGAGAGAGACTGTGTGAGATGTGTGCTCAGT-GGCTGGACGATGTGCTGCACATT 718  
 QY 255 AlaCyse---HsrThThMetEyrThMetCyseGluPheAspGluAsnMet 271  
 Db 719 ACATGTACTCATGTGAGTTGACAGAGACTGTGAGNCAGACGGAACGNCCTC 772  
 RESULT 10  
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 LOCUS BX394893 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens  
 DEFINITION CDNA clone CS0DC024YP19 3-PRIME, mRNA sequence.  
 ACCESSION BX394893  
 VERSION BX394893.2 GI:46921106  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 1095)  
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT On May 13, 2003 this sequence version replaced gi:30628356.  
 CONTACT: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and Ecor V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 1719.f  
 For more information about this cluster, see  
 http://www.genoscope.cns.fr/cdnas?CS0DC024CH1ONP1&c=1719.f.  
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 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and cloned into the Not I and Ecor V  
 sites of the pCMVSPORT 6 vector. Library was normalized."  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 7,06e-93 Length: 1095  
 Score: 1102.00 Matches: 236  
 Percent Similarity: 93.28% Conservative: 0  
 Best Local Similarity: 93.28% Mismatches: 16  
 Query Match: 76.47% Indels: 8  
 DB: 5 Gaps: 0  
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 QY 20 LeuPProSerGlyHisProGlnProAlaGlyAspAspAlaCyseSerValGlnIleuVal 39  
 Db 1042 CTGCCATCTGCA-CACTCTACGCCGCTGC-GATGAGC-TGCTCTGTGTGCAAGTCTCTGTC 986  
 QY 40 ProGlyLeuLysGlyAspAlaGlyGlyGlyAspLysGlyVala-ProGlyAyrProG 59  
 Db 985 CTGGCCTCAAGAGGGATCGGAGAGAGAGACAAAGGCGCCCGCGAGCGGCTGG 926

QY 59 YArValGlyProThrGlyGlyLysGlyAspMetGlyAspLysGlyGlyLysSerVa 79  
 Db 925 AAGAGTGGGCCCCACGGGAGAAAGAGACATGGGGGACAAAGAGACAGAAAGGACAGT 866  
 QY 79 LGLYARGHIGLYLysIleGlyProIleGlySerLysGlyGlyLysGlyAspSerGlyAs 99  
 Db 865 GGGTGTGATGAAATAATGTTGCTCCATGTGCTTAAGGTGAGAAAGAGATTTCCGGTGA 806  
 QY 99 pLIleGlyProProGlyProAsnGlyGlyProGlyLysProGlyLysSerGlnLeuAr 119  
 Db 805 CATGAG-CCCCCTGCTCTTAATGAGAACCGGCTCCCATGTAGTGCAG-ACCAGCG 748  
 QY 119 GLYAlaIleGlyLysLysMetAspAsnGlnValSerGlnLeuThrSerGlnLeuLysPhe1 139  
 Db 747 CAAGGCCATCGGGAGATGACCAACAGTCTCTCAGGTGACCGAGGCTCAAGTTCAT 688  
 QY 139 eLYAsnAlaValAlaGlyValArgLysLysLysLysLysLysLysLysLysLysG 159  
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 QY 159 uGLuLYArGlyTrpAlaAspAlaGlnLeuSerCyseGlyGlyValArgLysLysLysSerMe 179  
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 QY 179 tProLYAspGlyLysAlaAsnGlyLysMetAlaAlaTyrLeuAlaGlnAlaGlyLysAl 199  
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 Db 510 CCGTCTCTTCATCGGCATCAACGACTGAGAGAGAGGCGCTTCGTTGCTGACCA 451  
 QY 219 sSerPromeArGThrPheasnlySTrPaSerglyGluPProAsnAlaYrAspG 239  
 Db 450 CTCCCAATGGAGCTTCAACAAAGTGGCGAGGCGCAACATGCTTCAGACA 391  
 QY 239 uGLAspCyseValGluMetValAlaSerGlyGlyTrpAsnAspValAlaCyseHisThrTh 259  
 Db 390 GAGGACCTGCTGAGATGTGTGCTGCGGCTGAGAACCACTGCTGCCACACAC 331  
 QY 259 rMetEyrThMetCyseGluPheAspGlyAsnMet 271  
 Db 330 CATGACTTCATGTGTGAGTTGACAGAGACATG 294  
 RESULT 11  
 BX394625 1015 bp mRNA linear EST 01-MAY-2004  
 LOCUS BX394625 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens  
 DEFINITION CDNA clone CS0DC018YD07 5-PRIME, mRNA sequence.  
 ACCESSION BX394625  
 VERSION BX394625.2 GI:46920154  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 1015)  
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT On May 13, 2003 this sequence version replaced gi:30628263.  
 CONTACT: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and Ecor V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 1719.f  
 For more information about this cluster, see  
 http://www.genoscope.cns.fr/cdnas?CS0DC018CB04QP1&c=1719.f.

FEATURES  
source

Location/Qualifiers  
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/organism="Homo sapiens"  
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/clone="CSODC018YD07"  
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/clone\_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-cligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

## Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
9,896-93	1015	225	1	21	27	1
Score:	1100.00					
Percent Similarity:	82.78%					
Best Local Similarity:	82.42%					
Query Match:	76.34%					

US-09-806-277a-6 (1-271) x BX394625 (1-1015)

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Db 97 ATGAGGGGGAATCTGGCCCTGCTGCTTAATCACTGCGCTTCTCTCACTGCTG 156
QY 21 ProSerGlyHisProGlnProAlaGlyAsp AspAlaCysSerValGlnIleLeuValPr 40
Db 157 CCATCTGGACATCTCCACCGCGCTGGCCAAAGACGCCCTGCTGTGCMWCCCTGCTCC 216
QY 40 GGLYLeuYsgLYAspAlaGlyGlyValGlyAspLYsgLYAlaProGlyArgProGlyAr 60
Db 217 TGGCCTCAAGAGAGACMTG----- 235
QY 60 gValGlyProThrGlyGlyGlyAspMetGlyAspLYsgLYGlyGlySerValG 80
Db 236 -----GGGGMCMWGMGCMGCCCGGAGMGTGCG 264
QY 80 YArgHISGlyYsIleGlyProIleGlySerLYsgLYGlyGlyAspSerGlyAsp 100
Db 265 TCGTCATGAAATAATGCTCCATTCCTTAAGAGTGAAGAGATTCGGGTGACAT 324
QY 100 eGlyProProGlyProAsnGlyGlnProGlyLeuProCysGlyGlyCysSerGlnLeuArg 120
Db 325 AGGACCCCTGCTCTTAATGAGAAACAGGCTCCCATGTATGTTCAAGCCAGCTGCGCA 384
QY 120 sAlaIleGlyIleuMetAspAsnGlnValSerGlnLeuThrSerGlyLeuYsPheIle 140
Db 385 GGCCTATCGGGAGATGAGCAACAGGTCTCTCACTGACCAAGCGCTCAAGTTCACTCA 444
QY 140 sAsnAlaValAlaGlyValArgGlyThrGlySerLYsIleGlyLeuValLYsg 160
Db 445 GAAATGCTGTCCCGGTGTGCGGAGACGAGAGCAAGATCTAAGCTGCTGGAAGAGAG 504
QY 160 uLYsArgTYsAla AspAlaGlnLeuSerCysGlnGlyArgGlyGlyThreusertw 180
Db 505 GAAGCGCTACCGCGAGACCCCAAGCTGTCTCTGCAAGGCGGCGGCGGCGCTGAGCA 564
QY 180 rOLYsAspGlyAlaAlaAsnGlyLeuMetAlaAlaTYsLeuAlaGlnAlaGlyLeuAla 200
Db 565 CCAAGAGAGAGAGCTGCGCAATGCGCTGATGCGCGCATCTGCGCGM ACGGCGCTGCGCC 623
QY 200 rGValPheIleGlyIleAsnAspLeuGlyGlyGlyValAlaPheValTYsSerAspHis 220
Db 624 GTGCTTCATCGGATCAACACCTGAGAGAGAGGCGCTGCTGATCACTGACCACT 683
QY 220 eTPrometArgThPheAsnLYsTYsArgSerGlyGlnProAsnAspAlaTYsArg 240
Db 684 CCCCATGCGGAGCTTCMACAGTGGCGCAGGTCGAGCCCMACATGCTTACAGACAGG 743
QY 240 lueAspCysValGlyIleuMetValaSerGlyGlyTYsAsnAspValAlaCysHisThrTh 260

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Db

744 AGGACCTGCGTGGAGATGATGTCCTCGGCGGCTGGAGCAGAGTGGCTGCGACACCA 803

QY

260 eTYrPheMetCysGlyPheAspLYsgLYsennet 271

Db

804 TGTACTTCATGTGTGTAAGTGTGACAGAGACAATG 838

## RESULT 12

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Bi198782 823 bp mRNA linear EST 10-JUL-2001  
602759819F1 NIH\_MGC\_19 Homo sapiens cDNA clone IMAGE:4895213 5',  
mRNA sequence.  
Bi198782  
Bi198782.1 GI:14653803  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 823)  
NIH-MGC http://mgs.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strauberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov  
Plate: LNCMI780 row: e column: 06  
High quality sequence stop: 752.

## FEATURES

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/clone\_lib="NIH\_MGC\_19"  
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EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCAAGAG(G). Library constructed by Ling Hong  
in the laboratory of Gerald W. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC library."

## ORIGIN

## Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
1,176-92	823	233	1	6	33	3
Score:	1098.00					
Percent Similarity:	85.71%					
Best Local Similarity:	85.35%					
Query Match:	76.20%					

US-09-806-277a-6 (1-271) x Bi198782 (1-823)

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Db 70 ATGAGGGGGAATCTGGCCCTGCTGCTTAATCACTGCGCTTCTCTCACTGCTG 129
QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40
Db 130 CCATCTGGACATCTCAAGCGGCTGCGGATGAGCGCTGCTGTGCAAGATCTGCTCT 189
QY 41 GLYLeuYsgLYAspAlaGlyGlyValGlyAspLYsgLYAlaProGlyArgProGlyArg 60
Db 190 GGCCTC----- 195

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QY 61 ValGlyProThrGlyGluValGlyAspMetGlyAspGlyGlyGlySerValGly 80  
 Db 196 -----AAAGAGACATGGGGACAAAGAGACAGAGAGCGATGGGT 237  
 QY 81 ArgHISGlyValGlyProIleGlySerIleGlyGlyValGly-GlyAspSerGlyAsp11 100  
 Db 238 CGTCATGGAAAAATTGGTCCCATTTGGCTTAAGGTGAGAACAGAGATTCGGTGACAT 297  
 QY 100 eGlyProProGlyProAsnGlyGluProGlyLeuProGlyGlySerGlyLeuArgly 120  
 Db 238 AGGACCCCTGGTCTCTAATGAGAACAGAGCCCTCCCATGTGATGACAGCAGCTCGCAA 357  
 QY 120 sAlaIleGlyIleMetAspAsnGlyValSerGlyLeuThrSerGlyLeuValPheIlely 140  
 Db 358 GGCACATCGGGAGATGAGACACAGGCTCTCACTGACACAGAGCTCAATTCATCA 417  
 QY 140 sAsnAlaValAlaGlyValArgGlyThrGlySerIleIleIleLeuValGlyGly 160  
 Db 418 GAATGCTGTGGCGGGGTGGCGAGACGAGACAGAAATCTGCTGTGTAAAGAGGA 477  
 QY 160 uIlyArgIleValAspAlaGlyLeuSerGlyGlyGlyGlyGlyGlyThrLeuSerMetEpr 180  
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 DEFINITION CDNA clone CS0DC018Y07 3-PRIME, mRNA sequence.  
 ACCESSION BX394624  
 VERSION BX394624.2 GI:46877297  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 1071)  
 L1, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 Full-length cDNA libraries and normalization  
 Unpublished (2001)  
 On May 13, 2003 this sequence version replaced gi:30624327.  
 CONTACT: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seque@genoscope.cns.fr; Web: www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 1719.f  
 For more information about this cluster, see

FEATURES  
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 sites of the pCMVSPORT 6 vector. Library was normalized."  
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 Best Local Similarity: 83.27% Mismatches: 18  
 Query Match: 74.39% Indels: 27  
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 QY 29 GlyAspAspAlaCysSerValGlnIleLeuValProGlyLeuValGlyAspAlaGlyGlu 48  
 Db 966 GCGCATACGCTGTCTGTGTGCAATCTCTGCTCCCTGCGCTC----- 925  
 QY 49 LysGlyAspGlyGlyAlaProGlyArgProGlyArgValGlyProThrGlyGlyGly 68  
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 QY 69 AspMetGlyAspIleGlyGlyGlySerValGlyArgHISGlyValGlyProIle 88  
 Db 918 GACAT-GGGGACAAAGAACAGAAAGAGTGGGTCTTCATGAAAAATTGGTCCCAT 860  
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 Db 739 TTCTCTCAGCTGACGAGGCGTCAAGTTCATCAAAA-GGTGTGCGCGGTGGCGAG 681  
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 Db 441 CGCAGCGGTGAGCCCAACATGCTTACAGACGAGAGAGCTGGGTGAGATGGTGGCTCG 382



Qy 249 G1yG1yTTPaenAepValAlaCyshIshThrMetTyPheMetCyGluPheAspIys 268  
Db 381 GCGCGCTGGAACGAGCTGGCTGCGCACACCACTGATCTCATGTGTGAGTTTGACAAAG 322  
Qy 269 GluAenMet 271  
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DEFINITION mRNA sequence.  
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VERSION BP311981.1 GI:11259754  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 788)  
AUTHORS NIH-MGC http://mgs.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-remail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov  
Plate: L1CM1018 row: 0 column: 07  
High quality sequence stop: 703.  
Location/Qualifiers  
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/note="Organ: brain; Vector: pOT37; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Library constructed by Ling Hong  
in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

ORIGIN  
Alignment Scores:  
Pred. No.: 8.93e-90 Length: 788  
Score: 1067.00 Matches: 224  
Percent Similarity: 92.98% Conservative: 1  
Best Local Similarity: 92.56% Mismatches: 12  
Query Match: 74.05% Indels: 7  
DB: 2 Gaps: 1

US-09-806-277a-6 (1-271) x BP311981 (1-788)

Qy 1 MetAArgGlyAenLeuAlaLeuValG1yValLeuIleSerLeuAlaPheLeuSerLeu 20  
Db 75 ATGAGGGGGGAATCGGCCCTGTGAGCGCTTTAAATCAGCCCTGCGCTTCCTGCTCACTCGT 134

Qy 21 ProSerGlyHisProGlnProAlaG1yAspAspAlaCySerValGlnIleLeuValPro 40  
Db 135 CCATCTGGACATCTCTCAGCGCGCTGCGCATACCGCTCTGTGTGACATCTCTGCTCCT 194

Qy 41 G1yLeuIysG1yAspAlaG1yGluIysG1yAspIysG1yAlaProG1yArgProG1yArg 60

Db 195 GCGCTCAAGAGGAGTGGCGGAGAGAAAGAGACAAAGCGCCCGGACGCGCTTGAGAA 254  
Qy 61 ValG1yProThrG1yGluIysG1yAspMetG1yAspIysG1yGlnIysG1ySerValG1y 80  
Db 255 GTCGGCCCGACAGGAGAGAGAGACATGGGGAGCAAGAGACAGAAAGCGATGTGGGT 314  
Qy 81 ArgH1sG1yIysI1eG1yProI1eG1ySerIysG1yGluIysG1yAspSerG1yAspI1e 100  
Db 315 GGTCTATGAAAATTTGTTGCTCCATTTGCTCTAAAGGTAGAAAGAGATTTCCGATGATTA 374

Qy 101 G1yProProG1yProAenG1yGluProG1yLeuProCyG1yLucySerGlnLeuArgIys 120  
Db 375 GAGACCCCTGGTCTTATGAGAAACAGCGCTCCCATGTAGTGCACAGCTCGCAAG 434

Qy 121 AlalIeG1yGluMetAspAenGlnValSerGlnLeuThrSerGluLeuIysPheI1eIys 140  
Db 435 GCGATCGGGAGATGAGCAACAGGTCTTCACCTGACGACGACGACGATTCATCAAG 494

Qy 141 AspAlaValAlaG1yValArgG1yThrG1ySerIysI1eTyI1eLeuValIysGlu-G1 160  
Db 495 AATGCTTCCCGCGGTGTGCGCGAGACGAGAGCAAGATCTACTGCTGTGAGAGAGGA 554

Qy 160 U1yAspArgTyAlaAspAlaGlnLeuSerCyG1yArgG1yG1yThrLeuSerMetPr 180  
Db 555 GAAGCGCTACGCGGACGCGCAGCTGTCTCCAGGGCGCGGGGGCACGCTGAGACATGCC 614

Qy 180 U1yS-AspG1uAlaAlaAspG1yLeuMetAlaI1eI1eAlaG1yI1eAlaG1yLeuAla 200  
Db 615 CAAGTACGAGGCTGCCAAGGCGCTGTAGCCCATACCTGCGGCAAGCGCGCTGGGCC 674

Qy 200 rGValPheI1e-G1yI1eAspLeuG1yI1eG1yGluIys-G1yG1yAlaPheValTySerAspH1 219  
Db 675 GTGCTTTCATCGGCGATCAACGACTGTGAGAACGAGAGGGCGCTCTGTAACTGACCA 734

Qy 219 sSerProMetArgThrPheAsnIysI1eTyArgSerG1yGluProAsnAlaTyAsp 238  
Db 735 ATCCCATGCGGAC--CTTCACAAAGTGGCGCAC-GGTGAGCCA---AATGCTACGAC 786

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LOCUS BM547424  
DEFINITION AGENCOURT\_6507753 NIH\_MGC\_125 Homo sapiens cDNA clone IMAGE:5724382  
5', mRNA sequence.  
ACCESSION BM547424  
VERSION BM547424.1 GI:18781180  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1094)  
AUTHORS NIH-MGC http://mgs.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-remail.nih.gov  
Tissue Procurement: Invitrogen  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: L1AM12713 row: 1 column: 23  
High quality sequence stop: 619.  
Location/Qualifiers  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5724382"  
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/clone\_1lb="NIH\_MGC\_125"



/note="Organ: ovary (pool of 3) ; Vector: pCMV-Sport6;  
Site 1: EcorV (destroyed) ; Site 2: NotI; RNA source pool  
of three ovaries, from females ranging in age from 38 to  
49 yo. Library is oligo-dT primed and directionally cloned  
(EcorV site is destroyed upon cloning). Average insert  
size 2.1 kb, insert size range 1-3.5 kb. Library is  
normalized and enriched for full-length clones and was  
constructed by C. Gruber (Invitrogen). Research Genetics  
tracking code 036."

## ORIGIN

## Alignment Scores:

Pred. No.:	2.57e-86	Length:	1094
Score:	1032.00	Matches:	235
Percent Similarity:	72.11%	Conservative:	8
Best Local Similarity:	69.73%	Mismatches:	17
Query Match:	71.62%	Indels:	77
DB:	4	Gaps:	3

US-09-806-277a-6 (1-271) x BMS47424 (1-1094)

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QY      21 ProSerGIYHleProGIProAlaGIYAAspAlaCYsSerValGlnIleLeuValPro 40
DB      102 CCAATTTGACATCTTCAAGCCGCTGGCCATGACGCTTGTGTCAAGATCTCTGTCCT 161
QY      41 G1YLeuLYsGIYAAspAlaG1YGLYsGIYAAspLYsG1YAlaProG1YARsProG1YARg 60
DB      162 GGCCTCAAAAGGGGATCGCGGAGAGAAAGGAGACAAAGGGGCCCCCGGACGGCTTGAAAG 221
QY      61 ValG1YProThrG1YGLYsG1YAspMetG1YAspLYsG1YGLYsG1YSerValG1Y 80
DB      222 GTCCGCCCCACGGGAGAAAGAGACATGGGGGACAAAGACAGAAAGCGCATGTGGGT 281
QY      81 ArgH1sG1YLYsI1eG1YProI1eG1YSerLYsG1YGLYsG1YAspSerG1YAspI1e 100
DB      282 CGTCTATGAAAAAATTGGTCCCTTGGCTTAAAGGTGAGAAAGAGATTCCGGTACATA 341
QY      101 G1YProProG1YProAsnG1YGLYPro----- 109
DB      342 GGAACCCCTGGTCTTAATGAGAAACAGGCTCTTGGGACCGCAGATGAGAGAAAG 401
QY      109 ----- 109
DB      402 GCTGCTTGAAGTGTGCTTGGCGGTGTGACTTGGCTGAGTGTGAGTGGCTGAGATCAG 461
QY      109 ----- 109
DB      462 TGTCACTGACTGGCCGAGAGCATCCGCTCAGGGGCACTCCAGGCACTCAGCCAACTGA 521
QY      110 -----G1YLeuProCYsG1YCyase 116
DB      522 GGGGGCCGGACAAAGCCTCTGTGGAGACAGAAAGACCTGAGAGCCTCCCATGTGATGCAG 581
QY      116 TGI1eLeuArgLYsAlaI1eG1YGLYsG1YMetAspAsnGlnValSerGlnLeuThrSerG1Y 136
DB      582 CCAGCTGCGCAAGGCGCATCGAGATGAGACAAACAGGCTCTCTCAGCTGACCAAGAGAGCT 641
QY      136 ulYsPheI1eLYsAsnAlaValAlaG1YValArgLYsG1YLeuThrG1YSerLYsI1eTYrLeu 156
DB      642 CAAGTTCAACAAGATGTGTGCGCGGTGTGCGCGAGACGAGACAAAGATCTTACTGCT 701
QY      156 uValYsG1YGLYsArgTYrAlaAspAlaGlnLeuSer--CYsGlnG1YARg--G1YGLY 175
DB      702 GGTGAAGAGAGAAACGCTACGCGGACGCCCAAGCTGTCTTGGCAGGCCCCGGGGGGG 761
QY      176 ThrLeuSerMetProLYsAspG1YAlaAlaAsnG1YLeuMetAlaIaTYrLeuAla--G1 195
DB      762 ACCCTGACATGCCCCAAGAGACGAGGCTGCAATGCGCTGATGCGCGCATACCTGCGCCGA 821

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QY      195 nAlaG1YLeu-AlaArgValPheI1eG1YI1eAsnAspLeuG1YLYsG1YAla-Phe 214
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QY      215 ValTYrSer-AspH1sSerProMetArgThrPheAsnLYsTrp--ArgSerG1YGLYPr 233
DB      882 CGTACTCTGGACCACTCCCCCATGCGGAACTTCAACAAATGGCGGCAACGGGGGAAACC 941
QY      233 CAAsnAlaTYr--AspG1YGLYsValGlu--MetValAlaSerG1YGLY--Tr 251
DB      942 CACCAATGCTATGCAACCAAGAGAAATGCTGCAAAATTGTGGGCTTGGGCGGCTTG 1001
QY      251 PAsn-AspValAlaCYsH1sThrThrMet 260
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Job time : 3874 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 16, 2004, 20:47:53 ; Search time 8739 Seconds  
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Title: US-09-806-277A-13

Perfect score: 1253  
Sequence: 1 gggggcagctgtccctcgcggg.....gtcaagtcacaaaaaaaaa 1253

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4526729 seqs, 23644849745 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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9: gb\_pr:.\*  
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13: gb\_un:.\*  
14: gb\_vt:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1230	98.2	1238	6	AR252616 Sequence
2	1230	98.2	1238	6	AX403469 Sequence
3	1230	98.2	1238	6	AX454582 Sequence
4	1230	98.2	1238	6	AX491060 Sequence
5	1230	98.2	1238	9	AY358439 Homo sapi
6	1217	97.1	1248	9	BC000078 Homo sapi
7	1132	90.3	1341	6	BD103302 Novel col
8	949	75.7	1139	6	BD103303 Novel col
9	948	75.7	1139	6	BC009951 Homo sapi
10	879	70.2	1269	6	BD103330 Novel col
11	877	70.0	1067	6	BD103305 Novel col
12	813	64.9	813	6	BD103332 Novel col
13	807	64.4	1067	6	BD103306 Novel col
14	807	64.4	1197	6	BD103329 Novel col
15	807	64.4	1269	6	BD103331 Novel col
16	805	64.2	995	6	BD103304 Novel col
17	733	58.5	139357	9	AC010907 Homo sapi
18	685	54.7	735	6	BD103333 Novel col
19	615	49.1	741	6	BD103340 Novel col

20	613	48.9	663	6	BD103336 Novel col
21	543	43.3	663	6	BD103337 Novel col
22	543	43.3	669	6	BD103339 Novel col
23	543	43.3	741	6	BD103341 Novel col
24	541	43.2	591	6	BD103335 Novel col
25	477	38.1	477	6	BD103334 Novel col
26	425	33.9	708	6	CO716215 Sequence
27	342	27.3	619	6	BD103308 Novel col
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29	118	9.4	273	11	G24618 human STS w
30	50	4.0	89	6	AX920471 Sequence
31	50	4.0	89	6	BD056004 Sequence
32	31	3.2	813	6	BD103338 Novel col
33	40	3.2	1522	6	BD103307 Novel col
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35	38	3.0	246539	2	AC125638 Rattus no
36	36	2.9	36	6	AX403585 Sequence
37	36	2.9	36	6	AX403585 Sequence
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39	28	2.2	28	6	AR252703 Sequence
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45	22	1.8	22	6	AX403583 Sequence

#### ALIGNMENTS

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LOCUS AR252616 1238 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 356 from patent US 6478825.  
ACCESSION AR252616  
VERSION AR252616.1 GI:27300524  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1238)  
AUTHORS Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.  
TITLE Implant, method of making same and use of the implant for the  
treatment of bone defects  
JOURNAL Patent: US 6478825-A 356 12-NOV-2002;  
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source Location/Qualifiers  
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DB 1 GCGACGGGACAGACGCCCCGTTGCGCTTAGCGCGTCTCAGAGTTGTGTCTTGGCTTGG 60  
QY 84 CTCAGATGAGGGGGAATCTGGCCCTGGTGGGCGTTCTTAACACCTGGGCTTCTCTGCA 143  
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QY 204 GTTCCTGGCTCTCAAGAGGAGATGCGGAGAGAAAGGAGCAAAAGGCCCCCGGACGGCT 263  
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Db      241  GGAAGAGTCGGCCCGACCGAGAGAAAAAGAGCATGGGGAGCAAAAGAGCAGAAAGGCACT 300
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Qy      444  CGCAAGCCCATGGGAGATGACCAAGGCTCTTCACTGACCTGACCAAGGCTCAAGTTC 503
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Qy      504  ATCAAGATGCTGTGCGCGGTGTGGCGAGACGAGACCAAGATTAATCTCTGTGTAG 563
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Qy      564  GAGAGAACCGCTACGCGGACGCGCCAGCTGTCTTCCAGGCGCGCGGGGAGCAAGCTGAGC 623
Db      541  GAGAGAACCGCTACGCGGACGCGCCAGCTGTCTTCCAGGCGCGCGGGGAGCAAGCTGAGC 600
Qy      624  ATGCCCAAGACGAGGCTGCGCAATGGCTGTATGCGCGCATACCTGCGCAAGCCGCGCTG 683
Db      601  ATGCCCAAGACGAGGCTGCGCAATGGCTGTATGCGCGCATACCTGCGCAAGCCGCGCTG 660
Qy      684  GCCCGTCTTCAATGCGGATCAACGACCTGAGAAAGAGAGGCGCGCTTGTATCTTAC 743
Db      661  GCCCGTCTTCAATGCGGATCAACGACCTGAGAAAGAGAGGCGCGCTTGTATCTTAC 720
Qy      744  CACTCCCCCATGCGGACCTTCAACAAAGTGGCGAGCGGTGAGCCCAATGCTTACGAC 803
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Qy      804  GAGAGAGCTGCGTGGAGATGTGGCTTCGCGCGGCTGGAACGAGTGGCTTGCACACC 863
Db      781  GAGAGAGCTGCGTGGAGATGTGGCTTCGCGCGGCTGGAACGAGTGGCTTGCACACC 840
Qy      864  ACATGATCTTCAATGAGATTGAGCAAGAGAAACATGTAGGCTCAAGGCTGGGGCTGC 923
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Qy      984  CAGCCAGGAGACTGTCTCTGTGAAGGTGAGGCTCACTGATGAGGGCTGTGTCT 1043
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RESULT 2
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LOCUS
DEFINITION
Sequence 356 from Patent WO0073454.
ACCESSION
AX403469

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VERSION      AX403469.1  GI:21436970
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
1
Aabkenazi, A.J., Baker, K.P., Botstein, D., Desnovers, L., Baton, D.,
Ferrara, N., Gerber, H., Gertlisen, M., Goddard, A., Godowski, P.,
Grimaldi, C.O., Gurney, A.L., Kljavin, I., Napier, M.A., Pan, J.,
Paoni, N.F., Roy, M., Stewart, T.A., Tuma, D., Watanabe, C.K.,
Williams, P., Wood, W.I. and Zhang, Z.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL
Patent: WO 0073454-A 356 07-DEC-2000;
Genentech Inc. (US)
FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
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Query Match      98.2%; Score 1230; DB 6; Length 1238;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
24  GCGACGGGCGAGAGACCCCGTGGCTTACGCGCTGCTCAGAGTGGTGTCTGCTCGC 83
Db      1  GCGACGGGCGAGAGACCCCGTGGCTTACGCGCTGCTCAGAGTGGTGTCTGCTCGC 60
Qy      84  CTCAGATGAGGGGGAATTCGGCCCTGGTGGGCTTAAATCAAGCCCTGCTCTGCA 143
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Qy      144  CTGCTGCATCTGACATCTCTACCGGCTGGCGATGACGCTCTGTGACATCTC 203
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Db 661 GCCCGTGTCTTCATCGGCATCAAGCACTGGAGGAGGCGCTTCGTGTACTCTAC 720  
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Qy 804 GAGAGGACCTCGTGGAGATGATGATGCTCGGAGCGGCTGGAAGCAAGTGGCTGCAACAC 863  
Db 781 GAGAGGACCTCGTGGAGATGATGATGCTCGGAGCGGCTGGAAGCAAGTGGCTGCAACAC 840  
Qy 864 ACCATGTACTTCATGTGTGAGTTTGAACAAGGAACATGTGAGCTCAGGCTGGGCTGC 923  
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Qy 984 CAGCAGGAGAGCTGTCCTCTGTGAAAGGAGGAGCTCACTGATGAGAGGCTGTGTCT 1043  
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RESULT 3  
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DEFINITION AX454582  
ACCESSION AX454582.1 GI:21713915  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS 1 Baker, K.P., Ferrara, N., Gerber, H., Gerltzen, M.E., Goddard, A.,  
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,  
Pavoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.  
and Ye, W.  
TITLE Compositions and methods for the diagnosis and treatment of  
disorders involving angiogenesis  
JOURNAL Patent: WO 0208284-A 167 31-JAN-2002;  
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone  
(US) ; Gerber, Hanspeter (US) ; Gerltzen, Mary E. (US) ; Goddard,  
Audrey (US) ; Gurney, Paul J. (US) ; Gurney, Austin L. (US) ;  
Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)  
; Pavoni, Nicholas P. (US) ; Stephan, Jean-Philippe F. (US) ;  
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William  
I. (US)  
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VERSION	AX491060.1		
KEYWORDS	GI:22323867		
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ORGANISM	Homo sapiens (human)		
REFERENCE			
AUTHORS	1 Baker, K.P., Ferrara, N., Geber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gunney, A.L., Hillan, K.J., Marsters, S.A., Pan, J., Pooni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I. and Ye, W.		
TITLE	Compositions and methods for the diagnosis and treatment of disorders involving anglogenesis		
JOURNAL	Patent: WO 0200690-A 167 03-JAN-2002;		
FEATURES	Genentech, Inc. (US)		
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Best Local Similarity	100.0%; Pred. No. 0;		
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REFERENCE	Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,		
AUTHORS	Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,		
	Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Haas,P.E.,		

Heidens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, B., Sanchez, C., Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vages, A., Vandlen, R., Watanabe, C., Wiand, D., Woods, K., Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, M.I., and Godowski, P.  
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment  
Genome Res. 13 (10), 2265-2270 (2003)

JOURNAL  
PUBMED  
12975309  
2 (bases 1 to 1238)  
Clark, H.F.  
Direct Submission  
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA  
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Query Match 98.2%; Score 1230; DB 9; Length 1238;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GCGAGGGGAGGAGCGCCGCTTGCGCTAGCGGCTGCTAGAGATTGGTCTGCTCGG 83  
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1 (bases 1 to 1248)  
Strausberg, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
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Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Uadin, T.B., Toshiyuki, S.,  
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 Abramson, R.D., Muller, S.J., Bosak, S.A., McEwan, P.J.,  
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 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,  
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
 Butlerfield, Y.S., Krzywiński, M.I., Skalska, U., Smalls, D.E.,  
 Scherch, A., Schein, J.R., Jones, S.J. and Marra, M.A.  
 Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

# JOURNAL PUBMED REFERENCE AUTHORS TITLE JOURNAL

## REMARK COMMENT

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>  
 On Aug 20, 2003 this sequence version replaced gi:12652660.  
 Contact: MGC help desk  
 Email: [gcgabs-remail.nih.gov](mailto:gcgabs-remail.nih.gov)  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILML)  
 DNA Sequencing by: Institute for Systems Biology  
<http://www.systembiology.org>  
 contact: [amadan@systembiology.org](mailto:amadan@systembiology.org)  
 Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha  
 Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found  
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Query Match 97.1%; Score 1217; DB 9; Length 1248;  
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DEFINITION Novel collection.  
ACCESSION BD103302  
VERSION BD103302.1 GI:22648876  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1341)  
AUTHORS Wakamiya,N., Keshi,H., Otani,K., Sakamoto,T. and Kishi,Y.  
TITLE Novel collection  
JOURNAL Parent: MO 0181401-A 1 01-NOV-2001;  
FUSO PHARMACEUTICAL INDUSTRIES LTD,NOBUTAKA WAKAMIYA, HIROYUKI  
KESHI, KATSUKI OTANI,TAKASHI SAKAMOTO,YUICHIRO KISHI  
OS Homo sapiens (human)  
PN MO 0181401-A/1  
PD 01-NOV-2001  
PF 23-APR-2001 MO 2001JP003468  
PR 21-APR-2000 JP 00P 120358  
PI NOBUTAKA WAKAMIYA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI PI  
SAKAMOTO,  
PI YUICHIRO KISHI  
CC C07K14/47,C12N15/12,C12P21/02,A01K67/027,C07K16/18,G01N33/53  
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Db 270 GGGGAATCTGGCGCTGTGGGCTTCTAATACAGCTGCGCTTCTGTACTGTGCGCATC 329  
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DEFINITION Novel collection.  
ACCESSION BD103303  
VERSION BD103303.1 GI:22648877  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1139)  
AUTHORS Wakamiya,N., Keshi,H., Otani,K., Sakamoto,T. and Kishi,Y.  
TITLE Novel collection  
JOURNAL Parent: MO 0181401-A 2 01-NOV-2001;  
FUSO PHARMACEUTICAL INDUSTRIES LTD,NOBUTAKA WAKAMIYA, HIROYUKI  
KESHI, KATSUKI OTANI,TAKASHI SAKAMOTO,YUICHIRO KISHI

COMMENT	OS	Homo sapiens (human)
PN	MO 0181401-A/2	
PD	01-NOV-2001	
PF	23-APR-2001 WO 2001JP003468	
PR	21-APR-2000 JP 00P 120358	
PI	NOBUAKA MAKAMITA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI PI SAKAMOTO,	
PI	YUICHIRO KISHI	
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CC	Novel collection	
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ACCESSION			mRNA (CDNA clone MGC:141216 IMAGE:4125795), complete cds.
VERSION			BC009951
KEYWORDS			MGC
ORGANISM			MGC099951.2 GI:33871813
SOURCE			
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REFERENCE			
AUTHORS			Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1417)
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TITLE			12477932
JOURNAL			2 (bases 1 to 1417)
PUBMED			Strauberg, R.
REFERENCE			Submitted
AUTHORS			Submitted (02-JUN-2001) National Institutes of Health, Mammalian
TITLE			Gene Collection (MGC), Cancer Genomics Office, National Cancer
JOURNAL			Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
			USA
REMARK			NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT			On Aug 19, 2003 this sequence version replaced gi:14714411. Contact: MGC help desk Email: cgabbs-r@mail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/ Contact: nisc.mgc@nih.gov Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dierich, N.L., Grant, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legabadi, R.,

Maduro, Q. L., Mastello, C., Maskeri, B., Mastrian, S. D., McCloskey, J. C., McDowell, J., Pearson, R., Stantripp, S., Thomas, P. J., Touchman, J. W., Taurgeon, C., Vogt, J. L., Walker, M. A., Weherby, K. D., Wiggins, L., Young, A., Zhang, L. H. and Green, E. D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILM, at: <http://image.llnl.gov>  
Series: IRL Plate: 20 Row: f Column: 22  
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, similarity but not identity to protein.

## FEATURES

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RESULT 10
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LOCUS BD103330
DEFINITION Novel collection.
ACCESSION BD103330
VERSION BD103330.1
KEYWORDS MO 0181401-A/29.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1269)
AUTHORS Wakamiya, N., Keshi, H., Otani, K., Sakamoto, T. and Kishi, Y.
TITLES Novel collection
JOURNAL Patent: WO 0181401-A-29 01-NOV-2001;
FUSO PHARMACEUTICAL INDUSTRIES LTD, NOBUTAKA WAKAMIYA, HIROYUKI
KESHI, KATSUKI OTANI, TAKASHI SAKAMOTO, YUICHIRO KISHI
OS Homo sapiens (human)
PN MO 0181401-A/29
PD 01-NOV-2001
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PR 21-APR-2000 JP 00P 120358
PI NOBUTAKA WAKAMIYA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI PI
SAKAMOTO,
PI YUICHIRO KISHI
PC C07K14/47, C12N15/12, C12P21/02, A01K67/027, C07K16/18, G01N33/53
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708 GACCTGAGAGAGAGAGGCGGCTTGTGTAATCTGACCACTCCCATGCGAGACCTTGAC 767  
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811 GACCTGAGAGAGAGAGGCGGCTTGTGTAATCTGACCACTCCCATGCGAGACCTTGAC 870

768 AAGTGGCAGAGCAGTGAAGCCCAACATGCTTAACAGAGAGAGACTGCGTGAAGATGGTG 827  
Db AAGTGGCAGAGCAGTGAAGCCCAACATGCTTAACAGAGAGAGACTGCGTGAAGATGGTG 930

871 AAGTGGCAGAGCAGTGAAGCCCAACATGCTTAACAGAGAGAGACTGCGTGAAGATGGTG 930

828 GCTTGGGGGGCTGGAAGCAGCTGAGCTGCGCAGACCAATGTAATGATGTGAGATT 887  
Db GCTTGGGGGGCTGGAAGCAGCTGAGCTGCGCAGACCAATGTAATGATGTGAGATT 990

931 GCTTGGGGGGCTGGAAGCAGCTGAGCTGCGCAGACCAATGTAATGATGTGAGATT 990

888 GACCAAGAGAAATGAGAGCTCAGAGCTGAGGAGCTCCCATGAGGAGGAGCCCAATGCTCC 947  
Db GACCAAGAGAAATGAGAGCTCAGAGCTGAGGAGCTCCCATGAGGAGGAGCCCAATGCTCC 1050

991 GACCAAGAGAAATGAGAGCTCAGAGCTGAGGAGCTCCCATGAGGAGGAGCCCAATGCTCC 1050

948 GACAGGATGGCAGAGCAGAGCCCAACATGCTTAACAGAGAGAGACTGCGTGAAGATGGTG 1007  
Db GACAGGATGGCAGAGCAGAGCCCAACATGCTTAACAGAGAGAGACTGCGTGAAGATGGTG 1110

1051 GACAGGATGGCAGAGCAGAGCCCAACATGCTTAACAGAGAGAGACTGCGTGAAGATGGTG 1110

1008 AAGGATGAGAGCTCAGTGAAGAGAGCTGTTGTCTAAATCTGAGAAATGAGCTATGCTT 1067  
Db AAGGATGAGAGCTCAGTGAAGAGAGCTGTTGTCTAAATCTGAGAAATGAGCTATGCTT 1170

1111 AAGGATGAGAGCTCAGTGAAGAGAGCTGTTGTCTAAATCTGAGAAATGAGCTATGCTT 1170

1068 AAGAGAGAAATGAAAGTGTCTGAGGAGTCTGCTCTGAGAGAGAGAGATTTCATTAATCT 1127  
Db AAGAGAGAAATGAAAGTGTCTGAGGAGTCTGCTCTGAGAGAGAGAGATTTCATTAATCT 1230

1171 AAGAGAGAAATGAAAGTGTCTGAGGAGTCTGCTCTGAGAGAGAGAGATTTCATTAATCT 1230

1128 GATATTGATAGCCCAATGCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1166  
Db GATATTGATAGCCCAATGCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1269

1231 GATATTGATAGCCCAATGCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1269

RESULT 11  
BD103305 1067 bp DNA linear PART 27-AUG-2002  
LOCUS BD103305  
DEFINITION Novel collection.  
ACCESSION BD103305  
VERSION BD103305.1 GI:22648879  
KEYWORDS WO 0181401-A/4.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
1 (bases 1 to 1067)  
AUTHORS  
TITLE  
JOURNAL  
Wakamiya,N., Keshi,H., Otani,K., Sakamoto,T. and Kishi,Y.  
Novel collection  
Patent: WO 0181401-A 4 01-NOV-2001;  
FUSO PHARMACEUTICAL INDUSTRIES LTD,NOBUTAKA WAKAMIYA,HIROYUKI  
KESHI, KATSUKI OTANI,TAKASHI SAKAMOTO,YUICHIRO KISHI  
COMMENT  
OS Homo sapiens (human)  
PI WO 0181401-A/4  
PD 01-NOV-2001  
PE 23-APR-2001 WO 2001JP003468  
PR 21-APR-2000 JP 00P 120358  
PI NOBUTAKA WAKAMIYA,HIROYUKI KESHI,KATSUKI OTANI,TAKASHI PI  
SAKAMOTO,  
YUICHIRO KISHI  
PC C07K14/47,C12N15/12,C12P21/02,A01K67/027,C07K16/18,G01N33/53  
CC Novel collection Location/Qualifiers  
FH Key (141)..(803).  
FT CDS Location/Qualifiers  
1..1067  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Query Match 70.0%; Score 877; DB 6; Length 1067;  
Best Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0;  
Matches 877; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

290 AGAGAGCATGGGGGACAAAGAGCAGAAAGCAGTGTGGTCTCATGAAAAATTGGTCC 349  
Db AGAGAGCATGGGGGACAAAGAGCAGAAAGCAGTGTGGTCTCATGAAAAATTGGTCC 250

191 AGAGAGCATGGGGGACAAAGAGCAGAAAGCAGTGTGGTCTCATGAAAAATTGGTCC 250

350 CATTGGCTTAAAGGTGAGAAAGAGATTCCTGGTACATAGAACCCCTGGTCTTAATGG 409  
Db CATTGGCTTAAAGGTGAGAAAGAGATTCCTGGTACATAGAACCCCTGGTCTTAATGG 310

251 CATTGGCTTAAAGGTGAGAAAGAGATTCCTGGTACATAGAACCCCTGGTCTTAATGG 310

410 AGAACAGAGCCTCCCATGTGAGTGCAGAGCAGCTGCGCCCAAGAGCCATGAGAGATGAGCA 469  
Db AGAACAGAGCCTCCCATGTGAGTGCAGAGCAGCTGCGCCCAAGAGCCATGAGAGATGAGCA 370

311 AGAACAGAGCCTCCCATGTGAGTGCAGAGCAGCTGCGCCCAAGAGCCATGAGAGATGAGCA 370

470 CCAAGTCTCTCAGCTGACAGCAGAGCTCAAGTTCAATCAAGATGCTGTGCGCGGTGG 529  
Db CCAAGTCTCTCAGCTGACAGCAGAGCTCAAGTTCAATCAAGATGCTGTGCGCGGTGG 430

371 CCAAGTCTCTCAGCTGACAGCAGAGCTCAAGTTCAATCAAGATGCTGTGCGCGGTGG 430

530 CGAGAGCAGAGCAGAAATCTAATCTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 589  
Db CGAGAGCAGAGCAGAAATCTAATCTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 450

431 CGAGAGCAGAGCAGAAATCTAATCTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 450

590 GCTGTCTGCGAGAGGCGCGGAGGAGCAGCTGAGCAGATGCGCCAGAGAGAGAGAGAGAGAG 649  
Db GCTGTCTGCGAGAGGCGCGGAGGAGCAGCTGAGCAGATGCGCCAGAGAGAGAGAGAGAGAG 550

491 GCTGTCTGCGAGAGGCGCGGAGGAGCAGCTGAGCAGATGCGCCAGAGAGAGAGAGAGAGAG 550

650 CTTGATGAGCAGATCTGAGCAGAGCGGAGCTGAGCGCTGAGCTTCAATCGGCATCAACGA 709  
Db CTTGATGAGCAGATCTGAGCAGAGCGGAGCTGAGCGCTGAGCTTCAATCGGCATCAACGA 610

551 CTTGATGAGCAGATCTGAGCAGAGCGGAGCTGAGCGCTGAGCTTCAATCGGCATCAACGA 610

710 CTTGAGAGAGAGAGGCGCGCTTGTGTAATCTGTAACCACTCCCATGAGGAGAGAGAGAGAG 769  
Db CTTGAGAGAGAGAGGCGCGCTTGTGTAATCTGTAACCACTCCCATGAGGAGAGAGAGAGAG 670

611 CTTGAGAGAGAGAGGCGCGCTTGTGTAATCTGTAACCACTCCCATGAGGAGAGAGAGAGAG 670

770 GTGGCGAGCGGTGAGGCGCCCAATGCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 829  
Db GTGGCGAGCGGTGAGGCGCCCAATGCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 730

671 GTGGCGAGCGGTGAGGCGCCCAATGCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 730

830 CTGGGCGGCTGGAACAGAGCTGCTGCGCAGACCAATGTAATCTTCAATGTGTGAGTTGA 889  
Db CTGGGCGGCTGGAACAGAGCTGCTGCGCAGACCAATGTAATCTTCAATGTGTGAGTTGA 790

731 CTGGGCGGCTGGAACAGAGCTGCTGCGCAGACCAATGTAATCTTCAATGTGTGAGTTGA 790

890 CAAAGAGAAATGAGAGCTCAGGCTGAGGAGCTGCGCCATTTGAGGAGGAGAGAGAGAGAG 949  
Db CAAAGAGAAATGAGAGCTCAGGCTGAGGAGCTGCGCCATTTGAGGAGGAGAGAGAGAGAG 850

791 CAAAGAGAAATGAGAGCTCAGGCTGAGGAGCTGCGCCATTTGAGGAGGAGAGAGAGAGAG 850

Qy 950 AGGGTTGGCAGGAGCAGAGCCAGACATGTCGACGACGAGACCTGCTCCCTGTGTAA 1009  
Db 851 AGGGTTGGCAGGAGCAGAGCCAGACATGTCGACGACGAGACCTGCTCCCTGTGTAA 910  
Qy 1010 GGGTGGAGGCTCACTGATAGAGGCGCTGTGTCTAACTGAGAAATAGGCTATCTTAA 1069  
Db 911 GGGTGGAGGCTCACTGATAGAGGCGCTGTGTCTAACTGAGAAATAGGCTATCTTAA 970  
Qy 1070 GAGGAAATGAAAGTGTCTCTGGGGTGTCTGTCTGAAAGACAGATTTCAATCACTGT 1129  
Db 971 GAGGAAATGAAAGTGTCTCTGGGGTGTCTGTCTGAAAGACAGATTTCAATCACTGT 1030  
Qy 1130 ATTGTAGCCCAATGCTAT 1166  
Db 1031 ATTGTAGCCCAATGCTAT 1067

RESULT 12  
BD103332 813 bp DNA linear PAT 27-AUG-2002  
LOCUS BD103332 Novel collectin.  
DEFINITION BD103332  
ACCESSION BD103332.1 GI:22648906  
VERSION WO 0181401-A/31.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 813)  
AUTHORS Wakemiyu,N., Keshi,H., Otani,K., Sakamoto,T. and Kishi,Y.  
TITLE Novel collectin  
JOURNAL Patent: WO 0181401-A 31 01-NOV-2001;  
FUSO PHARMACEUTICAL INDUSTRIES LTD,NOBUTAKA WAKAMIYA, HIROYUKI  
KESHI, KATSUKI OTANI,TAKASHI SAKAMOTO, YUICHIRO KISHI  
OS Homo sapiens (human)  
PN WO 0181401-A/31  
PD 01-NOV-2001  
PF 23-APR-2001 WO 2001JP003468  
PR 21-APR-2000 JP 00P 120358  
PI NOBUTAKA WAKAMIYA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI PI  
SAKAMOTO,  
PI YUICHIRO KISHI  
PC C07K14/47,C12N15/12,C12P21/02,A01K67/027,C07K16/18,G01N33/53  
CC Novel collectin  
FH key  
FT source  
FT Location/Qualifiers  
1. 813  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="caxon:9606"

FEATURES  
Source  
1. 813  
Location/Qualifiers  
1. 813  
/organism="Homo sapiens (human)".

ORIGIN  
Query Match 64.9%; Score 813; DB 6; Length 813;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 90 ATGAGGGGGAATCTGGCCCTGGTGGCGCTTCAATCAGGCTGGCCCTGCTCACTGCTG 149  
Db 1 ATGAGGGGGAATCTGGCCCTGGTGGCGCTTCAATCAGGCTGGCCCTGCTCACTGCTG 60  
Qy 150 CCATCTGACATCTCAAGCCGGCTGGCGATGACGCGCTGCTGTGACATCTCTCTCCT 209  
Db 61 CCATCTGACATCTCAAGCCGGCTGGCGATGACGCGCTGCTGTGACATCTCTCTCCT 120  
Qy 210 GGCCTCAAAAGGGGATGCGGGAGAGAAAGGAGCAAAAGGCGCCCGGAGCGGCTTGAAGA 269  
Db 121 GGCCTCAAAAGGGGATGCGGGAGAGAAAGGAGCAAAAGGCGCCCGGAGCGGCTTGAAGA 180  
Qy 270 GTCCGCCCAACGGAGAAAAGAGACATGGGGGACAAAGAGACAGAAAGGACGTGGGGT 329

Db 181 GTCCGCCCAACGGAGAAAAGAGACATGGGGGACAAAGAGACAGAAAGGACGTGGGGT 240  
Qy 330 CCTCATGGAATAAATTGGTCCCATTTGGCTTAAAGTGAAAGAGATTTCCGGTGACATA 389  
Db 241 CGTCATGGAATAAATTGGTCCCATTTGGCTTAAAGTGAAAGAGATTTCCGGTGACATA 300  
Qy 390 GGACCCCTGGTCTCAATGAGAAACAGGCGCTCCCATGATGATGAGCAGCAGCTGGCGAAG 449  
Db 301 GGACCCCTGGTCTCAATGAGAAACAGGCGCTCCCATGATGATGAGCAGCAGCTGGCGAAG 360  
Qy 450 GCCATCGGGAGATGAGCAACAGGCTCTCTGAGTGAACAGCAGGCTCAAGTTCAATCAAG 509  
Db 361 GCCATCGGGAGATGAGCAACAGGCTCTCTGAGTGAACAGCAGGCTCAAGTTCAATCAAG 420  
Qy 510 AATGCTGTGCGCGGTGTGCGGAGACGAGAGCAAGATCTACCTGTGTGTAAGAGAGAG 569  
Db 421 AATGCTGTGCGCGGTGTGCGGAGACGAGAGCAAGATCTACCTGTGTGTAAGAGAGAG 480  
Qy 570 AAGGCTTACGGGAGACGCCAGCTGTCTGCGCAAGGGCGCGGGGGGACGCTGAGCATGCCC 629  
Db 481 AAGGCTTACGGGAGACGCCAGCTGTCTGCGCAAGGGCGCGGGGGGACGCTGAGCATGCCC 540  
Qy 630 AAGGAGAGGCTGGCAATGAGCTGTGATGAGCCGATACCTGAGCGCAAGCCGAGCTGGCCGT 689  
Db 541 AAGGAGAGGCTGGCAATGAGCTGTGATGAGCCGATACCTGAGCGCAAGCCGAGCTGGCCGT 600  
Qy 690 GTCTTCATCGGCATCAACGACCTGTGAGAGAGAGAGGCGGCTTGTGATCTTGAACCACTCC 749  
Db 601 GTCTTCATCGGCATCAACGACCTGTGAGAGAGAGAGGCGGCTTGTGATCTTGAACCACTCC 660  
Qy 750 CCATGAGGAGCCTTCAACAGATGGGCGAGCGGTGAGCCCAACATGCTTACAGAGAGAG 809  
Db 661 CCATGAGGAGCCTTCAACAGATGGGCGAGCGGTGAGCCCAACATGCTTACAGAGAGAG 720  
Qy 810 GACTGCGTGAAGATGATGAGCTGCGGCGGCTGGAACGACGCTGCGCACACCATG 869  
Db 721 GACTGCGTGAAGATGATGAGCTGCGGCGGCTGGAACGACGCTGCGCACACCATG 780  
Qy 870 TACTTCATGTGTGAGTTGACAGAGAAACATG 902  
Db 781 TACTTCATGTGTGAGTTGACAGAGAAACATG 813

RESULT 13  
BD103306 1067 bp DNA linear PAT 27-AUG-2002  
LOCUS BD103306 Novel collectin.  
DEFINITION BD103306  
ACCESSION BD103306.1 GI:22648880  
VERSION WO 0181401-A/5.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 1067)  
AUTHORS Wakemiyu,N., Keshi,H., Otani,K., Sakamoto,T. and Kishi,Y.  
TITLE Novel collectin  
JOURNAL Patent: WO 0181401-A 5 01-NOV-2001;  
FUSO PHARMACEUTICAL INDUSTRIES LTD,NOBUTAKA WAKAMIYA, HIROYUKI  
KESHI, KATSUKI OTANI,TAKASHI SAKAMOTO, YUICHIRO KISHI  
OS Homo sapiens (human)  
PN WO 0181401-A/5  
PD 01-NOV-2001  
PF 23-APR-2001 WO 2001JP003468  
PR 21-APR-2000 JP 00P 120358  
PI NOBUTAKA WAKAMIYA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI PI  
SAKAMOTO,  
PI YUICHIRO KISHI  
PC C07K14/47,C12N15/12,C12P21/02,A01K67/027,C07K16/18,G01N33/53  
CC Novel collectin  
FH key  
FT CDS  
FT Location/Qualifiers  
1(41)..(803).

FEATURES  
Location/Qualifiers  
1(41)..(803).

## SOURCE

1. 1067  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 64.4%; Score 807; DB 6; Length 1067;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 807; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

360 AAAGGTGAGAAAGAGATTCGGTGCATAGAACCCCTGGTCTTAATGAGAAACAGGC 419  
Db AAAGGTGAGAAAGAGATTCGGTGCATAGAACCCCTGGTCTTAATGAGAAACAGGC 320  
420 CTCCCATGTGATGATGACAGCTGGGCAAGCCATCGGGAGATGAGAACACAGGTCTCT 479  
Db CTCCCATGTGATGATGACAGCTGGGCAAGCCATCGGGAGATGAGAACACAGGTCTCT 380  
480 CAGGTGACCAAGGAGCTCAAGTTCTCAAGATGCTGCGGGTGTGCGGAGACGGAG 539  
Db CAGGTGACCAAGGAGCTCAAGTTCTCAAGATGCTGCGGGTGTGCGGAGACGGAG 440  
540 AGCAAGATCTACCTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 599  
Db AGCAAGATCTACCTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 500  
600 CAGGGCCCGGGGGGAG 659  
Db CAGGGCCCGGGGGGAG 560  
660 GCATACCTGCGGCAAGCGGCTGGCCCGGTCTTTCATCGGCATCAACGACTGGAGAG 719  
Db GCATACCTGCGGCAAGCGGCTGGCCCGGTCTTTCATCGGCATCAACGACTGGAGAG 620  
720 GAGGGCGCTTGTGTACTCTGACCACTTCCCATCGGACCTTCAACAGTGGCGGAC 779  
Db GAGGGCGCTTGTGTACTCTGACCACTTCCCATCGGACCTTCAACAGTGGCGGAC 680  
780 GGTGAGCCCAACAGCTTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 839  
Db GGTGAGCCCAACAGCTTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 740  
840 TGGAAAG 899  
Db TGGAAAG 800  
900 ATGTGAGCTTCAAGCTTGGGGCTGGCCATTTGGGGGCGCCCACTATGCTGAGAGAG 959  
Db ATGTGAGCTTCAAGCTTGGGGCTGGCCATTTGGGGGCGCCCACTATGCTGAGAGAG 860  
960 GGGACAG 1019  
Db GGGACAG 920  
1020 TCACAG 1079  
Db TCACAG 980  
1080 AAAGGTTCCTGGGGTGTGCTGTGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 1139  
Db AAAGGTTCCTGGGGTGTGCTGTGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 1040  
1140 CAATGTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1166  
Db CAATGTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1067

RESULT 14  
LOCUS BD103329 1197 bp DNA linear PAT 27-AUG-2002  
DEFINITION Novel collectin.  
ACCESSION BD103329  
VERSION BD103329.1 GI:22648903

## KEYWORDS

MO 0181401-A/28.  
SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 1197)  
Makamita, N., Keshi, H., Otsu, K., Sakamoto, T. and Kishi, Y.

## TITLES

Novel collectin  
Patient: MO 0181401-A 28 01-NOV-2001;

FUSO PHARMACEUTICAL INDUSTRIES LTD, NOBUTAKA WAKAMITSU, HIROYUKI

KESHI, KATSUKI OTANI, TAKASHI SAKAMOTO, YUICHIRO KISHI

## COMMENT

OS Homo sapiens (human)

PN MO 0181401-A/28

PP 01-NOV-2001

PR 23-APR-2001

PI 21-APR-2000 JP 00P 120358

PI NOBUTAKA WAKAMITSU, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI PI

## FEATURES

## SOURCE

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

# OM protein - nucleic search, using frame\_plus.p2n model

Run on: December 17, 2004, 03:37:49 ; Search time 588 Seconds  
(without alignments)  
2419.376 Million cell updates/sec

Title: US-09-806-277A-6

Perfect score: 1441

Sequence: 1 MRGNLALVGLISLAFSL.....NDVACHTTMTMCFEFDKEM 271

## Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Command line parameters:

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-DB=N Geneseq.235sep04 -OWT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR.SCORE=pct THR.MAX=100 -THR.MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pco -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=130 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database :

N Geneseq.235sep04:\*  
1: geneseqn1980s:\*  
2: geneseqn1980s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1441	100.0	813	6	ABA91201 Human col
2	1441	100.0	1238	3	Aa265084 Membrane
3	1441	100.0	1238	3	AaC58385 Human PRO
4	1441	100.0	1238	5	AAf44230 Human PRO
5	1441	100.0	1238	6	AbI88155 Human PRO
6	1441	100.0	1238	6	AbI95644 Human ang

7	1441	100.0	1238	8	ACA64399	ACA64399 Novel hum
8	1441	100.0	1238	8	ABX80858	ABX80858 Human sec
9	1441	100.0	1238	8	ACD44367	ACD44367 CDNA enco
10	1441	100.0	1238	8	ABX79538	ABX79538 Human sec
11	1441	100.0	1238	8	ACA93559	ACA93559 Novel hum
12	1441	100.0	1238	8	ABX81241	ABX81241 Novel hum
13	1441	100.0	1238	8	ACA93057	ACA93057 Novel hum
14	1441	100.0	1238	8	ABX17141	ABX17141 Human PRO
15	1441	100.0	1238	8	ACA67996	ACA67996 Novel hum
16	1441	100.0	1238	9	ACA88445	ACA88445 Human sec
17	1441	100.0	1238	9	ACD81952	ACD81952 CDNA enco
18	1441	100.0	1238	9	ADA37867	ADA37867 Human CDN
19	1441	100.0	1238	9	ADA21553	ADA21553 Human CDN
20	1441	100.0	1238	9	ADA10340	ADA10340 Human CDN
21	1441	100.0	1238	9	ADA17884	ADA17884 CDNA enco
22	1441	100.0	1238	9	ADA27992	ADA27992 Human CDN
23	1441	100.0	1238	9	ADA94572	ADA94572 Human CDN
24	1441	100.0	1238	9	ADA38797	ADA38797 Human CDN
25	1441	100.0	1238	9	ADA92918	ADA92918 Human CDN
26	1441	100.0	1238	9	ACH65513	ACH65513 Human CDN
27	1441	100.0	1238	9	ADA22479	ADA22479 Human CDN
28	1441	100.0	1238	9	ACD39503	ACD39503 Human sec
29	1441	100.0	1238	9	ADA06645	ADA06645 Human CDN
30	1441	100.0	1238	9	ADA39338	ADA39338 Human CDN
31	1441	100.0	1238	9	ADB96364	ADB96364 Human PRO
32	1441	100.0	1238	10	ADC57836	ADC57836 Human PRO
33	1441	100.0	1238	10	ADC55200	ADC55200 Human PRO
34	1441	100.0	1238	10	ADC12067	ADC12067 Human CDN
35	1441	100.0	1238	10	ADC56489	ADC56489 Human PRO
36	1441	100.0	1238	10	ADC07544	ADC07544 Human CDN
37	1441	100.0	1238	10	ADC11534	ADC11534 Human CDN
38	1441	100.0	1238	10	ADC14656	ADC14656 Novel hum
39	1441	100.0	1238	10	ADD08188	ADD08188 Novel hum
40	1441	100.0	1238	10	ADD82013	ADD82013 Human PRO
41	1441	100.0	1238	10	ADD07655	ADD07655 Novel hum
42	1441	100.0	1238	10	ADD82546	ADD82546 Human PRO
43	1441	100.0	1238	10	ADD10456	ADD10456 Human sec
44	1441	100.0	1238	10	ADD08726	ADD08726 Novel hum
45	1441	100.0	1238	10	ADD06975	ADD06975 Novel hum

## ALIGNMENTS

RESULT 1	ABA91201	standard; DNA; 813 BP.
ID	ABA91201	standard; DNA; 813 BP.
XX	ABA91201	
AC	ABA91201	
XX	ABA91201	
DT	19-FEB-2002	(first entry)
XX	Human collectin polynucleotide SEQ ID NO 45.	
DE	Human collectin polynucleotide SEQ ID NO 45.	
XX	Human; collectin; Cl-L2-1; Cl-L2-2; mouse; antibacterial; virulence;	
KW	protein therapy; infection; ds.	
XX	Homo sapiens.	
OS	Homo sapiens.	
XX	MO200181401-A1.	
PN	MO200181401-A1.	
XX	01-NOV-2001.	
PD	01-NOV-2001.	
XX	23-APR-2001; 2001WO-JP003468.	
PF	23-APR-2001; 2001WO-JP003468.	
XX	21-APR-2000; 2000JP-00120358.	
PR	21-APR-2000; 2000JP-00120358.	
XX	(FUSO ) FUSO PHARM IND LTD.	
PA	(FUSO ) FUSO PHARM IND LTD.	
XX	Wakamiya N, Keshi H, Ohtani K, Sakamoto T, Kishi Y,	
PI	Wakamiya N, Keshi H, Ohtani K, Sakamoto T, Kishi Y,	
XX	WPI; 2002-055345/07.	
DR	WPI; 2002-055345/07.	
XX	New collectin family proteins, designated Cl-L2-1 and Cl-L2-2, expressed	
PT	New collectin family proteins, designated Cl-L2-1 and Cl-L2-2, expressed	



PR 18-JUN-1998; 98US-0089801P.  
PR 18-JUN-1998; 98US-0089907P.  
PR 18-JUN-1998; 98US-0089908P.  
PR 19-JUN-1998; 98US-0089947P.  
PR 19-JUN-1998; 98US-0089948P.  
PR 19-JUN-1998; 98US-0089952P.  
PR 22-JUN-1998; 98US-0090246P.  
PR 22-JUN-1998; 98US-0090252P.  
PR 22-JUN-1998; 98US-0090254P.  
PR 23-JUN-1998; 98US-0090349P.  
PR 23-JUN-1998; 98US-0090355P.  
PR 24-JUN-1998; 98US-0090423P.  
PR 24-JUN-1998; 98US-0090431P.  
PR 24-JUN-1998; 98US-0090435P.  
PR 24-JUN-1998; 98US-0090444P.  
PR 24-JUN-1998; 98US-0090445P.  
PR 24-JUN-1998; 98US-0090461P.  
PR 24-JUN-1998; 98US-0090472P.  
PR 24-JUN-1998; 98US-0090535P.  
PR 24-JUN-1998; 98US-0090538P.  
PR 24-JUN-1998; 98US-0090540P.  
PR 24-JUN-1998; 98US-0090557P.  
PR 25-JUN-1998; 98US-0090676P.  
PR 25-JUN-1998; 98US-0090678P.  
PR 25-JUN-1998; 98US-0090688P.  
PR 25-JUN-1998; 98US-0090690P.  
PR 25-JUN-1998; 98US-0090691P.  
PR 25-JUN-1998; 98US-0090694P.  
PR 25-JUN-1998; 98US-0090695P.  
PR 25-JUN-1998; 98US-0090696P.  
PR 26-JUN-1998; 98US-0090863P.  
PR 26-JUN-1998; 98US-0090863P.  
PR 01-JUL-1998; 98US-0091358P.  
PR 01-JUL-1998; 98US-0091360P.  
PR 02-JUL-1998; 98US-0091478P.  
PR 02-JUL-1998; 98US-0091486P.  
PR 02-JUL-1998; 98US-0091519P.  
PR 02-JUL-1998; 98US-0091544P.  
PR 02-JUL-1998; 98US-0091626P.  
PR 02-JUL-1998; 98US-0091628P.  
PR 02-JUL-1998; 98US-0091633P.  
PR 02-JUL-1998; 98US-0091646P.  
PR 02-JUL-1998; 98US-0091673P.  
PR 07-JUL-1998; 98US-0091978P.  
PR 07-JUL-1998; 98US-0091982P.  
PR 09-JUL-1998; 98US-0092182P.  
PR 10-JUL-1998; 98US-0092472P.  
PR 20-JUL-1998; 98US-0093339P.  
PR 30-JUL-1998; 98US-0094651P.  
PR 04-AUG-1998; 98US-0095282P.  
PR 04-AUG-1998; 98US-0095285P.  
PR 04-AUG-1998; 98US-0095301P.  
PR 04-AUG-1998; 98US-0095302P.  
PR 04-AUG-1998; 98US-0095318P.  
PR 04-AUG-1998; 98US-0095321P.  
PR 04-AUG-1998; 98US-0095325P.  
PR 10-AUG-1998; 98US-0095916P.  
PR 10-AUG-1998; 98US-0095929P.  
PR 10-AUG-1998; 98US-0096012P.  
PR 11-AUG-1998; 98US-0096143P.  
PR 11-AUG-1998; 98US-0096146P.  
PR 12-AUG-1998; 98US-0096329P.  
PR 17-AUG-1998; 98US-0096757P.  
PR 17-AUG-1998; 98US-0096766P.  
PR 17-AUG-1998; 98US-0096768P.  
PR 17-AUG-1998; 98US-0096773P.  
PR 17-AUG-1998; 98US-0096791P.  
PR 17-AUG-1998; 98US-0096867P.  
PR 17-AUG-1998; 98US-0096891P.  
PR 17-AUG-1998; 98US-0096894P.  
PR 17-AUG-1998; 98US-0096895P.  
PR 17-AUG-1998; 98US-0096897P.  
PR 18-AUG-1998; 98US-0096949P.

PR 18-AUG-1998; 98US-0096950P.  
PR 18-AUG-1998; 98US-0096953P.  
PR 18-AUG-1998; 98US-0096960P.  
PR 18-AUG-1998; 98US-0097022P.  
PR 19-AUG-1998; 98US-0097141P.  
PR 20-AUG-1998; 98US-0097148P.  
PR 24-AUG-1998; 98US-0097661P.  
PR 26-AUG-1998; 98US-0097951P.  
PR 26-AUG-1998; 98US-0097952P.  
PR 26-AUG-1998; 98US-0097954P.  
PR 26-AUG-1998; 98US-0097955P.  
PR 26-AUG-1998; 98US-0097956P.  
PR 26-AUG-1998; 98US-0097974P.  
PR 26-AUG-1998; 98US-0097977P.  
PR 26-AUG-1998; 98US-0097978P.  
PR 26-AUG-1998; 98US-0097979P.  
PR 26-AUG-1998; 98US-0097986P.  
PR 26-AUG-1998; 98US-0098014P.  
PR 31-AUG-1998; 98US-0098525P.  
PR 16-SEP-1998; 98US-0100634P.  
PR 12-JAN-1999; 99US-0115565P.  
XX (GETH ) GENENTECH INC.  
PA  
XX  
PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
PI Wood W, Yuan J;  
XX WPI; 2000-072883/06.  
DR P-PSDB; AAY66738.  
XX  
PT Membrane-bound proteins and related nucleotide sequences.  
XX  
PS Claim 2; Fig 251; 822pp; English.  
XX  
CC The invention provides membrane-bound PRO polypeptides and  
CC polynucleotides encoding them. The PRO sequences of the invention were  
CC identified based on extracellular domain homology screening. The PRO  
CC sequences have homology with proteins including LDL receptors, TIE  
CC ligands and various enzymes. The membrane-bound proteins and receptor  
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
CC immunoadhesins, for instance, can be used as therapeutic agents to block  
CC receptor-ligand interactions. The membrane-bound proteins can also be  
CC employed for screening of potential peptide or small molecule inhibitors  
CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
CC are useful as hybridization probes, in chromosome and gene mapping and in  
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will  
CC also be useful for the preparation of PRO polypeptides, especially by  
CC recombinant techniques  
XX  
SQ Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 3,11e-90 Length: 1238  
Score: 1441.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0  
US-09-806-277A-6 (1-271) x AA265084 (1-1238)  
QY 1 MetAArgGlyAsnLeuAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeu 20  
DB 67 ATGAGGGGGAAATCTGGCCCTGTGGCGCTTAAATCAAGCCCTGCGCTTCTGCACTGCTG 126  
QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
DB 127 CCATCTGGACATCTCTCAAGCCGCGCGATACCGCTGCTGTGCAAGATCTGTCCT 186  
QY 41 GlyLeuLysGlyAspAlaGlyGlyLysGlyAspLysGlyAlaProGlyAspProGlyArg 60  
DB 187 GGCCTCAAGGGGATGCGGGAGAGAGAACAAAGCGCCCGCGCGCTGGAGA 246  
QY 61 ValGlyProThrGlyGlyLysGlyAspMetClyAspLysGlyGlnLysGlySerValGly 80

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Db      247 GTCCGCCCCCGAGGAGAAAAAGACATGGGGGACAAAGACGAAAGGACATGGTGGT
Qy      81 ArgHisGlyIleGlyProIleGlySerIleGlyIleGlyIleGlyIleGlyIle
Db      307 CGTCATGGAAAAATTTGGCTCCATGGCTCTAAAGGTGAAAGAGATTCCGGTGACATA
Qy      101 G1YProGlyProAspGlyIleProGlyIleProGlyIleProGlyIleProGlyIle
Db      367 GGACCCCTGCTCTAAATGAGAACACAGGCTCCCAATGATGATGACACCCAGCTGGCAG
Qy      121 A1a1leGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIle
Db      427 GCCATCGGGAGAGAGACCAACCAAGTCTCTAGCTGACGACGACGACGACGACGACG
Qy      141 AsnAlaValAlaGlyValArgGlyIleGlyIleGlyIleGlyIleGlyIleGlyIle
Db      487 AATGCTGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
Qy      161 LysArgIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle
Db      547 AAGCGCTACCGGAGCGCCAGCTCTCTGCGAGGCGCGCGCGCGCGCGCGCGCGCGCG
Qy      181 LysAspGlyIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle
Db      607 AAGGACGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
Qy      201 ValPheIleGlyIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle
Db      667 GTCTTCTTCGCGACCAACGACCTGAGAGAGAGGCGCGCTTCTGCTGCTGCTGCTGCT
Qy      221 ProMetArgIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle
Db      727 CCCATCGGACCTTCAACCAAGTGGCGAGCGGTAGCCCAACCAAGTGGCGAGGAG
Qy      241 AspCysValGlyIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle
Db      787 GACTGCGTGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
Qy      261 TyrPheMetCysGlyIleIleIleIleIleIleIleIleIleIleIleIleIle
Db      847 TACTTCATGTGTGAGTTGACCAAGAGAACATG 879

```

## RESULT 3

AAC58385

ID AAC58385 standard; cDNA; 1238 BP.

AC AAC58385;

DT 29-JAN-2001 (first entry)

DE Human PRO1182 nucleotide sequence SEQ ID NO:50.

Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;  
 Proliferation; tumorigenesis; identification; cancer; cytostatic;  
 neuroprotection; antiinflammatory; immunosuppressive;  
 immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;  
 neuronal disorder; glioma disorder; astrocytoma disorder; angiogenic;  
 hypochalamic disorder; glandular disorder; macropodag disorder;  
 epithelial disorder; retinal disorder; blastocoele disorder;  
 inflammatory disorder; immunologic disorder; ss.

XX Homo sapiens.

XX MO200053755-A2.

XX 14-SEP-2000.

XX 06-JAN-2000; 2000MO-US000376.

XX 08-MAR-1999; 99MO-US005028.

XX 02-JUN-1999; 99MO-US012252.

XX 23-JUN-1999; 99US-0141037P.

PR 07-JUL-1999; 99US-0143048P.  
 PR 26-JUL-1999; 99US-0145698P.  
 PR 30-NOV-1999; 99MO-US028313.  
 PR 20-DEC-1999; 99MO-US030911.  
 PR 05-JAN-2000; 2000MO-US000219.

XX (GENTH ) GENTECH INC.

XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;

XX Matanabe CK, Wood WI;

XX WPI; 2000-572270/53.

XX P-PSDB; AAB24075.

XX Thirty PRO polynucleotides encoding PRO polypeptides, useful in the

XX treatment, diagnosis and prevention of cancer.

XX Claim 50; Fig 37; 286pp; English.

CC The present invention describes an isolated antibody that binds to one of  
 CC the human PRO proteins designated PRO212, PRO290, PRO341, PRO535, PRO619,  
 CC PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009, PRO1025,  
 CC PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1187,  
 CC PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094, PRO2145 OR  
 CC PRO2198. PRO antagonists can be used to inhibit tumour cell growth. The  
 CC PRO polypeptides and nucleotides are useful in the treatment, diagnosis  
 CC and prevention of cancer. The antibodies and other anti-tumour compounds  
 CC maybe used to treat various conditions, including those characterised by  
 CC overexpression and/or activation of the amplified PRO genes. Exemplary  
 CC conditions or disorders to be treated with such antibodies and other  
 CC compounds include benign or malignant tumours (e.g., renal, liver,  
 CC kidney, bladder, breast, gastric, ovarian, colorectal, prostate,  
 CC pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas,  
 CC lymphoblastomas, and various head and neck tumours), leukaemias and  
 CC lymphoid malignancies, other disorders such as neuronal, gliat,  
 CC astrocytic, hypochalamic and other glandular, macrophageal, epithelial,  
 CC serosal and blastocoele disorders, and inflammatory, angiogenic and  
 CC immunologic disorders. AAC58242 to AAC58366 represent PCR primers and  
 CC hybridisation probes used in the isolation of the human PRO sequences.  
 CC AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human PRO  
 CC polynucleotide and protein sequences given in the exemplification of the  
 CC present invention

XX Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	Length:	Matches:
Score:	3.11e-90	1238
Percent Similarity:	1441.00	271
Best Local Similarity:	100.00%	Conservative: 0
Query Match:	100.00%	Mismatches: 0
DB:	3	Indels: 0
		Gaps: 0

US-09-806-277A-6 (1-271) x AAC58385 (1-1238)

```

Qy      1 MetArgG1YAsnIleuValIleGlyValIleIleSerIleuValIleIleuSerIleu
Db      67 ATAGGGGGAATTTGGCTTGGTGGGCTTCTTAATAGCTGGCTTCTCTGATGCTG
Qy      21 ProSerG1YH1aProGlnProIleGlyIleAspAspAlaCysSerValGlnIleuValPro
Db      127 CCATCTGACATCTCTAGCCGCTGCGATGACGCTGCTCTGTCGATGATCTCTGTCCT
Qy      41 G1YleuIleGlyIleAspAlaGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGly
Db      187 GGCCTCAAGGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
Qy      61 ValG1YProThrGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIle
Db      247 GTGCGCCCAACGGGAGAAAAAGACATGGGGGACAAAGAGAGAGAGAGAGAGAGAG
Qy      81 ArgHisGlyIleIleGlyProIleGlySerIleGlyIleGlyIleGlyIleGlyIle

```

Db 307 CGTATGAAATAATTGTCCTCCATTCGCTCTAAAGGTGAGAAAGAGATTCCGGTGACATA 366  
Qy 101 G1yProPog1yProAeng1yGluProg1yLeuProySg1uCySeSerGlnLeuArg1yS 120  
Db 367 GGACCCCTGCTGCTCAATGAGAACCAAGGCTCCCATGTGAGTGCAGCCACTGGCGAAG 426  
Qy 121 A1a1leg1yG1uMeAAspAeng1yValSerG1nLeuThrSerG1uLeu1yPhe1le1yS 140  
Db 427 GCCATCGGGAGATGAGCAACAGGCTCTCACTGACGACGAGCTCAAGTTCATCAAG 486  
Qy 141 AAsn1aVal1aG1yValArg1uThrG1uSer1y1e1yTrLeuLeuVal1yG1uG1u 160  
Db 487 AATGCTGTCGCGCTGCTCGGAGACGAGACCAAGATCTACCTGCTGTAAGAGAGAG 546  
Qy 161 LyAArg1yTr1aAAsp1aG1nLeuSerCySeG1nG1yArg1yG1yThrLeuSerMetPro 180  
Db 547 AAGCCTTCGCGGAGCGCCAGCTGCTCCAGCGGCGCCGCGGAGCACTGAGCATGCC 606  
Qy 181 LyAAspG1uA1aAAsnG1yLeuMeTr1aA1aTr1e1uA1aG1nA1aG1yLeuA1aArg 200  
Db 607 AAGAGCGAGGCTGCAATGCTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 666  
Qy 201 ValPhe1leg1y1eAAspAAspLeuG1u1ySg1uG1yA1aPheVal1ySerAAsp1aSer 220  
Db 667 GCTTCATCGGCATCAACGACTGAGAGAGAGGCGCTTCGTGTACTGTGACCATCC 726  
Qy 221 ProMeTr1aG1yTrPheAAsn1yS1yTrArgSerG1yG1uProAAsnA1aTr1aAspG1u 240  
Db 727 CCCATGCGGACCTTCACACAGGCGGAGCGGCTGAGCCCAATGCTTACGACGAGAG 786  
Qy 241 AAspCyVal1aG1uMeTr1aA1aSerG1yG1yTrPheAAspA1aA1aCyA1aTh1rMet 260  
Db 787 GACTGCGAGATGATGCTGCTGCGGCGCTGAGAGAGAGCTGCTGCTGCTGCTGCTGCTG 846  
Qy 261 TrPheMeTrCySg1uPheAAsp1ySg1uAAsnMet 271  
Db 847 TACTTCATGTGTGATTGACAGAGAGAAACATG 879

RESULT 4  
AAFA4230  
ID AAFA4230 standard; cDNA, 1238 BP.  
XX  
AC AAFA4230;  
XX  
DT 02-APR-2001 (first entry)  
XX  
DE Human PRO1182 (UNQ596) nucleotide sequence SEQ ID NO:356.  
XX  
KW Human; secreted and transmembrane protein; PRO; cytostratic; cell death;  
KW cancer; chromosomal mapping; gene mapping; tissue typing;  
KW diagnostic assay; ss.  
XX  
OS Homo sapiens.  
XX  
FN WO200073454-A1.  
XX  
PD 07-DEC-2000.  
XX  
PF 30-MAR-2000; 2000WO-US008439.  
XX  
PR 02-JUN-1999; 99WO-US012252.  
PR 23-JUN-1999; 98US-0141037P.  
PR 07-JUL-1999; 98US-0143048P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 28-JUL-1999; 99US-0146222P.  
PR 17-AUG-1999; 99US-0149396P.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 08-OCT-1999; 99US-0158663P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 16-DEC-1999; 99WO-US030095.

PR 20-DEC-1999; 99WO-US030911.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US000365.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,  
PI Ferrara N, Fong S, Garbar H, Gerltzen ME, Goddard A, Godowski PJ,  
PI Grimaldi CJ, Gurney AL, Kijavlin ID, Napier MA, Pan J, Paoni NF,  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
PI Zhang Z;  
XX  
XX WPI; 2001-032160/04.  
DR P-PSDB; AAB65261.  
XX  
XX PRO polynucleotides used to produce polypeptides used to target bioactive  
PT molecules such as toxins, radiolabels or antibodies, to specific cells,  
PT to cause targeted cell death.  
XX  
XX Claim 2; Fig 251; 935pp; English.  
XX  
XX The present invention describes human secreted and transmembrane PRO  
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins can  
CC be used for targeted delivery of bioactive molecules, such as toxins,  
CC radiolabels or antibodies, that cause cell death. PRO nucleotide  
CC sequences, and their fragments, can be used as hybridisation probes, in  
CC chromosomal and gene mapping, and in the generation of anti-sense RNA and  
CC DNA. They may also be used to produce transgenic animals which are used  
CC to develop and screen therapeutically useful reagents. The PRO nucleotide  
CC and protein sequence can be used for tissue typing and in treating  
CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAFA4270 to  
CC AAFA4470 represent PCR primers and hybridisation probes used in the  
CC isolation of human PRO sequences. AAFA4087 to AAFA4269 and AAB5154 to  
CC AAB6300 represent human PRO polynucleotide and protein sequences given  
CC in the exemplification of the present invention  
XX  
XX SQ Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;  
XX  
XX Alignment Scores:  
Pred. No.: 3,11e-90 Length: 1238  
Score: 1441.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 5 Gaps: 0  
XX  
XX US-09-806-277A-6 (1-271) x AAFA4230 (1-1238)  
Qy 1 MetArgG1yAAsn1eVal1aLeuVal1yG1yVal1e1le1Ser1eVal1aPhe1leuSer1e1u 20  
Db 67 ATGAGGGGGAATCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 126  
Qy 21 ProSerG1yH1aP1aProG1nProA1aG1yAAspAAsp1aCySeSerVal1aG1n1le1uVal1 40  
Db 127 CCATCTGACATCTCTCAAGCGGCTGCGAGTACCGCTGCTGTGCAAGATCTGTCTGCTCT 186  
Qy 41 G1yLeu1ySg1yAAspA1aG1yG1u1ySg1yAAsp1ySg1yA1aProG1yArgProG1yArg 60  
Db 187 GGCTCAAGAGGAGTGGCGGAG 246  
Qy 61 Val1yProThrG1yG1u1ySg1yAAspMeTr1yAAsp1ySg1yG1u1ySg1ySer1yG1y 80  
Db 247 GTCGCGCCCAAGGAG 306  
Qy 81 ArgH1aG1yS1e1leg1yPro1leG1ySer1ySg1yG1u1ySg1yAAspSerG1yAAsp1le 100

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Db 307 CGTATGAAAATTGGTCCCATGGCTTAAAGGTGAGAAAGAGTTCGGTGACATA 366
Qy 101 GTPProBroglyProAanglygluProGlyLeuProGlyLeuSerGlyLeuValGly 120
Db 367 GGACCCCTGGTCTTAAATGAGAACAGAGGCTCCCATGTAGTGCAGCGCTGATCAAC 426
Qy 121 AAlaIeglygluMetAaPaanglyValSerGlyLeuThrSerGlyLeuValPheLeu 140
Db 427 GCCATCGGGAGATGACACACAGCTCTCTCAGTGCAGCGAGCTCAAGTTCATCAAG 486
Qy 141 AaAlaValAlaGlyValArgGlyThrGlySerGlyLeuValPheLeuValGly 160
Db 487 AATGCTGCGCGGTGCGCGAGACGAGACGAGCAAGATCTCACTGCTGAGAGAGAG 546
Qy 161 LyAaArgTyrAlaAaPAlaGlyLeuSerGlyGlyValArgGlyThrLeuSerMetPro 180
Db 547 AAGGCTACGCGAGCGCGAGCTGCTGCGAGGCGCGCGGCGAGCGCTGAGCATGCC 606
Qy 181 LyAaPAlaValAlaAaanglyLeuMetAlaAlaTyrLeuAlaGlyLeuAlaArg 200
Db 607 AAGGACGAGGCTGCGCATGGCTGATGGCGCATACCTGGCGCAAGCGCGCTGGCCGT 666
Qy 201 ValPheIleGlyLeuAaAaPLeuGlyLeuGlyValAlaPheValTyrSerAaPHeSer 220
Db 667 GCTTCATCGGATCAACAGCTGAGAGAGAGGCGCGCTTCTGTACTGACCTGACCTCC 726
Qy 221 ProMetArgTyrPheAaAaPLeuTyrPArgSerGlyGlyProAaAaAlaTyrAaPAla 240
Db 727 CCCATCGGAGCTTCAACAGTGGCGAGCGCTGAGCGCAACATGCTACGAGAGAG 786
Qy 241 AaPcyValAlaGlyMetValAlaSerGlyGlyTyrPheAaPAlaAlaCyGlySerThrMet 260
Db 787 GACTCGGAGATGTGTGCTCGGCGCGCTGAGAGAGAGCGCTGCGCACCAACATG 846
Qy 261 TyrPheMetCysGlyPheAaPLeuGlyLeuMet 271
Db 847 TACTTCATGTGTGATTTGACAAAGAGAAACATG 879

RESULT 5
ABL88155
ID ABL88155 standard; cDNA; 1238 BP.
XX
AC ABL88155;
XX
DT 16-MAY-2002 (first entry)
XX
DE Human PRO1182 cDNA sequence SEQ ID NO:167.
XX
KW Human; angiogenesis; cardiact; cyrostatic; antiangiogenic; hypotensive;
XX gene therapy; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
XX vulnery; cardiovascular disorder; endochelial disorder; cancer;
XX angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
XX age-related macular degeneration; arterial restenosis; angina;
XX rheumatoid arthritis; myocardial infarction; thrombophlebitis;
XX lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
XX wound healing; chromosome mapping; gene mapping; gene; se.
XX
OS Homo sapiens.
XX
PN WO200200690-A2.
XX
PD 03-JAN-2002.
XX
PF 20-JUN-2001; 2001WO-US019692.
XX
PR 23-JUN-2000; 2000US-0213637P.
XX PR 20-JUL-2000; 2000US-0219556P.
XX PR 25-JUL-2000; 2000US-0220624P.
XX PR 25-JUL-2000; 2000US-0220664P.
XX PR 28-JUL-2000; 2000WO-US020710.
XX PR 02-AUG-2000; 2000US-0222695P.
XX PR 17-AUG-2000; 2000US-00643657.

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PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0249223P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 01-MAR-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-0086034.
PR 25-MAY-2001; 2001US-0086034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.

XX
XX (GETH ) GENENTECH INC.
XX
PI Baker KP, Ferrara N, Gerber H, Gertleen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Masters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
XX WPI; 2002-090516/12.
XX
DR P-FSDB; ABB84900.
XX
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial
XX infarction), endothelial or angiogenic disorders in a mammal.
XX
XX Claim 2; Fig 167; 565pp; English.
XX
XX
XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
XX ABB85003. The PRO proteins and polynucleotides have cardiact, cyrostatic,
XX antiangiogenic, hypotensive, vulnery and antiarteriosclerotic
XX activities, and can be used in gene therapy. The PRO polynucleotides,
XX proteins, agonists and antagonists are useful for treating or diagnosing
XX a cardiovascular, endochelial or angiogenic disorder in a mammal, e.g.
XX cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
XX atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
XX angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
XX angiogenesis (such as breast carcinoma and liver carcinoma), tumour
XX healing. The PRO polynucleotides have applications in molecular biology,
XX including use as hybridisation probes, and in chromosome and gene
XX mapping. ABL88259 to ABL88267 represent primers and probes used in the
XX exemplification of the present invention
XX
XX
XX Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 3,11e-90 Length: 1238
XX Score: 1441.00 Matches: 271
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 6 Gaps: 0
XX
XX US-09-806-277A-6 (1-271) x ABL88155 (1-1238)
XX
Qy 1 MetArgGlyLeuMetAlaValAlaGlyValLeuIleSerGlyLeuAlaPheLeuSerLeuLeu 20

```

67 ATGAGGGGAATCTGCGCCCTGCTGAGCGCTTATACAGCTGCGCTTCTCTGCTGCTG 126  
QY 21 ProSerGlyVhAEPProGlnProAlaGlyAspAlaCySerValGlnIleLeuValPro 40  
Db 127 CCATCTGACATCTCCACCGCGCTGCGCATGACGCTGCTGCTGCTGCTGCTGCTGCT 186  
QY 41 GILYLeuVhAEPAlaGlyValGlyValGlyValGlyValGlyValGlyValGlyValGly 60  
Db 187 GCGCTCAAGAGGAGTGGGAG 246  
QY 61 ValGlyProthGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyValGly 80  
Db 247 GTCGCGCCCAAG 306  
QY 81 ArgHISGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 100  
Db 307 GGTATGAGAAATTTGGTCTCCCTGCTTAAAGGTGAGAAAGAGATTCCTGCTGACATA 366  
QY 101 GILYProPogGlyProAsnGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 120  
Db 367 GGAACCCCTGCTGCTTAAAG 426  
QY 121 AlaIleGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 140  
Db 427 GCGATCGGAGAGATGAGACACAGGCTCTCTGCTGAGACAGGAGAGAGAGAGAGAGAG 486  
QY 141 AsnAlaValAlaGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 160  
Db 487 AATGCTGCTGCGCGGTGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546  
QY 161 LysAlaGlyValAlaAspAlaGlyValGlyValGlyValGlyValGlyValGlyValGly 180  
Db 547 AAGCGCTTACGCGAG 606  
QY 181 LysAspGlyValAlaAsnGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 200  
Db 607 AAGAGCGAGGCTGCAATGAGGCTGATGCGCGCATCTGCGAGAGAGAGAGAGAGAGAG 666  
QY 201 ValPheIleGlyValAlaAspLeuGlyValGlyValGlyValGlyValGlyValGlyVal 220  
Db 667 GCTTCATCGCGATCAAG 726  
QY 221 ProMetArgThrPheAsnLysPheArgSerGlyValProAsnAlaTyrAspGlnGlu 240  
Db 727 CCCATCGGAGAGCTTAAAG 786  
QY 241 AspCysValGlyMetValAlaSerGlyValGlyValGlyValGlyValGlyValGlyVal 260  
Db 787 GACTGCGTGGAGATGCTGCGCGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 846  
QY 261 TyrPheMetCysGlyPheAspLysGlyValGlyValGlyValGlyValGlyValGlyVal 271  
Db 847 TACTTCATGCTGAGATTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 879

RESULT 6  
ABL95644  
ID ABL95644 standard; cDNA; 1238 BP.  
XX  
XX ABL95644;  
XX  
DT 19-JUN-2002 (first entry)  
XX  
XX Human angiogenesis related cDNA PRO1182 SEQ ID NO: 167.  
XX  
XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
XX  
XX atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
XX  
XX cardiact; cytoskeletal; angiogenic; hypotensive; vulnerary;  
XX  
XX antiarteriosclerotic; gene; 86.  
XX  
XX Homo sapiens.  
XX  
XX MO200208284-A2.  
XX

PD 31-JAN-2002.  
XX  
XX 09-JUN-2001; 2001WO-US021735.  
XX  
XX 20-JUL-2000; 2000US-0219556P.  
PR 25-JUL-2000; 2000US-0220624P.  
PR 25-JUL-2000; 2000US-0220644P.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 02-AUG-2000; 2000US-0222695P.  
PR 17-AUG-2000; 2000US-00643657.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 04-AUG-2000; 2000WO-US023378.  
PR 07-SEP-2000; 2000US-0230978P.  
PR 18-SEP-2000; 2000US-00644610.  
PR 18-SEP-2000; 2000US-00665350.  
PR 24-OCT-2000; 2000US-0242922P.  
PR 08-NOV-2000; 2000US-00709238.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 22-JAN-2001; 2001US-00767609.  
PR 28-FEB-2001; 2001US-00796498.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 09-MAR-2001; 2001US-00802706.  
PR 14-MAR-2001; 2001US-00816744.  
PR 22-MAR-2001; 2001US-00816744.  
PR 05-APR-2001; 2001US-00828366.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 25-MAY-2001; 2001US-00866028.  
PR 25-MAY-2001; 2001US-00866034.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 30-MAY-2001; 2001US-00870574.  
PR 30-MAY-2001; 2001WO-US017443.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
XX  
XX (GETH ) GENENTECH INC.  
PA (BAKE ) BAKER K P.  
PA (FERR ) FERRARA N.  
PA (GERB ) GERBER H.  
PA (GERR ) GERRITSEN M E.  
PA (GODD ) GODDARD A.  
PA (GODO ) GODOWSKI P J.  
PA (GURN ) GURNEY A L.  
PA (HILL ) HILLMAN K J.  
PA (HILL ) HILLMAN K J.  
PA (MARS ) MARSTERS S A.  
PA (PANT ) PAN J.  
PA (PAON ) PAONI N F.  
PA (STEP ) STEPHAN J F.  
PA (WADA ) WATANABE C K.  
PA (WILL ) WILLIAMS P M.  
PA (WOOD ) WOOD W I.  
XX  
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,  
XX  
XX Godowski PJ, Gurney AL, Hillman KJ, Marsters SA, Pan J, Paoni NF,  
XX  
XX Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,  
XX  
XX WPI; 2002-171999/22.  
XX  
XX P-PSDB; ABB95506.  
XX  
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
XX  
XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
XX  
XX infarction), endothelial or angiogenic disorders in a mammal.  
XX  
XX Claim 1; Fig 167; 567pp; English.  
XX  
XX The present invention provides the protein and coding sequences of human  
XX  
XX PRO proteins. These are useful for treating or diagnosing a  
XX  
XX cardiovascular, endothelial or angiogenic disorder, including cardiac

CC hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a coding sequence of the invention

XX Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;

# Alignment Scores:

Score:	3.11e-90	Length:	1238
Percent Similarity:	1441.00	Matches:	271
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
		Gaps:	0

US-09-806-277A-6 (1-271) x ABL95644 (1-1238)

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QY 1 MethrGGLYAenLauAAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeuLeu 20
Db 67 ATGAGGGGGAATCGGCTGCTGAGGCGCTTCTTAATCAAGCTGCGCTTCTGCTCACTGCTG 126
QY 21 ProSerGIHSPGPGInProAlaGlyAAspAspAlaCySerValGlnIleLeuValPro 40
Db 127 CCATCTGACATCTCTCAAGCGGCTGGCGATGACCGCTCTCTGTGACAGATCTGCTCCT 186
QY 41 GlyLeuLysGlyAAspAlaGlyGlyLysGlyAAspLysGlyAlaProGlyAAspProGlyAAsp 60
Db 187 GAGCTCAAAAGGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246
QY 61 ValGlyProThrGlyGlyLysGlyAAspMetGlyAAspLysGlyGlyLysGlySerValGly 80
Db 247 GTGGGCCCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 306
QY 81 ArgHisGlyLysIleGlyProIleGlySerLysGlyGlyLysGlyAAspSerGlyAAspIle 100
Db 307 CGTATGGAATAATGTGCTCCATGCTCTTAAGGTGAGAGAGAGATTCGGTGACATA 366
QY 101 GlyProProGlyProAspGlyGlyLysProGlyLysProGlyLysGlyLysGlyLysGlyLys 120
Db 367 GAGCCCTCGTCTCTTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 426
QY 121 AlaIleGlyLysMetAAspAspGlnValSerGlnLeuThrSerGlyLysPheIleLys 140
Db 427 GCCATCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 486
QY 141 AsnAlaValAlaGlyValArgGlyLysIleThrSerLysIleThrLeuValLysGlyLys 160
Db 487 AATGCTGCGCGGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546
QY 161 LysArgGlyTyrAlaAspAlaGlnLeuSerCySerGlnGlyValArgGlyLysThrLeuSerMetPro 180
Db 547 AAGGCTAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 606
QY 181 LysAspGlnAlaAlaAsnGlyLysMetAlaIleTyrLeuAlaGlnAlaGlyLysAlaArg 200
Db 607 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 666
QY 201 ValPheIleGlyIleAsnAspLeuGlyLysGlyLysAlaPheValTyrSerAspHisSer 220
Db 667 GTCTTCATCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 726
QY 221 ProMetArgThrPheAsnLysTyrArgSerGlyGlyLysProAsnAlaTyrAspGlyLys 240
Db 727 CCCATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 786
QY 241 AspCyValGlyMetValAlaSerGlyLysTyrAspAspValAlaCySerIleThrThrMet 260
Db 787 GACTTCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 846
QY 261 TyrPheMetCySerLysPheAspLysGlyLysMet 271
Db 847 TACTTCATGCTGAGATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 879

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RESULT 7
ID AC64399
AC AC64399 standard; cDNA; 1238 BP.
XX
XX AC64399;
AC
XX
XX 17-JUN-2003 (first entry)
DT
XX
XX
XX Novel human secreted and transmembrane protein PRO1182 cDNA.
DE
XX
XX Human; secreted and transmembrane protein; cytosolic; anti-HIV;
XX vrinolide; hepatotropic; antiinflammatory; neuroprotective; gene therapy;
XX PRO; pharmaceutical; diagnostic; biosensor; bioreactor; malignancy;
XX cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; leukemia;
XX lymphoma; hepatitis B; multiple sclerosis; Crohn's disease;
XX drug screening; gene; ss.
XX
XX OS Homo sapiens.
XX
XX
XX US200300531-A1.
XX
XX
XX 02-JAN-2003.
XX
XX
XX 19-NOV-2001; 2001US-00989734.
XX
XX
XX 16-JUN-1997; 97US-0049787P.
XX
XX 17-OCT-1997; 97US-0062250P.
XX
XX 05-NOV-1997; 97WO-US020069.
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XX 12-NOV-1997; 97US-0065186P.
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XX 13-NOV-1997; 97US-0065311P.
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XX 24-NOV-1997; 97US-0066770P.
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XX 25-FEB-1998; 98US-0075945P.
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XX 20-MAR-1998; 98US-0078910P.
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XX 28-APR-1998; 98US-0083322P.
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XX 07-MAY-1998; 98US-0084600P.
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XX 28-MAY-1998; 98US-0087106P.
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XX 02-JUN-1998; 98US-0087607P.
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XX 02-JUN-1998; 98US-0087609P.
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XX 02-JUN-1998; 98US-0087759P.
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XX 03-JUN-1998; 98US-0087827P.
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XX 04-JUN-1998; 98US-0088021P.
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XX 04-JUN-1998; 98US-0088025P.
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XX 04-JUN-1998; 98US-0088026P.
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XX 04-JUN-1998; 98US-0088028P.
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XX 04-JUN-1998; 98US-0088029P.
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XX 04-JUN-1998; 98US-0088030P.
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XX 04-JUN-1998; 98US-0088033P.
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XX 04-JUN-1998; 98US-0088326P.
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XX 05-JUN-1998; 98US-0088167P.
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XX 05-JUN-1998; 98US-0088202P.
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XX 05-JUN-1998; 98US-0088212P.
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XX 05-JUN-1998; 98US-0088217P.
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XX 05-JUN-1998; 98US-0088655P.
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XX 10-JUN-1998; 98US-0088734P.
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XX 10-JUN-1998; 98US-0088738P.
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XX 10-JUN-1998; 98US-0088742P.
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XX 10-JUN-1998; 98US-0088810P.
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XX 10-JUN-1998; 98US-0088824P.
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XX 10-JUN-1998; 98US-0088826P.
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XX 11-JUN-1998; 98US-0088858P.
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XX 11-JUN-1998; 98US-0088861P.
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XX 11-JUN-1998; 98US-0088866P.
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XX 11-JUN-1998; 98US-0089105P.
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XX 12-JUN-1998; 98US-0089400P.
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XX 16-JUN-1998; 98US-0089512P.
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XX 16-JUN-1998; 98US-0089514P.
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XX 17-JUN-1998; 98US-0089532P.
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XX 17-JUN-1998; 98US-0089538P.
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XX 17-JUN-1998; 98US-0089588P.
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XX 17-JUN-1998; 98US-0089589P.
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XX 17-JUN-1998; 98US-0089600P.
XX
XX 17-JUN-1998; 98US-0089653P.

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PR 18-JUN-1998; 98US-0089801P.  
PR 18-JUN-1998; 98US-0089907P.  
PR 18-JUN-1998; 98US-0089908P.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 02-JUN-1999; 99WO-US012252.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 15-MAY-2000; 2000WO-US013358.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023528.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 28-AUG-2001; 2001US-00941992.  
XX  
PA (GENTH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,  
PI Ferrara N, Fong S, Gerber H, Gertlisen ME, Goddard A, Godowski PJ,  
PI Girmalai JC, Gurney AL, Kijavini J, Napier MA, Pan J, Paoni NF,  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
PI Zhang Z,  
XX  
XX WPI, 2003-352829/33.  
DR P-PSDB; AB072552.  
XX  
XX New genes and secreted and transmembrane polypeptides (e.g. PRO183 or  
PT PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's  
PT sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's  
PT disease.  
XX  
XX Claim 1, Fig 251; 663pp; English.  
XX  
XX The invention describes a new isolated nucleic acid molecule comprising  
CC the full length coding sequence of the DNA deposited with the American  
CC Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PTA, 819-PTA,  
CC 209439, 20133, etc.) or a sequence with at least 80% identity to a DNA  
CC encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are  
CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These  
CC are particularly useful for detecting or treating e.g. malignancies or  
CC cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma,

CC leukaemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's  
CC disease in mammals. The PRO polypeptides are useful in drug screening,  
CC particularly as targets for therapeutic intervention in these diseases.  
CC and in the diagnostic determination of the presence of these diseases.  
CC The PRO polypeptides are also useful as molecular weight markers, or for  
CC chromosome identification. The PRO genes are useful as hybridisation  
CC probes, or for screening libraries of human cDNA, genomic DNA or mRNA.  
CC The PRO genes may also be used in gene therapy, particularly for  
CC replacing a defective gene. This sequence encodes a novel human secreted  
CC and transmembrane PRO polypeptide  
XX  
SQ Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 3,11e-90 Length: 1238  
Score: 1441.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0  
US-09-806-277A-6 (1-271) x ACA64399 (1-1238)  
QY 1 MetArgGIYAenLauAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeu 20  
DB 67 ATGAGGGGGAATCTGGCCCTGCTGAGCTTAAATCAAGCTGGCCCTTCTCACTGCTG 126  
QY 21 ProSerGIYhISProGInPProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
DB 127 CCACTGTGACATCTCTCAAGCCGGCTGGCGATACCCCTCTCTGTGCAAGATCTCTCCCT 186  
QY 41 GlyLeuLySGlyAspAlaGlyGlyIuLySGlyAspLySGlyAlaProGlyYArgProGlyArg 60  
DB 187 GGCTCAAGAGGAGTATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246  
QY 61 ValGlyProThrGlyGlyIuLySGlyAspMetGlyAspLySGlyIuLySGlySerValGly 80  
DB 247 GTGGCCCGACGAG 306  
QY 81 ArgHisGlyLySIIleGlyProIleGlySerLySGlyIuLySGlyAspSerGlyAspIle 100  
DB 307 CGTATGGAATAATTTGGTCCATTGGCTTAAGGTGAAGAAGGANTTCGGTGACATTA 366  
QY 101 GlyProProGlyProAsnGlyGlyProGlyLeuProGlyGlyCysSerGlyLeuArgLyS 120  
DB 367 GGACCCCTCGTCTCTTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 426  
QY 121 AlaIleGlyIuMetLeuAspAsnGlnValSerGlnLeuThrSerGlyLeuLeuPheIleLyS 140  
DB 427 GCCATCGGGAGATGAGACCAAGGCTCTCAAGCTGACCAAGGAGCTCAAGTTCATCAAG 486  
QY 141 AsnAlaValAlaGlyValArgGlyIuThrGlySerLySIIleGlyLeuValLySGlyIu 160  
DB 487 AATGCTGTGCGCGGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546  
QY 161 LySArgTyAlaAspAlaGlnLeuSerCysGlnGlyArgGlyIuThrLeuSerMetPro 180  
DB 547 AAGGCTACGCGGAG 606  
QY 181 LySAspGlyAlaIleAsnGlyLeuMetValAlaTyIleuAlaGlnAlaGlyLeuAlaArg 200  
DB 607 AAGGACGAGGCTCCAAATGAGCTGATGAGCCCAATCTCGGAGAGAGAGAGAGAGAGAG 666  
QY 201 ValPheIleGlyIleAsnAspLeuGlyIuLySGlyAlaPheValTySerAspHisSer 220  
DB 667 GTCTTCATCGGCATCAACAGACTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 726  
QY 221 ProMetArgThrPheAsnLySTyrArgSerGlyIuProAsnAsnAlaTyAspGlyIu 240  
DB 727 CCATGCGGAGACTTCACACATGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 786  
QY 241 AspCysValGluMetValAlaSerGlyGlyTyrPheAspValAlaCysHisThrThMet 260

Db 787 GACTCGCTGAGATGATGCTCGGCGCTGAGAACGACGTGGCTGCCACACACCACATG 846  
Cy 261 TyPheMetCysGluPheAPlyGluAsMet 271  
Db 847 TACTTCATGTGTGAGTTTGACACGAGAACATG 879  
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ID ABX80858 standard; cDNA, 1238 BP.  
XX  
AC ABX80858;  
XX  
DT 22-APR-2003 (first entry)  
XX  
DE Human secreted/cranmembrane protein cDNA, #144.  
XX  
KM Human; gene; 88; PRO; secreted; transmembrane; pharmaceutical;  
KM diagnostic; biosensor; bioreactor; tumour; therapeutic; gene therapy;  
KM tumour-associated antigenic target; TAT; ADPPT;  
KM antibody-dependent enzyme mediated prodrug therapy; cytostatic.  
XX  
OS Homo sapiens.  
FM US2003027162-A1.  
XX  
PD 06-FEB-2003.  
XX  
PF 15-NOV-2001; 2001US-00997428.  
XX  
XX 16-JUN-1997; 97US-0049787P.  
PR 17-OCT-1997; 97US-0062250P.  
PR 05-NOV-1997; 97WO-US020069.  
PR 12-NOV-1997; 97US-0065186P.  
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PR 03-JUN-1998; 98US-0087827P.  
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PR 23-JUN-1998; 98US-0090355P.  
PR 24-JUN-1998; 98US-0090429P.  
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PR 24-JUN-1998; 98US-0090540P.  
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PR 02-JUL-1998; 98US-0091673P.  
PR 07-JUL-1998; 98US-0091978P.  
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PR 09-JUL-1998; 98US-0092472P.  
PR 10-JUL-1998; 98US-0093339P.  
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PR 04-AUG-1998; 98US-0095321P.  
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PR 10-AUG-1998; 98US-0095916P.  
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PR 10-AUG-1998; 98US-0096012P.  
PR 11-AUG-1998; 98US-0096143P.  
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PR 17-AUG-1998; 98US-0096766P.  
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PR 17-AUG-1998; 98US-0096897P.  
PR 18-AUG-1998; 98US-0096949P.  
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PR 18-AUG-1998; 98US-0096959P.

PR 18-AUG-1998; 98US-0096960P.  
PR 18-AUG-1998; 98US-0097022P.  
PR 19-AUG-1998; 98US-0097141P.  
PR 20-AUG-1998; 98US-0097218P.  
PR 24-AUG-1998; 98US-0097661P.  
PR 26-AUG-1998; 98US-0097952P.  
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PR 26-AUG-1998; 98US-0097971P.  
PR 26-AUG-1998; 98US-0097974P.  
PR 26-AUG-1998; 98US-0097978P.  
PR 26-AUG-1998; 98US-0097979P.  
PR 26-AUG-1998; 98US-0097986P.  
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PR 31-AUG-1998; 98US-0098525P.  
PR 16-SEP-1998; 98US-0100634P.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98US-0100858P.  
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PR 07-OCT-1998; 98WO-US021141.  
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PR 05-JAN-1999; 98WO-US001016.  
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PR 02-JUN-1999; 98WO-US012252.  
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PR 07-JUL-1999; 98US-0143048P.  
PR 20-JUL-1999; 98US-0144758P.  
PR 26-JUL-1999; 98US-0145698P.  
PR 28-JUL-1999; 98US-0146222P.  
PR 17-AUG-1999; 98US-0148396P.  
PR 15-SEP-1999; 98WO-US021090.  
PR 15-SEP-1999; 98WO-US021547.  
PR 08-OCT-1999; 98US-0158663P.  
PR 30-NOV-1999; 98WO-US028313.  
PR 01-DEC-1999; 98WO-US028301.  
PR 01-DEC-1999; 98WO-US028634.  
PR 16-DEC-1999; 98WO-US030095.  
PR 20-DEC-1999; 98WO-US030911.  
PR 05-JAN-2000; 98WO-US000219.  
PR 06-JAN-2000; 98WO-US000376.  
PR 11-FEB-2000; 98WO-US003565.  
PR 18-FEB-2000; 98WO-US004341.  
PR 22-FEB-2000; 98WO-US004414.  
PR 24-FEB-2000; 98WO-US004914.  
PR 24-FEB-2000; 98WO-US005004.  
PR 02-MAR-2000; 98WO-US005841.  
PR 10-MAR-2000; 98WO-US006319.  
PR 15-MAR-2000; 98WO-US006884.  
PR 20-MAR-2000; 98WO-US007377.  
PR 30-MAR-2000; 98WO-US008439.  
PR 15-MAY-2000; 98WO-US013358.  
PR 17-MAY-2000; 98WO-US013705.  
PR 22-MAY-2000; 98WO-US014042.  
PR 30-MAY-2000; 98WO-US014941.  
PR 02-JUN-2000; 98WO-US015264.  
PR 23-JUN-2000; 98WO-US015637P.  
PR 28-JUL-2000; 98WO-US020710.  
PR 11-AUG-2000; 98WO-US022031.  
PR 23-AUG-2000; 98WO-US023522.  
PR 24-AUG-2000; 98WO-US023328.

## Alignment Scores:

Pred. No.: 3,116-90  
Score: 1441.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
DB: 8  
Gaps: 0

US-09-806-277A-6 (1-271) x ABX80858 (1-1238)

Length: 1238

Matches: 271

Conservative: 0

Mismatches: 0

Indels: 0

QY 1 MetArngiYAsnLeuAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeu 20  
DB 67 ATGAGGGGAATCTGGCCCTG3TGGCGCTTCAATCAAGCTGGCCCTTGCTGACTGCTG 126  
QY 21 ProSerGIYHISProGlnProAlaGIYAspAspAlaCysSerValGlnIleLeuValPro 40  
DB 127 CCATGTGACATCTCCACACCGGCTGGCGATACAGCGCTCTCTGTGCAATCTGCTCCCT 186  
QY 41 GlyLeuLYSGIYAspAlaGlyGlyLeuLYSGIYAspLYSGIYAlaProGlyYArgProGlyArg 60  
DB 187 GGCCTCAAGAGGAGATGCGGAG 246  
QY 61 ValGIYProThrNGIYValLYSGIYAspMetGlyAspLYSGIYValLYSGIYSerValGly 80  
DB 247 GTGGCCCGACGAG 306  
QY 81 ArgHISGIYLYSILEGlyProIleGIYSerLYSGIYLYSGIYAspSerGIYAspIle 100  
DB 307 CGTATGAGAAAATTGGTCCATTTGGCTTAAAGGTGAGAGAGAGAGAGAGAGAGAGAGAG 366  
QY 101 GlyProProGIYProAsnGlyGlyProGlyLeuProCysGlyCysSerGlnLeuArgLYS 120  
DB 367 GGACCCCTGGTCCATGATGAG 426  
QY 121 AlaIleGIYGIYMetAspAsnGlnValSerGlnLeuThrSerGlnLeuLYSPheIleLYS 140  
DB 427 GCCATCGGGAGATGAGACACAGCTCTCTCAAGCTGACGACGAGCTCAAGTTCATCAAG 486  
QY 141 AsnAlaValAlaGlyValArgGlyIleThrGlySerLYSILEYrLeuLeuValLYSGIY 160  
DB 487 AATGCTGCGCGGTGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546  
QY 161 LysArgTYrAlaAspAlaGlnLeuSerCysGlnGlyArgGlyGlyTYrLeuSerMetPro 180  
DB 547 AAGCGCTACGCGGACGCGCCAGCTGCTGCCAGGCGCGGAGAGAGAGAGAGAGAGAGAG 606  
QY 181 LysAspGIYAlaAlaAsnGlyLeuMetAlaIleTYrLeuAlaGlnAlaGlyLeuAlaArg 200  
DB 607 AAGACGAGGCTGCCAATGCGCTGATGGCCGATCTCGGAGAGAGAGAGAGAGAGAGAGAG 666  
QY 201 ValPheIleGIYIleAsnAspLeuGlyLYSGIYAlaPheValTYrSerAspHisSer 220  
DB 667 GTCTTCATCGGATCTCAACGACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 726  
QY 221 ProMetArgThrPheAsnLYSTrpArgSerGlyGlyProAsnAsnAlaTYrAspGlyGlu 240  
DB 727 CCCATGCGGAGCTTCAACAGAGTGGCGAGCGGTGAGCCCAATGCTTACGACGAGAGAG 786  
QY 241 AspCysValGlyMetValAlaSerGlyGlyTYrPheAspValAlaCysHisThrThrMet 260  
DB 787 GACTGCGTGAAGATGTGGCTTGGGCGGCTGGAACGAGTGGCTTGCACACCAATG 846  
QY 261 TyrPheMetCysGlyPheAspLYSGIYAsnMet 271  
DB 847 TACTTCATGTGTGACTTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 879  
RESULT 9  
ACD44367  
ID ACD44367 standard, cDNA; 1238 BP.  
AC ACD44367;  
XX  
XX 10-SEP-2003 (first entry)  
DE cDNA encoding human PRO1182 polypeptide.  
XX  
XX  
KW Human; PRO polypeptide; secreted protein; transmembrane protein;  
KW genetic disorder; antibacterial; immunosuppressive; transgenic;  
KW gene therapy; gene; ss.  
OS Homo sapiens.  
XX  
XX  
PN US200212756-A1.

XX 12-SEP-2002.  
 PD 14-NOV-2001; 2001US-00991073.  
 XX 15-JUN-1997; 97US-0049787P.  
 PR 17-OCT-1997; 97US-0062250P.  
 PR 05-NOV-1997; 97US-0062250P.  
 PR 12-NOV-1997; 97US-0065186P.  
 PR 13-NOV-1997; 97US-0065311P.  
 PR 24-NOV-1997; 97US-0066770P.  
 PR 25-FEB-1998; 98US-0075945P.  
 PR 20-MAR-1998; 98US-0078910P.  
 PR 28-APR-1998; 98US-0083322P.  
 PR 07-MAY-1998; 98US-0084600P.  
 PR 28-MAY-1998; 98US-0087106P.  
 PR 02-JUN-1998; 98US-0087607P.  
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 PR 18-JUN-1998; 98US-0089801P.  
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 PR 18-JUN-1998; 98US-0089908P.  
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 PR 07-OCT-1998; 98US-0092114P.  
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 PR 05-JAN-1999; 99US-00000106.  
 PR 08-MAR-1999; 99US-00005028.  
 PR 02-JUN-1999; 99US-00012252.  
 PR 15-SEP-1999; 99US-00021090.  
 PR 15-SEP-1999; 99US-00021547.  
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 PR 01-DEC-1999; 99US-00028634.  
 PR 16-DEC-1999; 99US-00030095.  
 PR 20-DEC-1999; 99US-00030911.  
 PR 06-JAN-2000; 2000US-0000219.  
 PR 11-FEB-2000; 2000US-0003565.  
 PR 18-FEB-2000; 2000US-0004341.

PR 22-FEB-2000; 2000US-0004414.  
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 PR 24-FEB-2000; 2000US-0005004.  
 PR 02-MAR-2000; 2000US-0005841.  
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 PR 17-MAY-2000; 2000US-0013705.  
 PR 22-MAY-2000; 2000US-0014042.  
 PR 30-MAY-2000; 2000US-0014941.  
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 PR 24-AUG-2000; 2000US-0023328.  
 PR 08-NOV-2000; 2000US-0030952.  
 PR 01-DEC-2000; 2000US-0032678.  
 PR 28-FEB-2001; 2001US-0006520.  
 PR 01-JUN-2001; 2001US-0017800.  
 PR 20-JUN-2001; 2001US-0019692.  
 PR 29-JUN-2001; 2001US-0021066.  
 PR 09-JUL-2001; 2001US-0021735.  
 PR 28-AUG-2001; 2001US-00941992.  
 XX (BETH ) GENENTECH INC.  
 PA Ashkenazi AV, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Fong S, Gerber H, Gerltzen ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
 PI Zhang Z;  
 XX WPI; 2003-340824/32.  
 DR P-PSDB; ABO25998.  
 XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
 PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
 PT and are therapeutically useful for enhancing immune responses.  
 PS Claim 2; Fig 251; 661pp; English.  
 XX The present invention relates to the isolation of novel human PRO  
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO  
 CC polypeptides are secreted and transmembrane proteins. The PRO  
 CC polypeptides are useful for detecting other PRO polypeptides, for linking  
 CC bioactive molecules to cells expressing PRO polypeptides, for modulating  
 CC biological activities of cells expressing PRO polypeptides, and for for  
 CC identifying agonists or antagonists. The polynucleotide sequences  
 CC encoding PRO polypeptides are useful as hybridisation probes, in  
 CC chromosome and gene mapping, in the generation of antisense RNA and DNA,  
 CC in the preparation of PRO polypeptides, for generating transgenic animals  
 CC or knockout animals, to construct hybridisation probes for mapping the  
 CC gene which encodes the PRO polypeptide, and for the genetic analysis of  
 CC individuals with genetic disorders, in gene therapy, for chromosome  
 CC identification, as chromosome markers, and for generating probes for PCR,  
 CC Northern analysis, Southern analysis and Western analysis. The present  
 CC sequence encodes a human PRO polypeptide of the invention. Note: The  
 CC sequence data for this patent was obtained in electronic format directly  
 CC from the USPTO web site at seqdata.uspto.gov/psidbidentry.html  
 XX SQ Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 3,11e-90 Length: 1238  
 Score: 1441.00 Matches: 271  
 Percent Similarity: 100.008 Conservative: 0  
 Best Local Similarity: 100.008 Mismatches: 0  
 Query Match: 100.008 Indels: 0  
 DB: Gaps: 0  
 US-09-806-277A-6 (1-271) X ACD4367 (1-1238)

QY 1 MetArgGIYAenLeuAlaLeuValGlyValleuIleSerLeuAlaPheLeuSerLeuLeu 20  
Db 67 ATGAGGGGGAATCTGGCCCTGGTGGCGCTTCTAAACACCTGGCCCTTCTGTCATCTGCTG 126  
QY 21 ProSerGIYHleProGIleProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
Db 127 CCATCTGGACATCTCCACCGCGCTGGCGATGACGCTCTGCTGTCATCTGCTGCTCCCT 186  
QY 41 GlyLeuLysGIYAAspAlaGlyGlyLysGlyAspLysGlyAlaProGlyYArgProGlyArg 60  
Db 187 GGCCTCAAGGGGAGATGCGGAG 246  
QY 61 ValGlyProThrGlyGlyLysGlyLysMetGlyAspAspGlyAspGlyLysGlyLysGly 80  
Db 247 GTCCGCCCCACGGGAG 306  
QY 81 ArgHISGlyLysIleGlyProIleGlySerLysGlyLysGlyLysGlyAspSerGlyAspIle 100  
Db 307 CGTCAATGAAAAATTGGTCCCATTTGGCTCTAAAGGTGAGAGAGAGAGAGAGAGAGAGAT 366  
QY 101 GlyProProGlyProAsnGlyGlyLysProGlyLysProGlyLysGlyLysGlyLysGly 120  
Db 367 GGACCCCTGGTCTTAATGAG 426  
QY 121 AlaIleGlyGlyMetAspAsnGlyValSerGlyLysLeuThrSerGlyLysLeuLysPheIleLys 140  
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XX 03-OCT-2002.  
XX 19-NOV-2001; 2001US-00989721.  
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XX 02-JUN-1999; 99WO-US012252.  
XX 15-SEP-1999; 99WO-US021090.  
XX 30-NOV-1999; 99WO-US028313.  
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XX 01-DEC-1999; 99WO-US028634.  
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XX 20-DEC-1999; 99WO-US030911.  
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XX 06-JAN-2000; 2000WO-US000376.  
XX 11-FEB-2000; 2000WO-US003565.

PR 18-FEB-2000; 2000MO-US004341.  
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 PR 24-FEB-2000; 2000WO-US004514.  
 PR 24-FEB-2000; 2000WO-US005004.  
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 PR 28-JUL-2000; 2000WO-US020710.  
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 PR 23-AUG-2000; 2000WO-US023522.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 20-JUN-2001; 2001WO-US019692.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 PR 28-AUG-2001; 2001US-00941992.  
 PA (GETH ) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,  
 PI Ferrara N, Fong S, Gerber H, Gertsen ME, Goddard A, Godowski PJ,  
 PI Grimaldi JC, Gurney AL, Kijavitt TJ, Napier MA, Pan J, Paoni NF,  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
 PI Zhang Z;  
 XX WPI: 2003-155950/15.  
 DR P-PSDB; ABUS9007.  
 XX  
 PT New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184,  
 PT PRO361 or PRO846) useful as targets for therapeutic intervention in  
 PT cancers (e.g. lung or breast cancers), or for diagnosing these cancers.  
 PS Claim 2; Fig 251; 647pp; English.

XX The invention discloses isolated PRO secreted/transmembrane polypeptides  
 CC comprising a sequence without signal peptide and the nucleic acid  
 CC encoding them. The polypeptides can be used to raise antibodies that  
 CC specifically bind to the PRO polypeptide, for linking a bioactive  
 CC molecule to a cell expressing a PRO protein and for modulating at least  
 CC one biological activity of a cell. The PRO polypeptides or  
 CC polynucleotides are also useful as pharmaceuticals, diagnostics,  
 CC biosensors or bioreactors, for detecting or treating e.g. tumours in  
 CC mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or  
 CC rabbits as targets for therapeutic intervention in certain cancers (e.g.  
 CC colon, lung or breast cancers) and diagnostic determination of the  
 CC presence of these cancers. The PRO polypeptides are also useful as  
 CC molecular weight markers or for chromosome identification. The PRO genes  
 CC are useful as hybridisation probes or for screening libraries of human  
 CC cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene  
 CC therapy, particularly for replacing a defective gene. The sequences  
 CC presented in ABX79290-ABX79675 are the genes encoding, the primers  
 CC amplifying and the probes detecting the PRO polynucleotides of the  
 CC invention. Note: The sequence data for this patent is also available in  
 CC electronic format from USPTO at seqdata.uspto.gov/sequence.html

XX Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;

# Alignment Scores:

Pred. No.: 3,11e-90 Length: 1238  
 Score: 1441.00 Matches: 271  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0

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 Db 127 CCATCTGACATCTCAAGCCGCGCTGGCGATGAGCGCTGCTCTGACGATCTCTGCTCT 186  
 QY 41 GlyLeuIleGlyAspAlaGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 60  
 Db 187 GGCCTCAAGAGGATCGGAG 246  
 QY 61 ValGlyProThrGlyGlyValGlyValGlyValGlyValGlyValGlyValGlyValGly 80  
 Db 247 GTGCGCCCAAG 306  
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 Db 367 GGAACCCCTGGTCTAATGAG 426  
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 DT 16-JUL-2003 (first entry)  
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 DE Novel human secreted and transmembrane protein PRO1182 cDNA.  
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 KW PRO943; PRO1133; PRO1137; PRO1387; PRO5723; PRO1141; PRO3301;  
 KW PRO9940; PRO1181; PRO1170; PRO361; PRO846; bioactive molecule; toxin;

KM radiolabel; antibody; cell death; tissue typing; gene therapy;  
KM cytostatic; chromosome mapping; gene mapping; transgenic animal;  
KM knockout animal; immunohistochemical staining; gene; ss.  
XX  
XX Homo sapiens.  
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PD 30-JAN-2003.  
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PR 16-JUN-1997; 97US-0049787P.  
PR 17-OCT-1997; 97US-0062250P.  
PR 05-NOV-1997; 97WO-US02006P.  
PR 12-NOV-1997; 97US-0065186P.  
PR 13-NOV-1997; 97US-0065111P.  
PR 24-NOV-1997; 97US-0066770P.  
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PR 07-MAY-1998; 98US-0084600P.  
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PR 04-JUN-1998; 98US-0088021P.  
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 PR 11-FEB-2000; 2000MO-US003565.  
 PR 18-FEB-2000; 2000MO-US004341.  
 PR 22-FEB-2000; 2000MO-US004314.  
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 PR 10-MAR-2000; 2000MO-US005841.  
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 PR 02-JUN-2000; 2000MO-US015264.  
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 PR 28-JUL-2000; 2000MO-US020710.  
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## Alignment Scores:

Pred. No.: 3,11e-90 Length: 1238  
 Score: 1441.00 Matches: 271  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 0

US-09-806-277a-6 (1-271) x ACA93559 (1-1238)

QY 1 MetcArgGlyAsnLeuAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeu 20  
 DB 67 ATGAGGCGGGAATCTGCGCTGCTGCGGCGTTCTAATCAGCTGCGCTTCTGCACTGCTG 126  
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 QY 41 GlyLeuValGlyAspAlaGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 60  
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 DB 307 CGTCATGAG 366

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 DB 727 CCATCGGAGAGCTTCAACAG 786  
 QY 241 AspCysValGlyLeuValAlaSerGlyGlyTyrPheAsnValAlaCysHisThrThrMet 260  
 DB 787 GACTGCTGAGAGATGAGTGTGCTGCGGCGCTGGAACGAGTGTGCTGCCACACACATG 846  
 QY 261 TyrPheMetCysGlyLeuPheAspLysGlyAsnMet 271  
 DB 847 TACTCATGTGAGATTGAAGAGAGAGATG 879

RESULT 12  
 ID ABX81241 standard; DNA; 1238 BP.  
 XX ABX81241;  
 AC 22-APR-2003 (first entry)  
 DT XX  
 DE Novel human secreted or transmembrane protein PRO1155 DNA.  
 XX Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
 KW cardiac insufficiency disorder; cancer; tumour; immune response;  
 KW adrenal cortical capillary endothelial growth; c-fos induction;  
 KW vascular endothelial growth factor inhibition; VEGF inhibition;  
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
 KW retinal neurons cell survival; rod photoreceptor cell survival;  
 KW retinal disorder; retinitis pigmentosa; kidney disease;  
 KW mammalian kidney mesangial cell proliferation; Berger disease;  
 KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
 KW chondrocyte redifferentiation; sports injury; arthritis; gene; ds.  
 OS Homo sapiens.  
 XX US2003027985-A1.  
 PD 06-FEB-2003.  
 PE 14-NOV-2001; 2001US-00990562.  
 PF 16-JUN-1997; 97US-0049787P.  
 PR 17-OCT-1997; 97US-0062250P.  
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US-09-806-277A-6 (1-271) X ABX81241 (1-1238)

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Db	727	CCCATGCGGACCTTAAACAGTGGCGCAGCGGTGAGCCCAACATGCTTACGACGAGAG	786
Qy	241	AspCysVal1GluMetVal1AserylGlyTyrPaaAspVal1AcylsH1stHrMet	260
Db	787	GACTGCGTGAGATGTGTGGCCCTCGGCGCGCTGGAACGAGTGTGGCTGCCACACCATG	846
Qy	261	TyrPheMetCysGluPheAspLysGluMet	271
Db	847	TACTTCATGTGTGAGTTGACAGAGAACATG	879
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DT	16-JUL-2003	(first entry)	
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XX	Human, secreted and transmembrane protein; PRO, noctropic; neuroprotective; antiparkinsonian; cytosolic; gene therapy; chromosome mapping; gene mapping; transgenic animal; knock-out animal; neurodegenerative disorder; Parkinson's disease; Alzheimer's disease; gene; ss.		
XX	Homo sapiens.		
XX	US2003017476-A1.		
XX	23-JAN-2003.		
PF	20-NOV-2001; 2001US-00989724.		
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Alignment Scores: 3.11e-90

Pred. No.: Length: 1238

Score: 1441.00 Matches: 271  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
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US-09-806-277a-6 (1-271) x ACA93057 (1-1238)

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 Db CCACTCTGACATCTCTCAAGCCGCTGGCATGACCGCTGCTCTGTCAGATCTCTGCTCCT 186  
 QY 41 GlyLeuValGlyAspAlaGlyValGlyValAspValGlyAlaProGlyArgProGlyArg 60  
 Db GGCTTCAAGGGGATCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246  
 QY 61 ValGlyProThrGlyGlyValGlyValAspMetGlyAspValGlyValGlyValGlyVal 80  
 Db GTCCGGCCCAAGGAG 306  
 QY 81 ArgHisGlyValIleGlyProIleGlySerValGlyValGlyValAspSerGlyValAspIle 100  
 Db CGTATGGAGAAATTTGGTCCATTGCTCTAAAGGTGAGAAAGAGATTCGGTGACATA 366  
 QY 101 GlyProProGlyProAsnGlyGlyProGlyLeuProCysGlyCysSerGlnLeuArgLys 120  
 Db GGACCCCTGGTCTCTAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 426  
 QY 121 AlaIleGlyLeuMetAspAspGlnValSerGlnLeuThrSerGlnLeuValPheIleLys 140  
 Db GCCATCGGGGAGATGACACAGAGCTCTCTCAGCTGACAGAGAGAGAGAGAGAGAGAG 486  
 QY 141 AsnAlaValAlaGlyValArgGlyValThrGlySerValIleValLeuValValGlyGlu 160  
 Db AATCTGTGCGCGGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546  
 QY 161 LysArgGlyValAspAlaGlnLeuSerCysGlnGlyValArgGlyValThrLeuSerMetPro 180  
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 QY 181 LysAspGlnValAlaAsnGlyLeuMetAlaAlaValLeuValGlnAlaGlyLeuValArg 200  
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 QY 201 ValPheIleGlyIleAsnAspLeuGlyValGlyValAlaPheValTyrSerAspHisSer 220  
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 QY 221 ProMetArgThrPheAsnLysTrpArgSerGlyValProAsnAsnAlaValAspGlyGlu 240  
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 QY 241 AspCysValGlyMetValAlaSerGlyValTyrPheAspValAlaCysHisThrThMet 260  
 Db GACGCGCGGAGATGCTGCTGCGGCGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 846  
 QY 261 TyrPheMetCysGlyPheAspValGlyValGlyValGlyValGlyValGlyValGlyVal 271  
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RESULT 14

ABX17141 standard; cDNA; 1238 BP.

ABX17141;

04-FEB-2003 (first entry)

Human PRO polynucleotide #108.

XX Human; PRO; gene; ss; secreted polypeptide; transmembrane polypeptide;  
 KM toxin; radiolabel; cell death; gene mapping; chromosome mapping;  
 KM protein electrophoresis; genetic disorder; immunosuppressive; cytostatic;  
 KM antibacterial.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002123463-A1.  
 XX  
 PD 05-SEP-2002.  
 XX  
 PF 19-NOV-2001; 2001US-00989732.  
 XX  
 PR 16-JUN-1997; 97US-0049787P.  
 PR 17-OCT-1997; 97US-0062250P.  
 PR 05-NOV-1997; 97MO-US020069.  
 PR 12-NOV-1997; 97US-0065186P.  
 PR 13-NOV-1997; 97US-0065311P.  
 PR 24-NOV-1997; 97US-006770P.  
 PR 25-FEB-1998; 98US-0075945P.  
 PR 20-MAR-1998; 98US-0078910P.  
 PR 28-APR-1998; 98US-0083322P.  
 PR 07-MAY-1998; 98US-0084600P.  
 PR 02-JUN-1998; 98US-0087106P.  
 PR 02-JUN-1998; 98US-0087607P.  
 PR 02-JUN-1998; 98US-0087609P.  
 PR 02-JUN-1998; 98US-0087759P.  
 PR 03-JUN-1998; 98US-0087827P.  
 PR 04-JUN-1998; 98US-0088021P.  
 PR 04-JUN-1998; 98US-0088025P.  
 PR 04-JUN-1998; 98US-0088026P.  
 PR 04-JUN-1998; 98US-0088028P.  
 PR 04-JUN-1998; 98US-0088029P.  
 PR 04-JUN-1998; 98US-0088030P.  
 PR 04-JUN-1998; 98US-0088033P.  
 PR 04-JUN-1998; 98US-0088326P.  
 PR 05-JUN-1998; 98US-0088167P.  
 PR 05-JUN-1998; 98US-0088202P.  
 PR 05-JUN-1998; 98US-0088212P.  
 PR 05-JUN-1998; 98US-0088217P.  
 PR 09-JUN-1998; 98US-0088655P.  
 PR 10-JUN-1998; 98US-0088734P.  
 PR 10-JUN-1998; 98US-0088738P.  
 PR 10-JUN-1998; 98US-0088742P.  
 PR 10-JUN-1998; 98US-0088810P.  
 PR 10-JUN-1998; 98US-0088824P.  
 PR 11-JUN-1998; 98US-0088826P.  
 PR 11-JUN-1998; 98US-0088858P.  
 PR 11-JUN-1998; 98US-0088861P.  
 PR 11-JUN-1998; 98US-0088876P.  
 PR 12-JUN-1998; 98US-0089105P.  
 PR 16-JUN-1998; 98US-0089440P.  
 PR 16-JUN-1998; 98US-0089512P.  
 PR 16-JUN-1998; 98US-0089514P.  
 PR 17-JUN-1998; 98US-0089532P.  
 PR 17-JUN-1998; 98US-0089600P.  
 PR 17-JUN-1998; 98US-0089603P.  
 PR 18-JUN-1998; 98US-0089607P.  
 PR 18-JUN-1998; 98US-0089907P.  
 PR 16-SEP-1998; 98MO-US019330.  
 PR 17-SEP-1998; 98MO-US019437.  
 PR 07-OCT-1998; 98MO-US021141.  
 PR 01-DEC-1998; 98MO-US025106.  
 PR 05-JAN-1999; 99MO-US000106.  
 PR 08-MAR-1999; 99MO-US005028.  
 PR 02-JUN-1999; 99MO-US012252.  
 PR 15-SEP-1999; 99MO-US021090.  
 PR 15-SEP-1999; 99MO-US021547.

PR 30-NOV-1999; 99WO-US028313.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 01-DEC-1999; 99WO-US028634.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 20-DEC-1999; 99WO-US030911.  
 PR 06-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000376.  
 PR 11-FEB-2000; 2000WO-US003565.  
 PR 18-FEB-2000; 2000WO-US004341.  
 PR 22-FEB-2000; 2000WO-US004914.  
 PR 24-FEB-2000; 2000WO-US005004.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 10-MAR-2000; 2000WO-US006319.  
 PR 15-MAR-2000; 2000WO-US006884.  
 PR 20-MAR-2000; 2000WO-US007377.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 15-MAY-2000; 2000WO-US013358.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 11-AUG-2000; 2000WO-US022031.  
 PR 23-AUG-2000; 2000WO-US023522.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 20-JUN-2001; 2001WO-US019589.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 PR 28-AUG-2001; 2001US-00941992.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,  
 PI Ferrara N, Fong S, Gerber H, Gerltzen ME, Goddard A, Gadowski PJ,  
 PI Girmaldi JC, Gunney AL, Kijavlin IJ, Napier MA, Pan J, Paoni NF,  
 PI Roy MA, Stewart TA, Tumas D, Matanabe CK, Williams PM, Wood WJ,  
 PI Zhang Z;  
 XX  
 DR WPI, 2003-066810/06.  
 DR P-PSDB; AB010922.  
 PT Novel secreted and transmembrane polypeptide for modulating biological  
 PT activity of cell expressing the polypeptide, identifying agonists or  
 PT antagonists of polypeptide, and as molecular weight markers.  
 XX  
 PS Clalm 2, Fig 251; 655pp; English.  
 XX  
 CC The invention relates to a secreted and transmembrane polypeptide, termed  
 CC PRO polypeptide, and the polynucleotide encoding it. The polypeptide is  
 CC useful for detecting PRO polypeptides and for linking a bioactive  
 CC molecule to a cell expressing the above polypeptides, where the bioactive  
 CC molecule is a toxin, radiolabel or an antibody. The bioactive material  
 CC causes the death of the cell. The polypeptide is useful for identifying  
 CC agonists or antagonists of the PRO polypeptide, for preparing variants of  
 CC PRO, as a molecular weight marker for protein electrophoresis purposes  
 CC and the PRO polynucleotide is useful for recombinantly expressing those  
 CC markers. The polynucleotide is also useful as a hybridisation probe, in  
 CC chromosome and gene mapping, in generation of antisense RNA and DNA, in  
 CC the preparation of PRO polypeptide, for generating transgenic animals or  
 CC knockout animals which in turn are useful in the development and  
 CC screening of therapeutically useful reagents, to construct hybridisation  
 CC probes for mapping the gene which encodes PRO and for the genetic  
 CC analysis of individuals with genetic disorders, in gene therapy, for  
 CC chromosome identification, as a chromosome marker and for generating  
 CC probes for PCR, Northern analysis, Southern analysis and Western  
 CC analysis. This sequence represents a human PRO polynucleotide of the  
 CC invention  
 XX

SQ Sequence 1238 bp; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;  
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 Score: 1441.00 Matches: 271  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Gaps: 0  
 DB: 8  
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 DB 67 atgagggggaatctggccctggtggcgcttcaatcacaccctggccttctgctacatgctg  
 QY 21 Proserg1yhi:sprog1nProalaglYaspaap1aCysSerValgln1leuValPro 40  
 DB 127 ccaatctgacatctctcagcccgctggcgaatgacgcttctgctgacatctctgctt  
 QY 41 g1yleu1y8g1Yaspa1ag1YglulY8g1Yaspy8g1YalaproglYargProglYarg 60  
 DB 187 ggccctcaaaagggaatggcggaagagagagaaagcgccccggcgagcgcttgagga 246  
 QY 61 ValglYProthrng1YglulY8g1YaspmetglYasply8g1YglnY8g1YserValglY 80  
 DB 247 gtcggcccccacgggagaaaaagagacatgggggcaaaagacaaagagcagtgctgggt 306  
 QY 81 Argh1ag1YlY81leglYProglY8serY8g1YglulY8g1Yaspy8g1Yaspy1le 100  
 DB 307 cgtcatggaaaattggtgcttccatggctctttaaagtgagaaagaaatgctccggagacta 366  
 QY 101 g1YProProglYProa8ng1YgluProglYleuProCysgluY8serGlnleuArglys 120  
 DB 367 ggaacccctggtccttaatgagaaacaaagcctcccatgtgagtgagcagctggcgcaag 426  
 QY 121 Alal1leglYgluMetaspa8ng1nValserGlnleuthrserGlnleu1Ypheel1lys 140  
 DB 427 gccatcgggagagatggaaacacaggtctctcagctgacagcagcagctcaattctacaaG 486  
 QY 141 Asna1aVal1aag1Yvalarg1YthrGlnserY81leYrleu1YleuVal1Y8g1Yglu 160  
 DB 487 aatgctgctggccggctgtrggcggaacagagcagaaatcttactgctgtaagaagagag 546  
 QY 161 LysArgTYra1aaapa1ag1nleuSerCysgln1Yarg1Yg1YThrleuSerMetPro 180  
 DB 547 AAGGCTACGGGAGAGCGCCAGCTGTCCTGCCAGGGCGCGGGGAGAGCTGAGATGCC 606  
 QY 181 LysAspGlu1a1a1a8ng1YleuMetAla1aTYrleu1a1ag1n1a1Yleu1a1arg 200  
 DB 607 AAGGACGAGGCTGGCAATGAGCTGATGGCCCATACCTGGGCGCAAGCGGCGCTGGCCGT 666  
 QY 201 ValPheel1g1Y1leaspa8p1eug1ulY8g1Yal1aPheValTYrSerAspHisSer 220  
 DB 667 gttcttcatgcacatcacagcacttgagaaagagggccttctgtrtacttgcacactgcc 726  
 QY 221 ProMetArgThrPheasnu1YfTPArgSerG1YgluProa8naa1aTYrAspGlu 240  
 DB 727 cccatggcgagccttcaacaaatggcgagcggtgagcccaaatgcttgcagagagag 786  
 QY 241 AspCysVal1GluMetVal1a1aSerG1YglYrTPasnaapVal1aCY8HisThrMet 260  
 DB 787 GACTGCGGAGATGATGGCTCGGGCGGCTGGAAAGCAGTGGCGCTGCACACCACTAG 846  
 QY 261 TyrPheMetCysGluPheAsp1Y8g1Y8glnMet 271  
 DB 847 TACTTCAATGTGAGTCTTGAAGAAGAAACATG 879  
 RESULT 15  
 ID ACA67996  
 XX ACA67996 standard; cDNA; 1238 bp.  
 AC ACA67996;

XX 24-JUN-2003 (first entry)  
XX Novel human secreted and transmembrane protein PRO1182 cDNA.  
XX  
XX Human; secreted and transmembrane protein; gene therapy; PRO; PRO943;  
XX PRO183; PRO184; PRO185; PRO331; PRO1133; PRO363; PRO5723; PRO1387;  
XX PRO1114; PRO3301; PRO9940; PRO1181; PRO1170; PRO361; PRO846;  
XX bioactive molecule; toxin; radiolabel; antibody; cell death; cancer;  
XX autoimmune disease; chromosome mapping; gene mapping; transgenic animal;  
XX knockout animal; septic shock; gene; ss.  
XX Homo sapiens.  
XX OS  
XX US2002177164-A1.  
XX  
XX 28-NOV-2002.  
XX  
XX 20-NOV-2001; 2001US-00989293.  
XX  
XX 16-JUN-1997; 97US-0049787P.  
XX 17-OCT-1997; 97US-0062250P.  
XX 05-NOV-1997; 97MO-US02006S.  
XX 12-NOV-1997; 97US-0065186P.  
XX 13-NOV-1997; 97US-0065311P.  
XX 24-NOV-1997; 97US-0066770P.  
XX 25-FEB-1998; 98US-0075945P.  
XX 20-MAR-1998; 98US-0083322P.  
XX 28-APR-1998; 98US-0084600P.  
XX 07-MAY-1998; 98US-0087106P.  
XX 28-MAY-1998; 98US-0087607P.  
XX 02-JUN-1998; 98US-0087609P.  
XX 02-JUN-1998; 98US-0087609P.  
XX 02-JUN-1998; 98US-0087759P.  
XX 03-JUN-1998; 98US-0087827P.  
XX 04-JUN-1998; 98US-0088021P.  
XX 04-JUN-1998; 98US-0088026P.  
XX 04-JUN-1998; 98US-0088026P.  
XX 04-JUN-1998; 98US-0088029P.  
XX 04-JUN-1998; 98US-0088030P.  
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XX 04-JUN-1998; 98US-0088125P.  
XX 05-JUN-1998; 98US-0088167P.  
XX 05-JUN-1998; 98US-0088202P.  
XX 05-JUN-1998; 98US-0088212P.  
XX 05-JUN-1998; 98US-0088217P.  
XX 09-JUN-1998; 98US-0088655P.  
XX 10-JUN-1998; 98US-0088734P.  
XX 10-JUN-1998; 98US-0088738P.  
XX 10-JUN-1998; 98US-0088742P.  
XX 10-JUN-1998; 98US-0088810P.  
XX 10-JUN-1998; 98US-0088824P.  
XX 10-JUN-1998; 98US-0088826P.  
XX 11-JUN-1998; 98US-0088858P.  
XX 11-JUN-1998; 98US-0088861P.  
XX 11-JUN-1998; 98US-0088876P.  
XX 12-JUN-1998; 98US-0089105P.  
XX 16-JUN-1998; 98US-0089440P.  
XX 16-JUN-1998; 98US-0089512P.  
XX 16-JUN-1998; 98US-0089514P.  
XX 17-JUN-1998; 98US-0089538P.  
XX 17-JUN-1998; 98US-0089538P.  
XX 17-JUN-1998; 98US-0089598P.  
XX 17-JUN-1998; 98US-0089600P.  
XX 17-JUN-1998; 98US-0089609P.  
XX 17-JUN-1998; 98US-0089633P.  
XX 18-JUN-1998; 98US-0089801P.  
XX 18-JUN-1998; 98US-0089807P.  
XX 18-JUN-1998; 98US-0089908P.  
XX 16-SEP-1998; 98MO-US019330.  
XX 17-SEP-1998; 98MO-US019437.  
XX 07-OCT-1998; 98MO-US021141.

PR 01-DEC-1998; 98MO-US025108.  
PR 05-JAN-1999; 99MO-US000106.  
PR 08-MAR-1999; 99MO-US005028.  
PR 02-JUN-1999; 99MO-US012252.  
PR 15-SEP-1999; 99MO-US021090.  
PR 15-SEP-1999; 99MO-US021547.  
PR 30-NOV-1999; 99MO-US028313.  
PR 01-DEC-1999; 99MO-US028301.  
PR 01-DEC-1999; 99MO-US028634.  
PR 16-DEC-1999; 99MO-US030095.  
PR 20-DEC-1999; 99MO-US030911.  
PR 05-JAN-2000; 2000MO-US000219.  
PR 06-JAN-2000; 2000MO-US000376.  
PR 11-FEB-2000; 2000MO-US003565.  
PR 18-FEB-2000; 2000MO-US004341.  
PR 22-FEB-2000; 2000MO-US004414.  
PR 24-FEB-2000; 2000MO-US004914.  
PR 24-FEB-2000; 2000MO-US005004.  
PR 02-MAR-2000; 2000MO-US005841.  
PR 10-MAR-2000; 2000MO-US006319.  
PR 15-MAR-2000; 2000MO-US006884.  
PR 20-MAR-2000; 2000MO-US007377.  
PR 30-MAR-2000; 2000MO-US008439.  
PR 15-MAY-2000; 2000MO-US013358.  
PR 17-MAY-2000; 2000MO-US013705.  
PR 22-MAY-2000; 2000MO-US014042.  
PR 30-MAY-2000; 2000MO-US014941.  
PR 02-JUN-2000; 2000MO-US015264.  
PR 28-JUL-2000; 2000MO-US020710.  
PR 11-AUG-2000; 2000MO-US022031.  
PR 23-AUG-2000; 2000MO-US023522.  
PR 24-AUG-2000; 2000MO-US023328.  
PR 08-NOV-2000; 2000MO-US030952.  
PR 01-DEC-2000; 2000MO-US032678.  
PR 28-FEB-2001; 2001MO-US006520.  
PR 01-JUN-2001; 2001MO-US017800.  
PR 20-JUN-2001; 2001MO-US019692.  
PR 29-JUN-2001; 2001MO-US021066.  
PR 09-JUL-2001; 2001MO-US021735.  
PR 28-AUG-2001; 2001US-00941992.  
  
(GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Baker KP, Botstein D, Desnovere L, Eaton DL,  
PI Perrera N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,  
PI Grimaldi JC, Gurney AL, Kijavrin IU, Napier MA, Pan J, Paoi NF,  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
PI Zhang Z;  
XX  
XX WPI; 2003-328481/31.  
XX P-PSDB; AB061674.  
XX  
XX Claim 2; Fig 251; 654pp; English.  
XX  
XX The invention describes an isolated, secreted and transmembrane  
XX polypeptide (I), termed PRO polypeptide. (I) is useful for detecting  
XX PRO944, PRO183, PRO184, PRO185, PRO331, PRO1133, PRO363, PRO5723.  
XX PRO1387, PRO1114, PRO3301, PRO9940, PRO1181, PRO1170, PRO361 or PRO846  
XX polypeptide comprising contacting the sample with the polypeptide and  
XX determining formation of a polypeptide conjugate. (I) is also useful for  
XX linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a  
XX cell expressing the above polypeptides to cause cell death. (I) is also  
XX useful as a therapeutic agent e.g. for treating cancer and autoimmune  
XX disease. PRO is useful in assays to identify other proteins or molecules  
XX involved in binding interactions. The polynucleotide (II) encoding (I) is  
XX useful in chromosome and gene mapping, for generating transgenic animals  
XX or knockout animals which in turn are useful in the development and  
XX screening of therapeutically useful reagents, for the genetic analysis of  
XX individuals with genetic disorders, in gene therapy, for chromosome

CC Identification, and as a chromosome marker. An anti-(I)-antibody is  
CC useful in diagnostic assays for PRO, e.g. detecting its expression in  
CC specific cells, tissues or serum, for affinity purification of PRO, and  
CC for treating septic shock. This sequence encodes a novel human secreted  
CC and transmembrane PRO polypeptide  
XX

Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;

## Alignment Scores:

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Score:	1441.00	Matches:	271
Percent Similarity:	100.00%	Conservative:	0
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US-09-806-277a-6 (1-271) x ACA67996 (1-1238)

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Oy 21 ProSerGIYHAsProGInProAlaGIYAspAspAlaCySserValGlnIleuValPro 40
Db 127 CCATCTGGACATCTCAAGCCGGCTGGCGATGACGCTGCTGTGCAATCTCTCCCT 186
Oy 41 GILeulYbGILYAspAlaGILYILYbGILYAspLYbGILYAlaPProGILYArgProGILYArg 60
Db 187 GGCCTCAAGGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246
Oy 61 ValGILYProTHGILYILYbGILYAspMetGILYAspLYbGILYILYbGILYSerValGILY 80
Db 247 GTCGGCCCCACGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 306
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Db 307 CGTCATGGAGAAATTTGGTCCCATTTGCTCTTAAGGTGAGAAAGAGATTCGGGTGACATA 366
Oy 101 GILYProPProGILYProAsnGILYILYbProGILYLeuPProCYbGILYCySserGILYLeuArgLYb 120
Db 367 GGAACCCCTGTGCTTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 426
Oy 121 AlaIleGILYILYbMetAspAsnGILYValSerGILYLeuThrSerGILYLeuLYbPheIleLYb 140
Db 427 GCCATCGGGGAGATGAGACACAGGTCTCTCACTGACCAAGCACTCAAGTTCACTCAAG 486
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Db 487 AATGCTGTGCGCGGTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546
Oy 161 LYbArgTYrAlaAspAlaGILYLeuSerCYbGILYArgGILYTYrThrLeuSerMetPro 180
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Oy 201 ValPheIleGILYIleAsnAspLeuGILYbGILYAlaPheValTYrSerAspHisSer 220
Db 667 GTCTTCATCGGACATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 726
Oy 221 ProMetArgThrPheAsnLYbTYrArgSerGILYILYbProAsnAsnAlaTYrAspGILYILY 240
Db 727 CCCATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 786
Oy 241 AspCYbValGILYMetValAlaSerGILYTYrPheAsnAspValAlaCYbHisETHrThrMet 260
Db 787 GACTGCGTGAAGATGTGTGCTCGGCGGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 846
Oy 261 TyrPheMetCYbGILYbPheAspLYbGILYbMet 271
Db 847 TACTTCATGTGTGAGTTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 879
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Job time : 596 secs

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## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 17, 2004, 06:04:40 ; Search time 101 Seconds

(without alignments)  
1907.166 Million cell updates/sec

Title: US-09-806-277A-6

Perfect score: 1441  
Sequence: 1 MRGNALVGVLSLAFSL.....NDVACHTTMMCEKDKNM 271

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Command line parameters:

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-USER=US09806277@cgn\_1\_128@rnatc\_15122004\_101628\_29285 -NCPU=6 -ICPU=3  
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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6: /cgn2\_6/ptodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	716.5	49.7	1595	4	US-09-600-932-1
2	317.5	22.0	714	3	US-09-198-603C-26
3	304.5	21.1	900	3	US-09-198-603C-1
4	298.5	20.7	2318	4	US-09-620-312D-733
5	233	16.2	876	4	US-09-535-521-4
6	233	16.2	876	4	US-09-535-521-6
7	233	16.2	2851	4	US-09-535-521-1
8	233	16.2	2851	4	US-09-535-521-3
9	222.5	15.4	1333	3	US-09-227-357-51
10	217.5	15.1	624	4	US-09-535-521-19
11	217.5	15.1	624	4	US-09-535-521-21
12	212.5	14.7	6109	4	US-09-795-061-1

13	212	14.7	6200	4	US-09-795-061-3	Sequence 3, Appli
14	210.5	14.6	6674	4	US-09-620-312D-110	Sequence 110, App
15	210	14.6	6158	4	US-09-919-497-6	Sequence 6, Appli
16	206	14.3	1868	3	US-08-392-367B-1	Sequence 1, Appli
17	206	14.3	1868	3	US-08-893-467A-1	Sequence 1, Appli
18	205.5	14.3	9164	4	US-09-814-915A-80	Sequence 80, Appli
19	204.5	14.2	1323	4	US-09-023-655-813	Sequence 813, App
20	204.5	14.2	1560	3	US-09-453-702B-264	Sequence 264, App
21	204.5	14.2	61663	3	US-09-453-702B-62	Sequence 62, Appli
22	204	14.2	660	4	US-09-169-768-43	Sequence 43, Appli
23	204	14.2	3170	4	US-09-169-768-1	Sequence 1, Appli
24	204	14.2	3171	4	US-09-169-768-15	Sequence 15, Appli
25	204	14.2	3171	4	US-09-169-768-19	Sequence 19, Appli
26	204	14.2	3181	1	US-08-655-086-1	Sequence 1, Appli
27	204	14.2	3349	4	US-09-169-768-13	Sequence 13, Appli
28	204	14.2	3531	4	US-09-169-768-7	Sequence 7, Appli
29	204	14.2	3541	4	US-09-169-768-9	Sequence 9, Appli
30	204	14.2	4167	4	US-09-169-768-12	Sequence 12, Appli
31	204	14.2	4409	4	US-09-331-347C-22	Sequence 22, Appli
32	203.5	14.1	1416	1	US-07-621-091G-1	Sequence 1, Appli
33	203.5	14.1	1416	2	US-08-399-889-1	Sequence 1, Appli
34	203.5	14.1	1416	3	US-09-167-364-1	Sequence 1, Appli
35	203.5	14.1	1416	3	US-09-439-897-1	Sequence 1, Appli
36	201.5	14.0	2823	4	US-09-919-497-7	Sequence 7, Appli
37	201	13.9	2543	4	US-08-555-669-11	Sequence 11, Appli
38	201	13.9	2543	3	US-09-073-663-11	Sequence 11, Appli
39	200.5	13.9	9827	3	US-09-453-702B-66	Sequence 66, Appli
40	199.5	13.8	561	4	US-09-535-521-16	Sequence 16, Appli
41	199.5	13.8	561	4	US-09-535-521-18	Sequence 18, Appli
42	199.5	13.8	11481	3	US-09-453-702B-254	Sequence 254, App
43	199.5	13.8	45175	3	US-09-453-702B-116	Sequence 116, App
44	199	13.8	369	4	US-09-535-521-24	Sequence 24, Appli
45	199	13.8	369	4	US-09-535-521-26	Sequence 26, Appli

## ALIGNMENTS

RESULT 1  
US-09-600-932-1  
; Sequence 1, Application US/09600932  
; Patent No. 6787639  
; GENERAL INFORMATION:  
; APPLICANT: Wakamiya, No. 6787639utaka  
; TITLE OF INVENTION: NOVEL COLLECTIN  
; FILE REFERENCE: 19036/36615  
; CURRENT APPLICATION NUMBER: US/09/600, 932  
; CURRENT FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: PCT/JP98/03328  
; PRIOR FILING DATE: 1998-07-24  
; PRIOR APPLICATION NUMBER: JP 10-11281  
; PRIOR FILING DATE: 1998-01-23  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 1595  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (6)..(836)  
US-09-600-932-1

## Alignment Scores:

Pred. No.:	1,21e-63	Length:	1595
Score:	716.50	Matches:	129
Percent Similarity:	69.49%	Conservative:	60
Best Local Similarity:	47.43%	Mismatches:	76
Query Match:	49.72%	Indels:	7
DB:	4	Gaps:	3

US-09-806-277A-6 (1-271) x US-09-600-932-1 (1-1595)

Cy 1 MetArgGlyAsnLeuAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeuLeu 20



	APPLICANT : MOYER, Shawn S.	
	APPLICANT : RONNING, Michael T.	
	TITLE OF INVENTION : EXPRESSION OF MANNOSE-BINDING PROTEIN IN METHYLOTROPHIC	
	FILE OF INVENTION : YEAST	
	FILE REFERENCE : A7290	
	CURRENT APPLICATION NUMBER : US/09/198,603C	
	CURRENT FILING DATE : 1998-11-24	
	NUMBER OF SEQ ID NOS : 26	
	SOFTWARE : PatentIn Ver. 2.1	
	SEQ ID NO 1	
	LENGTH : 900	
	TYPE : DNA	
	ORGANISM : Human	
	US-09-198-603C-1	
	Alignment Scores:	
Pred. No. :	5.84e-22	Length: 900
Score:	304.50	Matches: 84
Percent Similarity:	44.73%	Conservative: 39
Best Local Similarity:	30.55%	Mismatches: 96
Query Match:	21.13%	Indels: 56
DB:	3	Gaps: 9
US-09-806-277A-6 (1-271) x US-09-198-603C-1 (1-900)		
Oy	17 LeuSerLeuLeuProSeGlyHlaPrOglInProAlaGly-----	29
Dd	74 GTTTCACACTCCCTCTCTCTCTCTAGTAGTGCGTAGCGTTTACTCAAAACTGT	133
Oy	30 -----AspaApAlaCySer-ValGlInIleuValProGlyLe	42
Dd	134 GACCTGTGAGATGCCCAAAGAAGCTGCCTGCACTGATTGCTGTAGCTCCAGCAT	193
Oy	42 ulvBgIvApAlaGlyGlvBgIvApBlyBgIvAlaPrOglvAArgvAlGI	62
Dd	194 C-----AACGGCTTCCAGGCAAGATGGCGCTGATGG	226
Oy	62 YProThrGlyGlvBgIvApBmetGlyApBlyBgIvGlvBgIvSeraValGIvArgHi	82
Dd	227 CACCAGGGAAGAAAAGGGGAACAAGC---CAAGGCTCAAGGCTTACAGAGCCCCC	283
Oy	82 BgIvLyvAlIgIvProIIgIvSerLyBgIvGlvBgIvApBserGlyApBIlgIvPr	102
Dd	284 TGSAAGTTGGGGCCT-----CCAGAAATCCAGGCGCTTGCGTCCACGAGACC	334
Oy	102 oProGlyProAenGlyGlvProGlyLeuProcysGlvucyBsSerGlnIeuAvGlvAlaIl	122
Dd	335 AAAAGGCCAAAAAGAGACCTTGA-----	359
Oy	122 eGlyGluMeArPaEnGlnValIsErglInIeuThrSerGluIeuLysPheIleYAsnaI	142
Dd	360 -AAAAAGTCGGATGTGATAGTAAGCTGTGCTCCACAAAGAAAGCTCTGCAAAACGA	418
Oy	142 aValAlaGlyvAl-----ArgGluThrGluSerLyvAl	153
Dd	419 AATGGCACGTATCAAAAAGTGGCTGACCTTCTCTGGGCAAAACAAGTTGGGAACAAGTT	478
Oy	153 eTyIleuIeuvallyBgIvGlvBgIvArgTyvAlaIAspAlaGlnIeuSerGylngIvAr	173
Dd	479 CTTCCTGACCAATGGTGAATAATATGACCTTTGAAAAAGTGAAGGCGCTTGtGTGCAAGTT	538
Oy	173 gGlyGlyThrIeuSerMetcProLyvAspGlvAlaIalaIngIlyIleuMecAlaAtyIle	193
Dd	539 CAAGGCGCTGTGGCCACCCCGAGGAATGCTSCAAGATAGGAGCCATTCAAGATTCAT	598
Oy	193 uAlaGlnAlaGlyIleuAlaArgvAlPheIIlgIvIleAnApBLeugIvBgIvGlyvAl	213
Dd	599 CAAGAG-----GAAGCCTTCTGGGCACTCACTGTAGGAAGACAGAGAGGCCA	646
Oy	213 aPheValTyvSerApRhlSerProMetvArg---ThrpheaInlySTPRvArgserGlyGI	232
Dd	647 GTTTGTG-----GATCTGACAGGAATATGACTGACTTACACAACTGAACAGAGGGTGA	700

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QY      232  UPProAAnaAaLaTyAsBgLuGluAbPCyVaLgUleValAlasergLyGLTPAS 2523
          |||||.....:|||||.....:|||||.....:|||||.....:
DB       701  ACCCAACAAAGCGTGGTTCTGTGAATGTGTATTGTTACTGAAAAATGGCCAGTGSA 760
          |||||.....:|||||.....:|||||.....:|||||.....:
QY      252  naSPvaLaLaCyShieThrThmerTyxPheMeCySglurPe 266
          |||||.....:|||||.....:|||||.....:|||||.....:
DB       761  TGAAGTCCCCGTGCCACCTCCCATTCGTGGCCGTCTGTAGTTCC 803
          |||||.....:|||||.....:|||||.....:|||||.....:

RESULT 4
US-09-620-312D-733
; Sequence 733, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
    APPLICANT: Tang, Y. Tom
    APPLICANT: Liu, Chenghua
    APPLICANT: Asundi, Vinod
    APPLICANT: Zhang, Jie
    APPLICANT: Ren, Feiyan
    APPLICANT: Chen, Rui-hong
    APPLICANT: Zhao, Qing A.
    APPLICANT: Wehrman, Tom
    APPLICANT: Xue, Aidong J.
    APPLICANT: Yang, Yonghong
    APPLICANT: Wang, Jian-Rui
    APPLICANT: Zhou, Ping
    APPLICANT: Ma, Junqing
    APPLICANT: Wang, Dunrui
    APPLICANT: Wang, Zhiwei
    APPLICANT: John Tillingshaat
    APPLICANT: Drmanac, Radotje T.
    TITLE OF INVENTION: No. 6569662el Nucleic Acids and
    TITLE OF INVENTION: Polypeptides
    FILE REFERENCE: 784CIP2B
    CURRENT APPLICATION NUMBER: US/09/620,312D
    PRIOR FILING DATE: 2000-07-19
    PRIOR APPLICATION NUMBER: 09/552,317
    PRIOR FILING DATE: 2000-04-25
    PRIOR APPLICATION NUMBER: 09/488,725
    PRIOR FILING DATE: 2000-01-21
    NUMBER OF SEQ ID NOS: 1105
    SOFTWARE: pt_FL_genes Version 1.0
    SEQ ID NO 733
    LENGTH: 2318
    TYPE: DNA
    ORGANISM: Homo sapiens
    FEATURES:
    NAME/KEY: CDS
    LOCATION: (663)..(1691)
    US-09-620-312D-733

Alignment Scores:
Pred. No.:      8,97e-21      Length:      2318
Score:          298.50      Matches:      83
Percent Similarity: 39.67%      Conservative: 38
Best Local Similarity: 27.21%      Mismatches: 119
Query Match:     20.71%      Indels:      65
DB:              4          Gaps:      9
US-09-806-277A-6 (1-271) x US-09-620-312D-733 (1-2318)

QY      21  ProSerGIyHISProGInProAlagLYaSPaPaLaCySSerValGlnIleLeuValPro 40
          |||||.....:|||||.....:|||||.....:|||||.....:
DB       792  CCACC GGCGCCCGCCAGGGGTCCAGAAGGTGCACAAGGATCCCAAGGACCC-----CCT 842
          |||||.....:|||||.....:|||||.....:|||||.....:
QY      41  GLYLeuLyBGlyAspAlaGLyLulysGLyAspLySGlyAlaAProGlyAngPro----- 58
          |||||.....:|||||.....:|||||.....:|||||.....:
DB       843  GGCCCAA CTGGCAACAAAGGACAGAAAGAGAAAGAGAGGGGGAGAGCTGGACCACTGGCCCT 902
          |||||.....:|||||.....:|||||.....:|||||.....:
QY      59  -----GLYarGVaLGlyProThrGIyLulysGLyAspMetGLYAspLySGly 74
          |||||.....:|||||.....:|||||.....:|||||.....:
DB       903  GCCGGTGAAGAGAGGCCCATTTGGACCAAGCTGTCCCCCCCAGAGACAGCGTGGCCGAAGCA 963
          |||||.....:|||||.....:|||||.....:|||||.....:
QY      75  GlmLyseGLySerValGLyArGHisGLyLisGLyLysIleGlyProIleGlySerLyBGlyLulys 94

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Db      963 TCTAAAGCTCCAGAGGCCCAAGGCTCCCGTGTCCCTGGGAAACCCGCGCTCAG 1022
Qy      95  G1YAspSerG1YAsp1Ieg1YProProG1YProAnG1Yg1uPProG1YLeuProCyseG1u 114
Db      1023 GGGCCCACTGGGAGACCAAGGCCCCCGGCCCAACAGAGGAACTCCCGGCGCT 1082
Qy      115  -----CySerG1uLeuArg1YAsp1Ieg1Yg1u----- 124
Db      1083 CAGGCGCTCCTGGCTTCAGAGGCTTCAGGCGCACTGGGAGGCGCTGGGCTGGA 1142
Qy      124  ----- 124
Db      1143 CCTGGGAGACTGCCAGGCTTGTGGGTACCAAGCATGCCAGGCCCAAGGCGCCCC 1202
Qy      125  -----MetAspAnG1nValSerG1n 131
Db      1203 GGGCCTCCTGGCCATCAGAGCGGTGGTGGCCCTGGCCCTGCAAGATGAGCCAAACCCG 1262
Qy      132 LeuThrSerG1uLeuYsPhe1IeYAsp1aVal1aG1YValArg1uThrG1uSer 151
Db      1263 GCACCGAGAGC-----AATGGCTGCCCGCTCACTGGAAGAACTTCACAGAC 1310
Qy      152 Ys1IeYLeuLeuVal1Yg1uG1uYsArg1Yr1aAsp1aG1nLeuSerCyseG1n 171
Db      1311 AATAGCTACTATTTTCTGCTGAGAAAGAAATTTTGAGATGCAAAAGCTTTCTGTGA 1370
Qy      172 G1YArg1Yg1Yr1eLeuSerMetProLYsAsp1u1a1aAnG1YLeuMet1a1a 191
Db      1371 GACAACTTCACACTCTGTTTCTAATAACACTAGAGAGAAACGAATGATATAAAAA 1430
Qy      192 TyrLeu1aG1n1aG1YLeu1aArg1YValPhe1IeG1Y1IeAnAsp1eG1u1Yg1u 211
Db      1431 CAGATG-----GTAGGAGAGAGAGACCACTGATGCGCTCACAGACTGACACGGTAA 1484
Qy      212 G1YAlaPheVal1YrSerAsp---HisSerProMetArg1YrPheAn1Yr1PArgSer 230
Db      1485 AACCAATGAAAGTGGCTGATGGACATCTCA-----GACTCAAAAAATTTGAAAGCT 1518
Qy      231 G1Yg1uProAnAsn-----AlaTyrAspG1uG1uAspCyseValG1uMetVal 246
Db      1539 GAGACGCGCGATTAACCTGGGTCAATGCGCATGGCGCAGAGAAAGCTGTGGCTGAT 1598
Qy      247 AlaSerG1Yg1YrPAspAspVal1aCyseHisThrMet1YrPheMetCyseG1uPhe 266
Db      1599 TATGCTGGCAGTGGACGATTTCCAAATGTGAAGCTCAATTAATTCATTGCGAAAA 1658
Qy      267 AspLYsG1uAsnMet 271
Db      1659 GACAGGAGAGACGTA 1673

```

RESULT 5  
US-09-535-521-4  
Sequence 4, Application US/09535521  
Patent No. 6410714

GENERAL INFORMATION:  
APPLICANT: Weber, Eric R.  
APPLICANT: McCall, Catherine A.  
TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGF RECEPTOR (CANINE CD23)  
FILE REFERENCE: AL-5  
CURRENT APPLICATION NUMBER: US/09/535,521  
EARLIER FILING DATE: 2000-03-24  
EARLIER APPLICATION NUMBER: 60/125,913  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 876  
TYPE: DNA  
ORGANISM: Canis familiaris  
FEATURE:  
NAME/KEY: CDS

LOCATION: (1)..(876)  
US-09-535-521-4

Alignment Scores:  
Pred. No.: 1,11e-14 Length: 876  
Score: 233.00 Matches: 68  
Percent Similarity: 40.08 Conservative: 37  
Best Local Similarity: 25.95 Mismatches: 110  
Query Match: 16.17 Indels: 47  
DB: 4 Gaps: 6

US-09-806-277a-6 (1-271) x US-09-535-521-4 (1-876)

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Qy      41  G1YLeu1YsG1YAsp1aG1Yg1uYsG1YAsp1YsG1YAlaProG1YArgProG1YArg 60
Db      75  GGTGACGTGGCGCTCTGGG---GCTGTGATGTTCATGCTGTGGGCGGCTGCTGAC 131
Qy      61  ValG1YProThrG1Yg1uYsG1YAspMetG1YAsp1YsG1Yg1uYsG1YsValG1Y 80
Db      132 CCGTCTCTCTTGTGGCAGAGGACACTGTACAGAACTGAAACAGCTGAGGCTCGCCG 191
Qy      81  ArgHisG1Ys1IeG1YPro1IeG1YSer1YsG1Yg1uYs-----G1YAspSer 97
Db      192 CGCCCAAGACGTCTCTCGGGTTTCCAAGACTTGAAGAACACACAGCTGACCAAGTGC 251
Qy      98  G1YAsp1Ie---G1YProProG1YProAnG1Yg1uPProG1YLeuPro-CyseG1uCyse 116
Db      252 CCAGAAATCCAGAGCTGCGCCAGGTGTCAAGACATGAAGAAATCAAGCTGAACAGAA 311
Qy      116  rG1nLeuArg1Ys1a1IeG1YLeuMetAspAnG1nValSerG1nLeuThrSerG1u 136
Db      312 GAATAGTAAAGCTCAGAGACTGTAGCTTCCAGAGACTGTGACTTGTCCGACT 371
Qy      136  u1YsPhe1IeYsAsp1aVal1aG1YValArg1uThr----- 149
Db      372 GAACAACTCAAGTCCAGAGCTTGAACAGAGAACACAGCCTTGACTTCACTGAGAG 431
Qy      149  ----- 149
Db      432 ACTCCAGAGAGAGTGAAGAGCTGTGATGACGTACACGTCCAGGCTCCAGATG 491
Qy      150  -----G1uSer1Ys1IeYr1eLeuVal1YsG1 159
Db      492 TAAAGTGTCCCTGAGAGAGTGTCAACTTCAGAGAGAGTGTCTACTTCGCGAGGA 551
Qy      159  uG1uYsArg1Yr1aAsp1aG1nLeuSerCyseG1nG1YArg1Yg1Yr1eLeuSer 179
Db      552 GCCCAAGAGTGTATCCAGGCGCGGTGTGCTGACCAAGCTGCAAGGCGGCTGGCAG 611
Qy      179  tProLYsAspG1u1a1aAsnG1YLeuMet1a1aTyrLeu1aG1n1aG1YLeu1 199
Db      612 CATCCACAGCCCAAGAGAGAGAGAGCTTCTGCGCAGATGCCAACAGAGAGG----- 666
Qy      199  aArgValPhe1IeG1Y1IeAnAsp1eG1uYsG1uG1YAlaPheVal1YrSerAsp1 219
Db      667  ---ACCTGATGTGCTCCGGAGCTGACAGAGAGGAGGAGTTTATGTGATGAGCA 722
Qy      219  sSerProMetArg1YrPheAn1Yr1PAspSerG1Yg1uPProAnAsp1aTyrAsp1 239
Db      723 GAACCCCTGT---AACTATGCAACTGCGCGCGCGGAGCCCAACAGCGGCGCAGGG 779
Qy      239  uG1uAspCyseValG1uMetVal1aAspSerG1Yr1PAspAspVal1aCyseHisThr 259
Db      780 CAGAGACTGCTGATGATGAGAGGCTCGGCGCAGTGGAAATGAGCGCTTCTGCGGAGCTC 839
Qy      259  rMet 260
Db      840 GCTG 843

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RESULT 6  
US-09-535-521-6/c  
Sequence 6, Application US/09535521  
Patent No. 6410714



QY 150 -----Glusterlyse11eTyrLeuValValysgl 159  
 Db 690 TAACAGTGCCTGAGAGAGTGTCTCAACTTCAGAGAGAGTGTCTTACTTCCGCGCAGGA 749  
 QY 159 uGluYsArgTyrAlaaspAlaGlnLeuSerCyseGlnGlyArgGlyGlyThrLeuSerMe 179  
 Db 750 GCCCAAGAGTGTGATCCAGGCGCGGTTTGCTGACAGCAAGTGTCAAGGCGCGCTGGCCAG 809  
 QY 179 tProlysaAspGluAlaalaanglyLeuMetAlaAlaTyrLeuAlaGlnlaGlyLeuAl 199  
 Db 810 CATCCACAGCAG 864  
 QY 199 aArgValPheAlleGlyIleasnaAspLeuGluValGlyAlaPheValTyrSerAspH 219  
 Db 865 ---ACCTGATGTGGCTCCGCGGACTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 920  
 QY 219 sSerProMetArgThrPheAsnlySTrPArGSeGlyGluProAsnaAsnaAlaTyrAspG 239  
 Db 921 GAACCCCTG---AACTATAGCAACTGTGCGGCGCGGAGGCCCAACAGCGGCGCAGAG 977  
 QY 239 uGluAspCyseValaGlnMetValaIaSerGlyGlyTyrAsnaAspValaIaCyseHsThr 259  
 Db 978 CGAGGACTGCTGTATGATGACAGGCGCTCGGCGCAGTGAATGACGCTTCTGCGCAGCTC 1037  
 QY 259 rMet 260  
 Db 1038 GCTG 1041

## RESULT 8

US-09-535-521-3/c  
 ; Sequence 3, Application US/09535521  
 ; Patent No. 6410714  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weber, Eric R.  
 ; APPLICANT: McCall, Catherine A.  
 ; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGB RECEPTOR (CANINE CD23)  
 ; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF  
 ; FILE REFERENCE: AL-5  
 ; CURRENT APPLICATION NUMBER: US/09/535,521  
 ; CURRENT FILING DATE: 2000-03-24  
 ; EARLIER APPLICATION NUMBER: 60/125,913  
 ; EARLIER FILING DATE: 1999-03-24  
 ; NUMBER OF SEQ ID NOS: 26  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 3  
 ; LENGTH: 2851  
 ; TYPE: DNA  
 ; ORGANISM: Canis familiaris  
 US-09-535-521-3

## Alignment Scores:

Score: 5.76e-14 Length: 2851  
 Percent Similarity: 233.00 Matches: 68  
 Best Local Similarity: 40.08% Conservative: 37  
 Query Match: 16.17% Mismatches: 110  
 DB: 4 Indels: 47  
 Gaps: 6

US-09-806-277A-6 (1-271) x US-09-535-521-3 (1-2851)

QY 41 G1YleuYsG1YAspAlaG1YG1YAspYsG1YAlaProG1YArgProG1YArg 60  
 Db 2579 GGTCAGACTGGCGCTGCTGGG---GCTGGTACTGTATGATGTGGCGCGGCTGCTGAC 2523  
 QY 61 ValG1YProThrG1YG1YAspMetG1YAspYsG1YG1YAspYsG1YValG1Y 80  
 Db 2522 CTTGCTCTCTCTTCTGGCAGACAGGACACTGTACAAATCTGAAAGCTGAGAGCTGGCCG 2463  
 QY 81 ArgH1sG1Ys11eG1YPro11eG1YSer1YsG1YG1Ys-----G1YAspSer 97  
 Db 2462 CGCCCAAGAGCTCTCTGGGTTTCCAAGAGCTTGAAAGACACAGCGTGAACGATGGC 2403

QY 98 G1YAsp11e---G1YProProG1YProAsnG1YGluProG1YLeuPro-CyseG1YCyse 116  
 Db 2402 CCAGAAATCCAGAGCTGCGCGAGGTGTACAGAGCATGAGAGAAATCCAGCTAACAGAA 2343  
 QY 116 rGlnLeuAsG1YAla11eG1YlumeCyseAsnaGlnVala1SerG1YLeuThrSerG1ule 136  
 Db 2342 GAAGATGAAGAGCTCAGAGCTCTGAGCTCTCCCAAGAACTGTAGTCACTTGTTCGACCT 2283  
 QY 136 uLyPhe11eYsAsnaAlaVala1aG1YAlaArgG1YThr----- 149  
 Db 2282 GAACAACTCAAGTCCAGAGCTTGAACGAGAGAAACACAGAGCTTCATTCAGTGAAG 2223  
 QY 149 ----- 149  
 Db 2222 ACTCCAGAGAGAGTGAAGAGAGTGTGATGAGTACAGTGTCCAGCGCTCCAGAGT 2163  
 QY 150 -----Glusterlyse11eTyrLeuValValysgl 159  
 Db 2162 TAACAGTGCCTGAGAGAGTGTCTCAACTTCAGAGAGAGTGTCTTACTTCCGCGCAGGA 2103  
 QY 159 uGluYsArgTyrAlaaspAlaGlnLeuSerCyseGlnGlyArgGlyGlyThrLeuSerMe 179  
 Db 2102 GCCCAAGAGTGTGATCCAGGCGCGGTTTGCTGACAGCAAGTGTCAAGGCGCGCTGGCCAG 2043  
 QY 179 tProlysaAspGluAlaalaanglyLeuMetAlaAlaTyrLeuAlaGlnlaGlyLeuAl 199  
 Db 2042 CATCCACAGCAG 1988  
 QY 199 aArgValPheAlleGlyIleasnaAspLeuGluValGlyAlaPheValTyrSerAspH 219  
 Db 1987 ---ACCTGATGTGGCTCCGCGGACTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1932  
 QY 219 sSerProMetArgThrPheAsnlySTrPArGSeGlyGluProAsnaAsnaAlaTyrAspG 239  
 Db 1931 GAACCCCTG---AACTATAGCAACTGTGCGGCGCGGAGGCCCAACAGCGGCGCAGAG 1875  
 QY 239 uGluAspCyseValaGlnMetValaIaSerGlyGlyTyrAsnaAspValaIaCyseHsThr 259  
 Db 1874 CGAGGACTGCTGTATGATGACAGGCGCTCGGCGCAGTGAATGACGCTTCTGCGCAGCTC 1815  
 QY 259 rMet 260  
 Db 1814 GCTG 1811

## RESULT 9

US-09-227-357-51  
 ; Sequence 51, Application US/09227357  
 ; Patent No. 6342581  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fischer et al.  
 ; TITLE OF INVENTION: 123 Human Secreted Proteins  
 ; FILE REFERENCE: P2010P1  
 ; CURRENT APPLICATION NUMBER: US/09/227,357  
 ; CURRENT FILING DATE: 1999-01-08  
 ; EARLIER APPLICATION NUMBER: PCT/US98/13684  
 ; EARLIER FILING DATE: 1998-07-07  
 ; EARLIER APPLICATION NUMBER: 60/051,926  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/052,793  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/051,925  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/051,929  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/052,803  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/052,732  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/051,931  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/051,932  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/051,916

EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,930  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,918  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,920  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,733  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,795  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,919  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,928  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/055,722  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,723  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,948  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,949  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,953  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,950  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,947  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,964  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/056,360  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,684  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,984  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,954  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/058,785  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,664  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,660  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,661  
NUMBER OF SEQ ID NOS: 672  
SOFTWARE: PatentIn Ver. 2.10  
SEQ ID NO 51  
LENGTH: 1333  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (485)  
OTHER INFORMATION: n equals a,t,g, or c  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (486)  
OTHER INFORMATION: n equals a,t,g, or c  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (493)  
OTHER INFORMATION: n equals a,t,g, or c  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (496)  
OTHER INFORMATION: n equals a,t,g, or c  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (587)  
OTHER INFORMATION: n equals a,t,g, or c

FEATURE:  
NAME/KEY: SITE  
LOCATION: (633)  
OTHER INFORMATION: n equals a,t,g, or c  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (1330)  
OTHER INFORMATION: n equals a,t,g, or c  
US-09-227-357-51  
Alignment Scores:  
Pred. No.: 2,35e-13 Length: 1333  
Score: 222.50 Matches: 56  
Percent Similarity: 48.18% Conservative: 10  
Best Local Similarity: 40.88% Mismatches: 40  
Query Match: 15.44% Indels: 31  
DB: 3 Gaps: 6  
US-09-806-277a-6 (1-271) x US-09-227-357-51 (1-1333)  
QY 2 ArgglyAenLeuAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeuPro 21  
DB 161 CGGGTATAT---CAGTTGAAGAGAGAACTACTCCCCAGGTATATCTGAGCATTCCT 217  
QY 22 SerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValProGly 41  
DB 218 ---GGCTTGCTCGACCTCCAGGGCCC-----CCTGGA 247  
QY 42 LeuLygIAspAlaGlyGlyValGlyAspLygIAspAlaProGlyArgProGlyArgVal 61  
DB 248 GCAATGTTCCCTCCGCGCCCATGTCGATCGGCTTCAGAGAGATGTAGAAC 307  
QY 62 GlyProThrGlyGlyValGlyAsp----- 69  
DB 308 GCACAGAAAGAGAGAAAGTGAAGAAAGCACTGAGTTGAGAGTGAAGTGAACCG 367  
QY 70 MetGlyAspLygIValGlyValGlySerValGlyArgHisGlyValGlyProIleGly 89  
DB 368 CTAGTCTTCCCGGTGAAGAGGAGCCAGAGAGACTGCGAAGAAAGAACCCATGAGA 427  
QY 90 SerLygIValGlyValGlyAspSerGlyAspIleGlyProProGlyProAsnGly----- 107  
DB 428 CCAAGGAGAGAGAAAGAGAGTGTGATTCCTCTTCGACCAAGGAGACACNNA 487  
QY 108 -----GluProGlyLeuPro-----CysGlyCysSerGlnLeu 118  
DB 488 TGATANTGTGAGACCCGGGCTGCTGAGTTGACATGTGGAAGCATC 538  
RESULT 10  
US-09-535-521-19  
; Sequence 19, Application US/09535521  
; Patent No. 6410714  
; GENERAL INFORMATION:  
; APPLICANT: Weber, Eric R.  
; APPLICANT: McCall, Catherine A.  
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)  
; FILE REFERENCE: AL-5  
; CURRENT APPLICATION NUMBER: US/09/535,521  
; EARLIER FILING DATE: 2000-03-24  
; EARLIER APPLICATION NUMBER: 60/125,913  
; EARLIER FILING DATE: 1999-03-24  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 624  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1) .. (624)  
US-09-535-521-19

## Alignment Scores:

Pred. No.:	2,63e-13	Length:	624
Score:	217.50	Matches:	52
Percent Similarity:	41.92%	Conservative:	31
Best Local Similarity:	26.26%	Mismatches:	73
Query Match:	15.09%	Indels:	42
DB:	4	Gaps:	3

US-09-806-277a-6 (1-271) x US-09-535-521-19 (1-624)

```

QY 101 GLYProProGlyProAhnGlyGluProGlyLeuPro-CysGluCysSerGlnLeuArgly 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 12 GGGTCCCAAGGTGTCAAGACATGAAGAAATCCAACTGAACAGAGAAATGAAGC 71
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 120 sAlaIleGlyGluMetAspAhnGlnValSerGlnLeuThrSerGlnLeuLysPheIlely 140
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 72 TCAGAGCTGTGAGCTTCCCAAGACCTGTGACCTTGCTGGACCTGAACAACCTCA 131
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 140 sAenAlaValAlaGlyValArgGluThr----- 149
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 132 GTCCCAAGCTTGAACGAGAAAGACACAGCTTGATTCATCTGAGAGACTCCAGAGGA 191
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 149 ----- 149
DB 192 GGTGAGAAAGCTGTGATGAGCTACACGTGTCCACGGCTCCAGTGTAAACAGTCCC 251
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 150 -----GluSerIleIleTyrLeuLeuValIleGluGluLysArgly 163
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 252 TGAGAAAGTGTCTCAACTCCAGAGAAAGTGTCTACTCTCCGCGAGAGGCCCAAGATG 311
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 163 rAlaAspAlaGlnLeuSerCysGlnGlyArgGlyGlyThrLeuSerMetProLysAspG 183
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 312 GATCCAGGCGCGGTTGGCTGCAGCAAGCTGCAAGGGCGGCTGGCCAGCATCCACGCCA 371
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 183 uAlaAlaAsnGlyLeuMetAlaIleTyrLeuAlaGlnAlaGlyLeuAlaArgValPheI 203
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 372 AGAGAGAGAGAGACTTCTCGCCGAGGTATGCCAACAGAAAGGCC-----ACCTGGAT 422
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 203 eGlyIleAsnAspLeuGluLysGluGlyAlaPheValTyrSerAspHisSerProMetAr 223
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 423 TGGCTCCGCGGACTGCGACAGAGAGGGGAGTTATCTGATGACAGAAACCCCTG-- 480
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 223 gThrPheAsnLysTyrPArgSerGlyGluProAsnAsnAlaTyrAspGluGluAspCysVa 243
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 481 -AACTATGCAACTGGCGGCCCGGAGCCCAACAACGGGGCCAGGGCCAGGACTGCGT 539
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 243 lGluMetValAlaSerGlyGlyTyrPAsnAspValAlaCysHisThrThreMet 260
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 540 GATGATGCAAGGCTCGGGGCAGTGAATGACGCTTGTGGCGGAGCTGCTG 591
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

## RESULT 11

US-09-535-521-21/c

Sequence 21, Application US/09535521

Patent No. 6410714

GENERAL INFORMATION:

APPLICANT: Weber, Eric R.

TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)

FILE REFERENCE: AL-5

CURRENT APPLICATION NUMBER: US/09/535,521

EARLIER FILING DATE: 2000-03-24

EARLIER APPLICATION NUMBER: 60/125,913

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 21

LENGTH: 624

TYPE: DNA

ORGANISM: Canis familiaris

US-09-535-521-21

Alignment Scores:

## Pred. No.:

Pred. No.:	2,63e-13	Length:	624
Score:	217.50	Matches:	52
Percent Similarity:	41.92%	Conservative:	31
Best Local Similarity:	26.26%	Mismatches:	73
Query Match:	15.09%	Indels:	42
DB:	4	Gaps:	3

US-09-806-277a-6 (1-271) x US-09-535-521-21 (1-624)

```

QY 101 GLYProProGlyProAhnGlyGluProGlyLeuPro-CysGluCysSerGlnLeuArgly 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 613 GGGTCCCAAGGTGTCAAGACATGAAGAAATCCAACTGAACAGAGAAATGAAGC 554
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 120 sAlaIleGlyGluMetAspAhnGlnValSerGlnLeuThrSerGlnLeuLysPheIlely 140
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 553 TCAGAGCTGTGAGCTTCCCAAGACCTGTGACCTTGCTGGACCTGAACAACCTCA 494
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 140 sAenAlaValAlaGlyValArgGluThr----- 149
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 493 GTCCCAAGCTTGAACGAGAAAGACACAGCTTGATTCATCTGAGAGACTCCAGAGGA 434
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 149 ----- 149
DB 433 GGTGAGAAAGCTGTGATGAGCTACACGTGTCCACGGCTCCAGTGTAAACAGTCCC 374
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 150 -----GluSerIleIleTyrLeuLeuValIleGluGluLysArgly 163
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 373 TGAGAAAGTGTCTCAACTCCAGAGAAAGTGTCTACTCTCCGCGAGAGGCCCAAGATG 314
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 163 rAlaAspAlaGlnLeuSerCysGlnGlyArgGlyGlyThrLeuSerMetProLysAspG 183
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 313 GATCCAGGCGCGGTTGGCTGCAGCAAGCTGCAAGGGCGGCTGGCCAGCATCCACGCCA 254
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 183 uAlaAlaAsnGlyLeuMetAlaIleTyrLeuAlaGlnAlaGlyLeuAlaArgValPheI 203
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 253 AGAGAGAGAGAGACTTCTCGCCGAGGTATGCCAACAGAAAGGCC-----ACCTGGAT 203
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 203 eGlyIleAsnAspLeuGluLysGluGlyAlaPheValTyrSerAspHisSerProMetAr 223
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 202 TGGCTCCGCGGACTGCGACAGAGAGGGGAGTTATCTGATGACAGAAACCCCTG-- 145
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 223 gThrPheAsnLysTyrPArgSerGlyGluProAsnAsnAlaTyrAspGluGluAspCysVa 243
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 144 -AACTATGCAACTGGCGGCCCGGAGCCCAACAACGGGGCCAGGGCCAGGACTGCGT 86
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 243 lGluMetValAlaSerGlyGlyTyrPAsnAspValAlaCysHisThrThreMet 260
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 85 GATGATGCAAGGCTCGGGGCAGTGAATGACGCTTGTGGCGGAGCTGCTG 34
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

## RESULT 12

US-09-795-061-1

Sequence 1, Application US/09795061

Patent No. 6759528

GENERAL INFORMATION:

APPLICANT: Greenspan, Daniel S

TITLE OF INVENTION: Pro-Alpha 3 (V) Collagen Genes

FILE REFERENCE: 960296, 96781

CURRENT APPLICATION NUMBER: US/09/795,061

EARLIER FILING DATE: 2001-02-26

NUMBER OF SEQ ID NOS: 24

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 1

LENGTH: 6109

TYPE: DNA

ORGANISM: Mus musculus

FEATURE:

NAME/KEY: CDS

LOCATION: (82)..(5298)

US-09-795-061-1

Alignment Scores:

Pred. No.:	2.06e-11	Length:	6109
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Score: 212.50 Matches: 55  
Percent Similarity: 44.59% Conservative: 15  
Best Local Similarity: 35.03% Mismatches: 51  
Query Match: 14.75% Indels: 37  
DB: 4 Gaps: 4

US-09-806-277A-6 (1-271) x US-09-795-061-1 (1-6109)

QY 23 G1YH1SPROG1NPRO1AG1YASPAAPALACYSERVALG1N1LEUVALPROG1YLEU 42  
DB 4213 GGCCCTCCAGGGGCCCTCGGCCACCTGGC-----CTCCCTGGGCTG 4254  
QY 43 LYSG1YAPALAG1YGL1YULYSG1YASPLYSG1YALAPROG1YARGPROG1YARGVALG1Y 62  
DB 4355 AAGGAGAGTGTCTGGCCCCAAGGGGAGAGAGGCCCATTTGGCTTAATAGGCTCATTTGGT 4314  
QY 63 PROTHRG1YULYSG1YASPMETG1YASPLYA-----73  
DB 4315 CCCCCAGGGAGGCGCGGTGAGAAAGGCATCAGGGGTTGCCAGGTGTGAGGGCCCCCA 4374  
QY 74 -----G1YGL1YSG1YSERVALG1YARG 81  
DB 4375 GGCCCTCAGGAGACCTGTCTCTCCCTGTCTGTGCTGTAGTCACTGGGCCC 4434  
QY 82 H1SG1YVSL1EG1YPRO1LEG1YSE1YSG1YGL1YULYSG1YASP-----96  
DB 4435 CCAGGTGTGGGCGCCCTGTGGACAGAAAGGCTCCAAAGGATCCCGGAGTCTTTGGT 4494  
QY 97 ---SERGLYAP1LEG1YPRO1PROG1YPROANG1YGL1YULYSG1YLEU1YLEU1YSG1YULY 115  
DB 4495 CCTGTGTGAGACCTCGGACACAGCGGCTCTCTGTCTCCCGGTTCTCCGGTGAAGTG 4554  
QY 116 SERGL1YULYSG1YASPMETG1YASPLYA-----A1AL1EG1YULYSG1YSERVALG1YARG 132  
DB 4555 CATGGCTGCGGACGCGCGCATCTGTGTGACGACACCTGGAAGGTGGCTGAGAGAGTG 4614  
QY 133 TH1SERGL1YULYSG1YASPMETG1YASPLYA-----A1AL1EG1YULYSG1YSERVALG1YARG 149  
DB 4615 ATGGCTTCACTGAA-TTCACTGAGCTTGAGCTGACGAGTTCAGAGTTCAGAGACC 4664

## RESULT 13

US-09-795-061-3  
Sequence 3, Application US/09795061  
Patent No. 6759528  
GENERAL INFORMATION:  
APPLICANT: Greenspan, Daniel S  
APPLICANT: Imamura, Yasutada  
TITLE OF INVENTION: Pro-Alpha 3 (V) Collagen Genes  
FILE REFERENCE: 960296.96781  
CURRENT APPLICATION NUMBER: US/09/795.061  
CURRENT FILING DATE: 2001-02-26  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 3  
LENGTH: 6200  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (87)..(5321)  
US-09-795-061-3

## Alignment Scores:

Pred. No.: 2,37e-11 Length: 6200  
Score: 212.00 Matches: 54  
Percent Similarity: 43.33% Conservative: 11  
Best Local Similarity: 36.00% Mismatches: 41  
Query Match: 14.71% Indels: 44  
DB: 4 Gaps: 5

US-09-806-277A-6 (1-271) x US-09-795-061-3 (1-6200)

QY 23 G1YH1SPROG1NPRO1AG1YASPAAPALACYSERVALG1N1LEUVALPROG1YLEU 42

DB 4221 GGCCCTCTGGCCCCCTGGGCCCTTGGC-----CTCCAGGGGCTG 4262  
QY 43 LYSG1YAPALAG1YGL1YULYSG1YASPLYSG1YALAPROG1YARGPROG1YARGVALG1Y 62  
DB 4263 AAGGAGAGTGTCTGGCCCCAAGGGGAGAGAGGCCCATTTGGATTTGATGTGCTCATTTGGC 4322  
QY 63 PROTHRG1YULYSG1YASPMETG1YASPLYA-----73  
DB 4323 CCCCCGAGAGAGTGTGAGAAAGATCAGGGGTTGCCAGGCGTGCAGGACCCCT 4382  
QY 74 G1YGL1YSG1YSERVALG1YARGH1YVSL1E-----85  
DB 4383 GTCTCCAAAGGAGACCTGTCTCCCTGTGTCCATTTGGCTTCTGGGCCACCTGGGCCC 4442  
QY 86 -----G1YPRO1LEG1YSE1YSG1YGL1YULYSG1YASP-----96  
DB 4443 CCAGGTGTGGGCGCCCTCTAGACAGAAAGGCTCAAAAGGCTCCGGGGTCCATGGGC 4502  
QY 97 ---SERGLYAP1LEG1YPRO1PROG1YPROANG1YGL1YULYSG1YLEU1YLEU1YSG1YULY 115  
DB 4503 CCCCCGTGAGACACTGAGACTGACAGGCCACAGGCCCCCGGGTGCCTGCGAGAGTG 4562  
QY 116 SERGL1YULYSG1YASPMETG1YASPLYA-----A1AL1EG1YGL1 124  
DB 4563 CATGGCTGCGGACGCGCGCGCTTGTCTCCAGTCCCGCTTCCAGTGTGAGAGGCGGC 4622  
QY 125 METASPMANG1YASPMETG1YASPLYA-----A1AL1EG1YGL1 134  
DB 4623 CTGAGAGAGTGTGGCTGCGCTGCTCATG 4652

## RESULT 14

US-09-620-312D-110  
Sequence 110, Application US/09620312D  
Patent No. 6569662  
GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Liu, Chenghua  
APPLICANT: Asundi, Vinod  
APPLICANT: Zhang, Jie  
APPLICANT: Ren, Feiyan  
APPLICANT: Chen, Rui-hong  
APPLICANT: Zhao, Qing A.  
APPLICANT: Weinman, Tom  
APPLICANT: Xue, Aiding J.  
APPLICANT: Yang, Yonghong  
APPLICANT: Wang, Jian-Rui  
APPLICANT: Zhou, Ping  
APPLICANT: Ma, Yundong  
APPLICANT: Wang, Dunrui  
APPLICANT: Wang, Zhiwei  
APPLICANT: John Tillinghast  
APPLICANT: Drmanac, Radjole T.  
TITLE OF INVENTION: No. 6569662el Nucleic Acids and  
TITLE OF INVENTION: Polypeptides  
FILE REFERENCE: 784CIP28  
CURRENT APPLICATION NUMBER: US/09/620.312D  
CURRENT FILING DATE: 2000-07-19  
PRIOR APPLICATION NUMBER: 09/552,317  
PRIOR FILING DATE: 2000-04-25  
PRIOR APPLICATION NUMBER: 09/488,725  
PRIOR FILING DATE: 2000-01-21  
NUMBER OF SEQ ID NOS: 1105  
SOFTWARE: PL\_FL\_genes Version 1.0  
SEQ ID NO 110  
LENGTH: 6674  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1312)..(6330)  
NAME/KEY: misc\_feature

LOCATION: (1) ... (6674)  
OTHER INFORMATION: n = a, t, c or g  
US-09-620-312D-110

## Alignment Scores:

Align. No.: 3,73e-11 Length: 6674  
Score: 210.50 Matches: 46  
Percent Similarity: 44.54% Conservative: 7  
Best Local Similarity: 38.66% Mismatches: 31  
Query Match: 14.61% Indels: 35  
DB: 4 Gaps: 2

US-09-806-277A-6 (1-271) x US-09-620-312D-110 (1-6674)

QY 23 GYHISProGInProAlaGlyAspAspAlaCySerValGlnIleValProGlyLeu 42  
DB 4654 GGGCTTACCTGGAGAAAAAGGTGACAAAGC-----CTCCCGAGATTG 4695  
QY 43 LysGlyAspAlaGlyGlyValAspLysGlyValAlaProGlyArgValGly 62  
DB 4696 GATGGCATCCCTGGTGTCAAGAGAGACAGGCTTCTGAGACTCTGGCCCAAGGC 4755  
QY 63 ProThrGlyGlyLysGlyAsp-----69  
DB 4756 CCAGCTGGCCAGAAAGGGAGCCAGCATGATGAAATCCCGGGTCAGCAGAGAGAAG 4815  
QY 70 -----MetGlyAspLys 73  
DB 4816 GGTGACCAAGCTTACCAAGAGAGATTCCAGGGTTTCCAGGGCCAAAGAGAGAAA 4875  
QY 74 GlyGlyLysGlySerValGlyArgHisGlyLysIleGlyProIleGlySerLysGly 93  
DB 4876 GCTTCAAGAGGTGAGTGGTGTCCAGAGATTACCCGGAGCCAGAAATTCCTGATCC 4935  
QY 94 LysGlyAspSerGlyAspIleGlyProProGlyProAsnGlyLysProGlyLeuPro 112  
DB 4936 AAAGAGAGCAAGGATTCATGGTCTCCGGGCCCCAGGAGACAGCCGGGTTACCG 4992

## RESULT 15

US-09-919-497-6  
Sequence 6, Application US/09919497  
Patent No. 6773883  
GENERAL INFORMATION:  
APPLICANT: Mutter, George L.  
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER  
FILE REFERENCE: B0801/7225  
CURRENT APPLICATION NUMBER: US/09/919,497  
PRIORITY FILING DATE: 2001-07-31  
PRIOR APPLICATION NUMBER: US 60/221,735  
NUMBER OF SEQ ID NOS: 100  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 6  
LENGTH: 6158  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: Unsure  
LOCATION: (2434) .. (2434)  
OTHER INFORMATION: n = a, c, g or t/u  
US-09-919-497-6

## Alignment Scores:

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Score: 210.00 Matches: 81  
Percent Similarity: 34.11% Conservative: 36  
Best Local Similarity: 23.62% Mismatches: 100  
Query Match: 14.57% Indels: 126  
DB: 4 Gaps: 13

US-09-806-277A-6 (1-271) x US-09-919-497-6 (1-6158)

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DB 4446 GAGCAACCTGCTGCTTATGGAGACTCTCTGCG-----TTACTGCTCTC 4487  
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DB 4488 AAAGTGAGCCCTGGCTCCCAAGGGGTGAAGAGGACATCTGTTAATATGGCTGATTTGGT 4547  
QY 63 ProThrGlyGlyLysGlyAspMetGlyAspLys-----73  
DB 4548 CTTCCAGAGAAAGAGGAGAAAAAGGTGACCGAGGCTCTCCGAACTCAAGATCTCCA 4607  
QY 74 GlyGlyLysGlySerValGlyArgHisGlyLysIleGlyProIle-----88  
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QY 89 -----GlySerLysGly 92  
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QY 93 GlyLysGlyAspSerGlyAspIleGlyProProGlyProAsnGlyValLysProGly-----110  
DB 4728 CAGAAAGTGACATGATGCTTCCAGGGCTCTGAGCTTCAGGTCACCTGATGAATC 4787  
QY 111 -----LeuProCySerGlyLysSerGln-----117  
DB 4788 ATTCAAGCTTACCATCTTGTCTCCAAAAAGAGAGACATCTGAAGCATGCA 4847  
QY 118 -----LeuArgLysAlaIleGlyLys 124  
DB 4848 GCAGATGACAGATGATATATCTTGTATCTCTGATGATGAGAAATATTTGGTCTC 4907  
QY 125 MetAspAsnGlnValSerGlnLeuThrSerGlyLeuLysPheIleLysAsnAlaValAla 144  
DB 4908 CTC---AATTCCTGAAACAGACATCGAGCATATGAATTTCCATGGTACTCAGACC 4964  
QY 145 GlyValArgGlyLysThrGlySerLysIleTyrLeuLeu-----ValLysGlyLys 161  
DB 4965 AATCCAGCCCACTGTGAAGACCTGCAACTCAGCATCTGATCTCCAGATGGTGA 5024  
QY 162 ArgTyrAlaAspAlaGlnLeuSerCySerGly-----172  
DB 5025 TATTTGATTTGATCTTACCAAGGTTGCTCAGAGATCTCTCAAGTTATCTGTAATTTTC 5084  
QY 173 ---ArgGlyGlyThrLeuSerMetProLysAspGlyAlaAlaAsnGlyLeuMetAlaAla 191  
DB 5085 ACATCTGGTGTGAGACTTGATTTATCCAGAAATAATCTGAGGA-----5132  
QY 192 TyrLeuAlaGlnAlaGlyLeuAlaArgValPheIleGlyIleAsnAspLeuGlyLysGly 211  
DB 5133 -----GTAAGAATTTCAATCATGCGCAAAAGGAG 5159  
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QY 232 GluProAsnAsnAlaTyrAsp---GluGlyAspCyValGlyMetVal-----246  
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QY 247 -----AlaSerGly 249  
DB 5256 CTGAATCTTGAAGCTCTGCTCGCAAAATTTACCTACCACTGATCATCAGCA 5315  
QY 250 GlyTyrAspAspValAlaCyHisThr-----ThrMetLysPheMetCySerGlyPhe 266  
DB 5316 GCTGTGATGATGTGATCATCAGAAAGTTATGACAAAGCACTTGCTTCTGGGATCAAT 5375  
QY 267 AspLysGlyLys 269  
DB 5376 GATGAGAG 5384

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Mon Dec 20 08:22:14 2004

us-09-806-277a-6.rnt

Page 11

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 17, 2004, 03:40:34 ; Search time 5448 Seconds

(without alignments)  
2352.333 Million cell updates/sec

Title: US-09-806-277a-6

Perfect score: 1441

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9083458

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45  
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: gp\_hcg:\*  
3: gp\_in:\*  
4: gp\_om:\*  
5: gp\_ov:\*  
6: gp\_pat:\*  
7: gp\_ph:\*  
8: gp\_pl:\*  
9: gp\_pr:\*  
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11: gp\_ro:\*  
12: gp\_sy:\*  
13: gp\_un:\*  
14: gp\_vl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1441	100.0	813	6	BD103332 Novel col
2	1441	100.0	1238	6	AR252616 Sequence
3	1441	100.0	1238	6	AX403469 Sequence
4	1441	100.0	1238	6	AX454582 Sequence

5	1441	100.0	1238	6	AX491060	Sequence
6	1441	100.0	1238	9	AY358439	Homo sapi
7	1441	100.0	1248	9	BC000078	Homo sapi
8	1441	100.0	1341	6	BD103302	Novel col
9	1405	97.5	1417	9	BC009951	Homo sapi
10	1331	92.4	813	6	BD103338	Novel col
11	1331	92.4	1522	6	BD103307	Novel col
12	1289	89.5	741	6	BD103341	Novel col
13	1289	89.5	1269	6	BD103331	Novel col
14	1286	89.2	741	6	BD103340	Novel col
15	1286	89.2	1269	6	BD103333	Novel col
16	1234.5	85.7	735	6	BD103333	Novel col
17	1234.5	85.7	1139	6	BD103303	Novel col
18	1216	84.4	708	6	CQ716215	Sequence
19	1144	79.4	669	6	BD103339	Novel col
20	1144	79.4	1197	6	BD103329	Novel col
21	1138	79.0	1272	5	BC056052	Xenopus laevis
22	1095	76.0	663	6	BD103336	Novel col
23	1095	76.0	1067	6	BD103305	Novel col
24	1082.5	75.1	663	6	BD103337	Novel col
25	1082.5	75.1	1067	6	BD103306	Novel col
26	965	67.0	591	6	BD103335	Novel col
27	965	67.0	995	6	BD103304	Novel col
28	840	58.3	477	6	BD103334	Novel col
29	805	55.9	139357	9	AC010907	Homo sapi
30	776.5	53.9	175475	2	AC123631	Mus muscu
31	757	52.5	246539	2	AC125638	Rattus no
32	716.5	49.7	1594	9	AB002631	Homo sapi
33	716.5	49.7	1595	6	E29008	Novel colle
34	716.5	49.7	1686	6	AX959723	Sequence
35	715.5	49.7	1594	6	CQ719085	Sequence
36	710.5	49.3	1016	6	CQ767629	Sequence
37	710.5	49.3	1016	6	AX376032	Sequence
38	710.5	49.3	1016	6	AX359038	Homo sapi
39	703.5	48.8	867	10	AB016429	Mus muscu
40	691.5	48.0	212049	5	BX005484	Zebrafish
41	422	29.3	141262	9	AC080033	Homo sapi
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43	422	29.3	234922	2	AC097055	Rattus no
44	413.5	28.7	166860	10	AC115924	Mus muscu
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#### ALIGNMENTS

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LOCUS	BD103332	Novel collectin.				
DEFINITION	BD103332	Novel collectin.				
ACCESSION	BD103332.1	GI:22648906				
VERSION	BD103332.1	GI:22648906				
KEYWORDS	WO 0181401-A/31.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
TITLE	Wakamiya, N., Keshi, H., Otani, K., Sakamoto, T. and Kishi, Y.					
JOURNAL	Novel collectin					
COMMENT	Patent: WO 0181401-A 31 01-NOV-2001; FUSO PHARMACEUTICAL INDUSTRIES LTD, NOBUTAKA WAKAMIYA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI SAKAMOTO, YUICHIRO KISHI OS Homo sapiens (human) PN WO 0181401-A/31 PD 01-NOV-2001 PF 23-APR-2001 WO 2001JP003468 PR 21-APR-2000 JP 00P 120358 PI NOBUTAKA WAKAMIYA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI PI SAKAMOTO, PI YUICHIRO KISHI PC C07K14/47, C12N15/12, A01K67/027, C07K16/18, G01N33/53 CC Novel collectin FH Key Location/Qualifiers					

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 /organism='Homo sapiens (human)'.  
 Location/Qualifiers  
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 /mol\_type='genomic DNA'  
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 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 Gaps: 0

US-09-806-277a-6 (1-271) x BD103332 (1-813)

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 Db 1 ATGAGGGGGGAAATCTGGCCCTGGTGGCGGTTCTAATCAAGCTGCGCTTCTGTCACTGCTG 60  
 QY 21 ProSerGlyHisProGlnProAlaGlyAAspAspAlaCysSerValGlnIleLeuValPro 40  
 Db 61 CCATCTGGAACATCTCTACGCGGCTGGCGATGACCGCTGCTGTGCAATCTGTCTCT 120  
 QY 41 GlyLeuLysGlyAAspAlaGlyGluLysGlyAAspLysGlyAlaProGlyAAspProGlyAAsp 60  
 Db 121 GGCTCTAAAGGGGATGCGGGAG 180  
 QY 61 ValGlyProThrGlyGluLysGlyAAspMetGlyAAspLysGlyGluLysGlySerValGly 80  
 Db 181 GTCCGCCCCCAGGAG 240  
 QY 81 ArgHisGlyLysIleGlyProIleGlySerLysGlyGluLysGlyAAspSerGlyAAspIle 100  
 Db 241 CGTATGGAAGAAATTTGGTCCATTTGGCTCTAAAGTGAAGAGAGAGAGAGAGAGAGAGAG 300  
 QY 101 GlyProProGlyProAsnGlyGluProGlyLeuProCysGlyGlyCysSerGlnLeuAAspLys 120  
 Db 301 GAGACCCCTGGTCTTAATGAG 360  
 QY 121 AlaIleGlyGluMetLysAsnGlnValSerGlnLeuThrSerGlnLeuLysPheIleLys 140  
 Db 361 GCCATCGGGAGATGACCAACAGAGTCTCTCAAGTCAAGAGAGAGAGAGAGAGAGAGAGAG 420  
 QY 141 AsnAlaValAlaGlyValArgGluThrGluSerLysIleTyrLeuLeuValLysGluGlu 160  
 Db 421 AATGCTGTCCGCGGTGTGGCGAG 480  
 QY 161 LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyArgGlyGlyTyrThrLeuSerMetPro 180  
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 QY 181 LysAspGluAlaAlaAsnGlyLeuMetAlaIleTyrLeuAlaGlnIleGlyLeuAlaArg 200  
 Db 541 AAGAGACAGAGCTGCGCATGAGCTGATGCGCATGAGCTGAGAGAGAGAGAGAGAGAGAGAG 600  
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 Db 601 GTCTTCATCGGCATCAAG 660  
 QY 221 ProMetArgThrPheAsnLysTyrArgSerGlyGluProAsnAsnAlaIleTyrAspGluGlu 240  
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 QY 241 AspCysValGluMetValAlaSerGlyGlyTyrPheAsnAspValAlaCysHisSerThrMet 260  
 Db 721 GACTGCGTGGAGATGGGCTCGGGCGGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780  
 QY 261 TyrPheMetCysGluPheAspLysGluAsnMet 271

Db 781 TACTTCATGCTGAGTGTGACAG 813

RESULT 2  
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 LOCUS AR252616 1238 bp DNA linear PAT 20-DEC-2002  
 DEFINITION Sequence 356 from patent US 6478825.  
 AR252616  
 VERSION AR252616.1 GI:27300524  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 1238)  
 WINTERBOTTOM, J.M., SHIMP, L., BOYCE, T.M. and KASE, D.  
 Implant, method of making same and use of the implant for the  
 treatment of bone defects  
 Patent: US 6478825-A 356 12-NOV-2002;  
 Location/Qualifiers  
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JOURNAL  
 FEATURES  
 source

## ORIGIN

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US-09-806-277a-6 (1-271) x AR252616 (1-1238)

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 QY 61 ValGlyProThrGlyGluLysGlyAAspMetGlyAAspLysGlyGluLysGlySerValGly 80  
 Db 247 GTCCGCCCCCAGGAG 306  
 QY 81 ArgHisGlyLysIleGlyProIleGlySerLysGlyGluLysGlyAAspSerGlyAAspIle 100  
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 VERSION AX403469.1 GI:21436970  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 Asakazaki, A., Baker, K.P., Botstein, D., Desnover, L., Eaton, D.,  
 Ferrara, N., Gerber, H., Gerritsen, M., Goddard, A., Godowski, P.,  
 Grimaldi, C.J., Gurney, A.L., Kijavich, I., Napier, M.A., Pan, J.,  
 Paoni, N.F., Roy, M., Stewart, T.A., Tunnas, D., Watanabe, C.K.,  
 Williams, P., Wood, W.I., and Zhang, Z.  
 Secreted and transmembrane polypeptides and nucleic acids encoding  
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 Patent: WO 0073454-A 356 07-DEC-2000;  
 JOURNAL Genentech Inc. (US)  
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 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 Gaps: 0  
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QY 101 GIyProProGIyProAsnGIyGIuPProGIyLeuProCySgIuCYrSerGIuLeuArGIyS 120  
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 ORGANISM Homo sapiens (human)  
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 REFERENCE 1 Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,  
 Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,  
 Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.,  
 and Ye, W.  
 Compositions and methods for the diagnosis and treatment of  
 disorders involving angiogenesis  
 Patent: WO 0208284-A 167 31-JUN-2002;  
 JOURNAL Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone  
 (US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,  
 Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;  
 Hillan, Kenneth J. (US) ; Marsters, Scott A. (US) ; Pan, James (US)  
 ; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;  
 Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William  
 I. (US)  
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Percent Similarity: 100.00%  
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US-09-806-277a-6 (1-271) x AX454582 (1-1238)

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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

# REFERENCE

1 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 Baker, K.P., Ferrera, N., Gerber, H., Gerritzen, M.E., Goddard, A.,  
 Godowski, P.J., Guney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,  
 Paoni, N.F., Stephan, U.P., Watanabe, C.K., Williams, P.M., Wood, W.I.  
 and Ye, W.  
 Compositions and methods for the diagnosis and treatment of  
 disorders involving angiogenesis  
 Patent: WO 0200690-A 167 03-JAN-2002;  
 Genentech, Inc. (US)

# TITLE

Compositions and methods for the diagnosis and treatment of  
 disorders involving angiogenesis  
 Patent: WO 0200690-A 167 03-JAN-2002;  
 Genentech, Inc. (US)

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 VERSION AY358439.1  
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 REFERENCE 1 (bases 1 to 1238)  
 Clark,H.F., Gurney,A.L., Adaya,E., Baker,K., Baldwin,D., Brush,J.,  
 Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,  
 Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Haas,P.E.,  
 Heidens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,  
 Lee,J., Lewis,L., Liao,D., Mark,M., Robble,E., Sanchez,C.,  
 Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,  
 Stinson,J., Vagte,A., Vandlen,R., Watanabe,C., Wiesand,D., Woods,K.,  
 Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,  
 Goddard,A., Wood,W.I. and Godowski,P.  
 The Secreted Protein Discovery Initiative (SPDI), a Large-Scale  
 Effort to Identify Novel Human Secreted and Transmembrane Proteins:  
 A Bioinformatics Assessment  
 Genome Res. 13 (10), 2265-2270 (2003)  
 JOURNAL PUBMED 12975309  
 REFERENCE 2 (bases 1 to 1238)  
 Clark,H.F.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,  
 Inc., 1 DNA Way, South San Francisco, CA 94080, USA  
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 REFERENCE 1 (bases 1 to 1248)  
 Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,  
 Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,  
 Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,  
 Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,

Diatchenko, L., Marasina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loguigliano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.D., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fehey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickerson, M.C., Rodriguez, A.C., Grimod, J., Schmutz, J., Myers, R.M., Buetterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 12477932

2 (bases 1 to 1248)  
Strauberg, R.  
Direct Submission  
Submitted (03-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
On Aug 20, 2003 this sequence version replaced gi:12652660.  
Contact: MGC help desk  
Email: [gcgaps-remail.nih.gov](mailto:gcgaps-remail.nih.gov)  
Tissue Procurement: ATCC  
cDNA Library Preparation: Rubin Laboratory  
DNA Sequencing by: The I.M.A.G.E. Consortium (LNLN)  
<http://www.systemsbio.org>  
contact: [amadan@systemsbio.org](mailto:amadan@systemsbio.org)  
Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.lnl.gov>  
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US-09-806-277A-6 (1-271) x BC000078 (1-1248)

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SOURCE  
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Contact: nhec.mgc@nhgri.nih.gov  
 Akter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
 Blakeley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,  
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,  
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Clone distribution: MGC clone distribution information can be found  
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 ADAOLSCGGRGTLSPMDKDEANGLMAVLAQGLARVFGINDLEKGEAVVSDHSP  
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## CDS

## gene

## ORIGIN

Alignment Scores:  
 Pred. No.: 5.4e-84 Length: 1417  
 Score: 1405.00 Matches: 271  
 Percent Similarity: 90.94% Conservative: 0  
 Best Local Similarity: 90.94% Mismatches: 27  
 Query Match: 97.50% Gaps: 1

US-09-806-277a-6 (1-271) x BC009951 (1-1417)

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 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
 207 CCATCTGCACATCTCCAGCCGCTGCGATGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 266  
 41 GlyLeuValGlyAspAlaGlyValGlyValGlyValGlyValGlyValGlyValGlyValGly 60  
 267 GGCCTCAAAAGGAGATGCGGAGAGAAAGGAGACAAAGGCGCCCGGAGCGGCTTGAAGA 326  
 61 ValGlyProThrGlyGlu-Lys-----GlyAspMetGlyAspValGly 74  
 327 GTGCGGCCCAAGGAGAAAGGAGAGCAAGTCAAGCCAGTGTGACAGCTTGCATCTCCAA 386  
 68 -----GlyAspMetGlyAspValGly 74  
 387 AAGGAGTGCACCTGCTGCTTTGTAGAAATGGGATCACAGGAGCATGGGGGAGCAAAAGG 446

74 YGlnlyGlySerValGlyArgHisGlyLysIleGlyProIleGlySerIleGlyGly 94  
 Db 447 ACAGAAAGCAGATGTTGGTGTCTCATGAAATAATTTGCTCCATGTGCTTAAAGGTAGAA 506  
 QY 94 eGlyAspSerGlyAspIleGlyProProGlyProAsnGlyGluProGlyLeuProCysG1 114  
 Db 507 AGAGATTCGGTGTACATGAGACCCCTGTGTCTTAATGAGAAACAGGCTCCCATGTGA 566  
 QY 114 uCysSerGlnLeuValGlyAlaIleGlyGluMetAspAsnGlnValSerGlnLeuThse 134  
 Db 567 GTCCAGCCAGCTGCGGAGGCGCATCGGGAGATGAGCAACAGGCTCTCCACCTGACCG 626  
 QY 134 rGluLeuValPheIleValAsnAlaValAlaGlyValArgGluThrGlnSerIleIleTy 154  
 Db 627 CGAGCTCAAGTTCTATCAAAATGCTGTCCGCGGTGTGCGGAGACGAGAGCAAGATCTA 686  
 QY 154 rLeuLeuValIleGlyGluIleValArgValPheIleGlyIleAsnAspLeuGluIleGlyValAlaPh 214  
 Db 687 CCGTGTGTGAG 746  
 QY 174 YGlyThrLeuSerMetProIleAspGluAlaAlaAsnGlyLeuMetAlaAlaTyIleuAl 194  
 Db 747 GGGCAGCTGAGCATGCCCAAGAGCAGGCTGCAATGCTGATGCGCATACCTGCGC 806  
 QY 194 aGlnAlaGlyLeuAlaArgValPheIleGlyIleAsnAspLeuGluIleGlyValAlaPh 214  
 Db 807 GCAAGCCGGCTGCGCGGTGTCTTATCGGATCAACAGCTTGGAGAGAGAGAGAGAGAGAG 866  
 QY 214 eValTySerAspHisSerProMetArgThrPheAsnIleValArgSerGlyGluProAs 234  
 Db 867 CGTGATCTGTGACCATCTCCCGCATGCGGAGCTTCAACAAGTGGCGGAGTGTAGCCCA 926  
 QY 234 nAlaAlaTyArgGluGluAspCysValGluMetValAlaSerGlyGlyThrAsnAspVa 254  
 Db 927 CAATGCTTCAG 986  
 QY 254 lAlaCysHisThrThrMetTyPheMetCysGluPheAspValGluAsnMet 271  
 Db 987 GGCTGCGACCAACACCATGACTTCAATGTGTGATTTGACAGAGAGAACATG 1038

RESULT 10  
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 DEFINITION BD103338  
 ACCESSION BD103338  
 VERSION BD103338.1 GI:22648912  
 KEYWORDS WO 0181401-A/37.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.  
 1 (bases 1 to 813)  
 REFERENCES  
 1 Makamita, N., Keshi, H., Ocani, K., Sakamoto, T. and Kishi, Y.  
 Novel collectin  
 Patent: WO 0181401-A 37 01-NOV-2001;  
 FUSO PHARMACEUTICAL INDUSTRIES LTD, NOBUTAKA WAKAMITVA, HIROYUKI  
 KESHI, KATSUKI OTANI, TAKASHI SAKAMOTO, YUICHIRO KISHI  
 COMMENT  
 OS Mus musculus (mouse)  
 PN WO 0181401-A/37  
 PD 01-NOV-2001  
 PF 23-APR-2001 WO 2001P003468  
 PR 21-APR-2000 JP 00P 120358  
 PI NOBUTAKA WAKAMITVA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI PI  
 SAKAMOTO.  
 PT YUICHIRO KISHI  
 PC C07K14/47, C12N15/12, C12P21/02, A01K67/027, C07K16/18, G01N33/53  
 CC Novel collectin  
 FH Key  
 FT source  
 FT location/Qualifiers  
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## FEATURES

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/organisms="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"

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Percent Similarity:	96.51%
Best Local Similarity:	91.88%
Query Match:	92.37%
DB:	6
Length:	813
Matches:	249
Conservative:	12
Mismatches:	10
Indels:	0
Gaps:	0

US-09-806-277A-6 (1-271) x BD103338 (1-813)

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Db	1	ATGATGAGGGAGCTGGCTCTTCCAGGCAATGCTGATTAAGCTGGCTTTCCCTGCTGCTG	60
QY	21	ProSeRgIyHLeProGIInProAlaGIyAaSPaSPaLlCySeSeRgAlGInIleLeuValPro	40
Db	61	CCATCTGGATGTCCTTCAGCAGACACACAGAGAGCGCTGCTCTGTGCAGATTCTGTGCCC	120
QY	41	GIyLeuLySeGIyASpAlaGIyGIyulLySeGIyASpLySeGIyAlaProGIyArProGIyArG	60
Db	121	GCGCTCAAAAGGGGATGCGAGAGAAAGGAGACAAAGAGAGCCCAAGAGCGGCCAGGAGA	180
QY	61	ValGIyProThGIyGIyulLySeGIyASpMetGIyASpLySeGIyGIyulLySeGIySeRValGIy	80
Db	181	GTCCGGCCCTCAAGGAGAAAGAGACATGTGGGGACAAAGAGACAGAAAGGCACCTGTGGC	240
QY	81	ArGHlAGLyLyaIISeGIyProIISeGIySeRLeYSeGIyGIyulLySeGIyAaSPeSeRgIyASpIle	100
Db	241	CGCCATGGAAAAATTGGTCCCATTTGGCCGCAAAAGGTGAAGAAAGAGATTCTGGTGAATATC	300
QY	101	GIyProProGIyProAaenGIyGIuProGIyLeuProCySeGIyLycySeSeRGIInLeuArGIyLys	120
Db	301	GGAGCCCCCTGGCCCGACGTGAGAACCTGGATATTCATGTGATGTGCAGTCACTGAGAGAG	360
QY	121	AlaIISeGIyLumecaSPaenGIInValSeRGIInLeuThSeRGIuLeuLySPheIIeLys	140
Db	361	GCTATTGGGGAATGAGACAAACGAGCTCACTCACTACACTGACTAAATTCAATAAAA	420
QY	141	AenAlaValAlaGIyValaRgGIuThRGIuSeRLeYIleThLeuLeuValLySGIuGIu	160
Db	421	AATGCTGTTGCTGGCTGGCGCGAGACTGAGAGCAAGTCTACTCTGCTGGTGAAGAGAGAG	480
QY	161	LySaRgTYrAlaASpAlaGIInLeuSeRcySeGIInLyArGIyGIyThRLeuSeRmetPro	180
Db	481	AAGCGGTAGCAGATGCCAGAGTGTCTCGCAAGCCGAGGGGGACACTGACATATGCC	540
QY	181	LySaSPaRGIuAlaAlaenGIyLeuMetAlaAlaTYrLeuAlaGIInalagIyLeuAlaArg	200
Db	541	AAAGACGAGCGAGCCCATGGCTCGATGGCTCTACTCTGGCACAGGCTGGCCCTGGCCCCA	600
QY	201	ValPheIISeGIyIIeAenAaSPeLeuGIyLySGIyAlaPheValTYrSeSaSPHlSeSer	220
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QY	221	ProMetArGThR-PheAenLySTrPaRgSeRGIyGIuProAaenAaAlaTYrAaSPeGIuGIu	240
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QY	241	AaSPCySeValGIuMetAlaAlaSeRGIyGIyTPaSaAaSPaValAlaCySPHlSTHTrMet	260
Db	721	GACTGTGTGGAATAGTGGCTCTCAAGGTGGCTGGAAGAATGTGGCTGCCACATTAACATG	780
QY	261	TYrPheMetCySeGIuPheAaSPySGIyAaenMet	271
Db	781	TACTTCATGTGGAGTTTGACAAAGGAACCTTG	813

LOCUS	BD103307	1522 bp	DNA	linear	PAT 27-AUG-2002
DEFINITION	Novel collectin.				
ACCESSION	BD103307				
VERSION	BD103307.1	GI:22648881			
KEYWORDS	WO 0181401-A/6.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1522)				
AUTHORS	Wakamaya, N., Keshi, H., Otani, K., Sakamoto, T. and Kishi, Y.				
TITLE	Novel collectin				
JOURNAL	Patent: WO 0181401-A 6 01-NOV-2001;				
	FUSO PHARMACEUTICAL INDUSTRIES LTD, NOBUTAKA WAKAMITSA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI SAKAMOTO, YUICHIRO KISHI				
COMMENT	OS Mus musculus (mouse)				
	PN	WO 0181401-A/6			
	PD	01-NOV-2001			
	PF	23-APR-2001	WO 2001JP003468		
	PR	21-APR-2000	JP 00P 120358		
	PI	NOBUTAKA WAKAMITSA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI SAKAMOTO,			
	PI	YUICHIRO KISHI			
	PC	C07K14/47, C12N15/12, C12P21/02, A01K67/027, C07K16/18, G01N33/53			
	CC	Novel collectin	Location/Qualifiers		
	FT	Key	(157). (969).		
	FT	CDS	Location/Qualifiers		
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ORIGIN					
Alignment Scores:					
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Query Match:	92.37%	Indels:	0		
DB:	6	Gaps:	0		
US-09-806-277A-6 (1-271) x BD103307 (1-1522)					
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QY	21	Pro	Ser	G	I
DB	217	CCAT	CTG	ATG	CTG
QY	41	Gly	Leu	Leu	Val
DB	277	GGC	CTC	AAA	GGG
QY	61	Val	Gly	Pro	Thr
DB	337	GTC	GCC	CTT	ACA
QY	81	Arg	His	Gly	Leu
DB	397	CGC	CAT	GGA	AAA
QY	101	Gly	Pro	Pro	Gly
DB	457	GGA	CCC	CTG	CCC
QY	121	Ala	Ile	Gly	Met
DB	517	GCT	ATG	GGG	AGG
QY	141	Asn	Ile	Val	Ala

Db 577 AATGCTGTTGCTGCGCGGAGCACTGAGCAAGATCTTCTGCTGTAAGAAGAG 636  
Qy 161 LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyArgGlyGlyThrLeuSerMetPro 180  
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Qy 181 LysArgGlyAlaAlaAsnGlyLeuMetAlaAlaTyrLeuAlaGlnAlaGlyLeuAlaArg 200  
Db 697 AAGAAGCGAGCGCAATGCGCTGATGCTTCATACCTGCGACAGGCTGGCTGCCCGA 756  
Qy 201 ValPheIleGlyIleAsnAspLeuGlnGlyGlyAlaPheValTyrSerAspHisSer 220  
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Db 817 CCCATGCGAGACCTTCAACAGAGTGGCGAGTGAAGGCCCAACAGCCTATGATGAGAG 876  
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Db 877 GACTGTGTGAGATGATGCTGCTGAGTGGCTGGAATGATGTGGCTGCACATTAACATG 936  
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## RESULT 12

BD103341 741 bp DNA 1linear PAT 27-AUG-2002  
LOCUS Novel collectin.  
DEFINITION BD103341  
ACCESSION BD103341.1 GI:22648915  
VERSION WO 0181401-A/40.  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 741)  
AUTHORS Wakamaya,N., Keshi,H., Otani,K., Sakamoto,T. and Kishi,Y.  
TITLE Novel collectin  
JOURNAL Patent: WO 0181401-A 40 01-NOV-2001;  
FUSO PHARMACEUTICAL INDUSTRIES LTD, NOBUTAKA WAKAMIYA, HIROYUKI  
KESHI, KATSUKI OTANI, TAKASHI SAKAMOTO, YUICHIRO KISHI

## COMMENT

OS Homo sapiens (human)  
PN WO 0181401-A/40  
PD 01-NOV-2001  
PF 23-APR-2001 WO 2001JP003468  
PR 21-APR-2001 JP 00P 120358  
PI NOBUTAKA WAKAMIYA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI  
SAKAMOTO, YUICHIRO KISHI  
PC C07K14/47, C12N15/12, C12P21/02, A01K67/027, C07K16/18, G01N33/53  
CC Novel collectin  
PP Key  
FT source 1..741  
FT Location/Qualifiers  
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## ORIGIN

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Pred. No.: 1,23e-76 Length: 741  
Score: 1289.00 Matches: 247  
Percent Similarity: 91.14% Conserves: 0  
Best Local Similarity: 91.14% Mismatches: 0  
Query Match: 89.45% Indels: 24  
DB: 6 Gaps: 1

US-09-806-277A-6 (1-271) x BD103341 (1-741)

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Qy 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
Db 61 CCATCTGGACATCTCTCAGCGCGCTGGCGATGAGCGCTGCTCTGTGCAAGATCTGTCCT 120  
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Db 121 GGCCTCAAGAGGATGCGGGAGAGAAAGGAGACAAAGCCGCCCGGACGGCTGGAAGA 180  
Qy 61 ValGlyProThrGlyGlyLysGlyAspMetGlyAspLysGlyGlyLysSerValGly 80  
Db 181 GTGGGCCCCAGGAGAA-----  
Qy 81 ArgHisGlyLysIleGlyProIleGlySerLysGlyGlyLysGlyAspSerGlyAspIle 100  
Db 199 -----AAGGTGAGAAAGAGATTCGGTGACATA 228  
Qy 101 GlyProProGlyProAlaGlyGlyProGlyLeuProCysGlyLysSerGlnLeuArgLys 120  
Db 229 GGAACCCCTGCTCTATGAGAAACAGGCTCCCATGTGATGCGACGCGCTGCGCAG 288  
Qy 121 AlaIleGlyLysMetAspAsnGlnValSerGlnLeuThrSerGlnLeuLysPheIleLys 140  
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Qy 141 AsnAlaValAlaGlyValArgGlyThrGlnSerLysIleTyrLeuLeuValLysGluGlu 160  
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Qy 161 LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyArgGlyGlyThrLeuSerMetPro 180  
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## RESULT 13

BD103331 1269 bp DNA 1linear PAT 27-AUG-2002  
LOCUS Novel collectin.  
DEFINITION BD103331  
ACCESSION BD103331.1 GI:22648905  
VERSION WO 0181401-A/30.  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1269)  
AUTHORS Wakamaya,N., Keshi,H., Otani,K., Sakamoto,T. and Kishi,Y.  
TITLE Novel collectin  
JOURNAL Patent: WO 0181401-A 30 01-NOV-2001;  
FUSO PHARMACEUTICAL INDUSTRIES LTD, NOBUTAKA WAKAMIYA, HIROYUKI

COMMENT  
KESHI, KATSUKI OTANI, TAKASHI SAKAMOTO, YUICHIRO KISHI  
OS Homo sapiens (human)  
PD WO 0181401-A/30  
PD 01-NOV-2001  
PF 23-APR-2001 WO 2001JP003468  
PR 21-APR-2000 JP 00P 120358  
PI NOBUTAKA WAKAMIYA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI PI  
SAKAMOTO,  
PI YUICHIRO KISHI  
PC C07K14/47, C12N15/12, C12P21/02, A01K67/027, C07K16/18, G01N33/53  
CC Novel collection  
FH Key  
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Best Local Similarity: 91.14% Mismatches: 0  
Query Match: 89.45% Indels: 24  
Gaps: 1  
US-09-806-277A-6 (1-271) x BD103331 (1-1269)  
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QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
DB 335 CCATCTGGACATCTCTCAAGCCGCTGGCCCATGACGCTCTGCTGTCAGATCTCTCCCT 384  
QY 41 GlyLeuLysGlyAspAlaGlyGlyLysGlyAspLysGlyAlaProGlyArgProGlyArg 60  
DB 385 GGCCCTCAAGGGGATGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 444  
QY 61 ValGlyProThrGlyGlyLysGlyAspMetGlyAspLysGlyGlyLysGlySerValGly 80  
DB 445 GTCCGCCCCACCGGAGAA----- 462  
QY 81 ArgHisGlyLysIleGlyProIleGlySerLysGlyLysGlyAspSerGlyAspIle 100  
DB 463 -----AAAGGTGAGAAAGAGATTCCGGTACAT 492  
QY 101 GlyProProGlyProAsnGlyGlyLysProGlyLysProCysGlyCysSerGlnLeuArgLys 120  
DB 493 GGACCCCTCGTCTTAATGAGAACAGAGCTCCCATGTGATGAGCAGCTGCGCAG 552  
QY 121 AlaIleGlyLysMetAspAsnGlnValSerGlnLeuThrSerGlnLeuLysPheIleLys 140  
DB 553 GCCATCGGGAGATGAGAACAGAGTCTCTCAGCTGACAGCAGGACCTCAAGTTCACTCAAG 612  
QY 141 AsnAlaValAlaGlyValArgGlyLysThrGlySerLysIleTyrLeuLeuValLysGlyLys 160  
DB 613 AATGCTGTGCGCGGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 672  
QY 161 LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyArgGlyLysThrLeuSerMetPro 180  
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QY 221 PrometArgThrPheAsnLysTyrArgSerGlyGlyLysProAsnAsnAlaTyrArgGlyLys 240  
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QY 261 TyrPheMetCysGlyLysPheAspLysGlyLysMet 271  
DB 973 TACTTCACTGTGTGATTTGACAGAGAGACATG 1005  
RESULT 14  
BD103340 741 bp DNA linear PAT 27-AUG-2002  
BD103340  
LOCUS Novel collection.  
DEFINITION Novel collection.  
BD103340  
VERSION BD103340.1 GI:22648914  
KEYWORDS WO 0181401-A/39.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 741)  
AUTHORS Wakamiya,N., Keshi,H., Otani,K., Sakamoto,T. and Kishi,Y.  
TITLE Novel collection  
JOURNAL Patent: WO 0181401-A 39 01-NOV-2001;  
FUSO PHARMACEUTICAL INDUSTRIES LTD, NOBUTAKA WAKAMIYA, HIROYUKI  
KESHI, KATSUKI OTANI, TAKASHI SAKAMOTO, YUICHIRO KISHI  
COMMENT  
OS Homo sapiens (human)  
PN WO 0181401-A/39  
PD 01-NOV-2001  
PF 23-APR-2001 WO 2001JP003468  
PR 21-APR-2000 JP 00P 120358  
PI NOBUTAKA WAKAMIYA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI PI  
SAKAMOTO,  
PI YUICHIRO KISHI  
PC C07K14/47, C12N15/12, C12P21/02, A01K67/027, C07K16/18, G01N33/53  
CC Novel collection  
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Pred. No.: 1,946-76 Length: 741  
Score: 1286.00 Matches: 247  
Percent Similarity: 91.14% Conservative: 0  
Best Local Similarity: 91.14% Mismatches: 0  
Query Match: 89.24% Indels: 24  
Gaps: 1  
US-09-806-277A-6 (1-271) x BD103340 (1-741)  
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Qy      101 GilyProProGlyProAsnGlyGlyLupProGlyLeuProGlyGlyGlyGlyGlyGlyGlyGlyGly 120
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Qy      161 LyAArgTyrlAaAspAlaGlnLeuSerCyseGlnGlyArgGlyGlyThrlleuSerMetPro 180
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Qy      201 ValPhe11leglylAenAspLeuGlyLysGlyGlyAlaPheValTyrlSerAspHisSer 220
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DEFINITION Novel collectin.
ACCESSION BD103330
VERSION   BD103330.1 GI:22648904
KEYWORDS  WO 0181401-A/29.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
          1 (bases 1 to 1269)
REFERENCE Makamiya,N., Keshi,H., Ocani,K., Sakamoto,T. and Kishi,Y.
TITLE     Novel collectin
AUTHORS   Patent: WO 0181401-A 29 01-NOV-2001.
JOURNAL   FUSO PHARMACEUTICAL INDUSTRIES LTD, NOBUTAKA WAKAMIYA, HIROYUKI
          KESHI, KATSUKI OTANI, TAKASHI SAKAMOTO, YUICHIRO KISHI
          OS Homo sapiens (human)
          PN WO 0181401-A/29
          PD 01-NOV-2001
          PF 23-APR-2001 WO 2001JP003468
          PR 21-APR-2000 JP 00P 120358
          PI NOBUTAKA WAKAMIYA, HIROYUKI KESHI, KATSUKI OTANI, TARASHI PI
          SAKAMOTO,
          PI YUICHIRO KISHI
          PC C07K14/47, C12N15/12, C12P21/02, A01K67/027, C07K16/18, G01N33/53
          CC Novel collectin
          FH Key Location/Qualifiers
          FT CDS Location/Qualifiers
          (265)..(1005).
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            /db_xref="taxon:9606"

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Alignment Scores:
Pred. No.:      3,4e-76
Score:          1286.00
Percent Similarity: 91.14%
Best Local Similarity: 91.14%
Query Match:    89.24%
DB:              6
Gaps:            1

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Qy      21 ProSerGlyYHisProGlnProAlaGlyAspAspAlaCyseValGln1leuValPro 40
Db      325 CCATCTGACATCTCAGCGGCTGGCGATGACGCTGTGTGACAGATCTGTGCTCCT 384
Qy      41 GlyLeuLysGlyAspAlaGlyGlyLysGlyAspLyGlyAlaProGlyArgProGlyArg 60
Db      385 GGCTCTC-----
Qy      61 ValGlyProThrGlyGlyLysGlyAspMetGlyAspLyGlyGlyLysGlySerValGly 80
Db      391 -----AAAGGACATGGGGGCAAGACAGAAAGGACATGTGGT 432
Qy      81 Arghisgilyysilegylproilleglyserlysgilyulysgilyaspsergilyasp1le 100
Db      433 CGTCATGGAATAATGGTCCCATTTGGCTCTAAAGGTGAGAAAGAGATTCCGGTGACATA 492
Qy      101 GilyProProGlyProAsnGlyGlyLupProGlyLeuProGlyGlyGlyGlyGlyGlyGlyGlyGly 120
Db      493 GAGCCCCCTGGTCTCTAATGAGAACCAAGGCTTCCATGAGTGCAGCCAGCTGCGCAG 552
Qy      121 A1a1leglylumeCaspasnGlyValserGlyleuThrsGlyleuValPhe11lys 140
Db      553 GCCATCGGGGAGATGAGACCAAGGCTCTCAGCTGACCAAGGAGGCTCAATCAACAG 612
Qy      141 AenAlaValAlaGlyValArgGlyLthrGlySerlySileTyrlleuVallysglyGly 160
Db      613 AATGCTGTGCGCGGTGTGCGGAGACGAGACAGATCTACCTGTGTGAGAGAGAG 672
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Search completed: December 17, 2004, 08:55:15  
Job time : 5456 secs

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DR MPI: 2000-317516/27.  
DR P-PsDB: AAY79510.  
XX  
XX Novel carboxylate-associated proteins used for the prevention and  
PT treatment of autoimmune/inflammatory disorders of e.g. the  
PT gastrointestinal and reproductive systems.  
PS  
PS Claim 9; Page 94; 104pp; English.  
XX  
XX The present sequence is that of cDNA coding for a novel human  
CC carboxylate-associated protein, termed CRBP-6 (see AAY79510). The cDNA  
CC (Inveco clone 2821011) was initially identified in adrenal tumour cDNA  
CC library ADRHUT06. CRBP-6 has chemical and structural similarity with  
CC bovine lung surfactant protein D (32% identity). CRBP-6 is expressed in  
CC the liver, kidney, ovary, gut, adrenal gland and secretory epithelium.  
CC The invention provides CRBP-1 to -7 polynucleotides (see AAZ94941-48)  
CC and polypeptides (see AAY79505-11), as well as expression vectors, host  
CC cells, antibodies, agonists and antagonists. These are used in the  
CC diagnosis, treatment or prevention of disorders associated with CRBP  
CC expression, especially autoimmune or inflammatory disorders,  
CC gastrointestinal disorders, infectious disorders, reproductive disorders,  
CC neurological disorders, eye disorders and cell proliferative disorders,  
CC including cancer. CRBP polynucleotides are useful sources of probes and  
CC primers which can be used to detect CRBP in a sample from a patient.  
CC They may also be administered as part of a gene therapy regime.  
XX  
XX Sequence 1253 BP; 287 A; 328 C; 400 G; 238 T; 0 U; 0 Other;

Query Match	100.0%	Score 1253;	DB 3;	Length 1253;
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Matches 1253; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

[illegible]

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Db	661	CATACCTTGGCGCAAGCCGGGCTTGCCCGGTCTTTCATTCGAGATCAACGACCTGGAGAAG	720
Qy	721	AGGGGCGCTTGSTGTACTCTGACACACTCCCCCATGGGGACCTTCAACAAGTGGGGCGACGG	780
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Qy	781	GTGAGCCCCAACATGCTTACGACAGAGGAGCTGCGTGAAGATGTGGCTCGGGCGGCT	840
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Qy	901	TGTGAGCCTCAGGCTGGGGGCTGCCCATTTGGGGGGCCCACTGTCCTCGACAGGTTGGCAG	960
Db	901	TGTGAGCCTCAGGCTGGGGGCTGCCCATTTGGGGGGCCCACTGTCCTCGACAGGTTGGCAG	960
Qy	961	GGAACGAGCCCAACATGCTGTCGACAGAGGAGCTGTCCTCTTGTGAAGGGTGGAGGCT	1020
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XX	AD	ADI60324;	
XX	DT	15-APR-2004 (first entry)	
XX	DE	Secreted polypeptide encoding gene splice variant #57.	
XX	XX	de; gene; osteopathic; vulnary; cytostatic; gene therapy; diagnosis;	
XX	KW	forensic; gene mapping; mutation identification; biodiversity;	
XX	KW	chromosome marker; immune response; myeloid cell disorder;	
XX	KW	lymphoid cell disorder; bone cartilage; tendon; ligament;	
XX	KW	nerve tissue growth; wound healing; burns; incision; ulcer; cancer.	
XX	OS	Homo sapiens.	
XX	PN	WO2003025142-A2.	
XX	PD	27-MAR-2003.	
XX	PF	18-SEP-2002; 2002WO-US029636.	
XX	PR	18-SEP-2001; 2001US-0323349P.	
XX	PR	16-SEP-2002; 2002US-00323349.	
XX	PA	(HYSB-) HYSBQ INC.	



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PR 31-AUG-1998; 98US-0098252P.  
PR 16-SEP-1998; 98US-0100634P.  
PR 12-JAN-1999; 99US-0115565P.  
XX (GETH ) GENENTECH INC.  
XX  
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
PI Wood WT, Yuan J;  
XX  
XX WPI; 2000-072883/06.  
XX P-PSDB; AAY66738.  
XX  
XX Membrane-bound proteins and related nucleotide sequences.  
XX  
XX Claim 2; Fig 251; 822pp; English.  
PS

XX The invention provides membrane-bound PRO polypeptides and  
CC polymucleotides encoding them. The PRO sequences of the invention were  
CC identified based on extracellular domain homology screening. The PRO  
CC sequences have homology with proteins including LDL receptor, TIR  
CC ligands and various enzymes. The membrane-bound proteins and receptor  
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
CC immunoadhesins, for instance, can be used as therapeutic agents to block  
CC receptor-ligand interactions. The membrane-bound proteins can also be  
CC employed for screening of potential peptide or small molecule inhibitors  
CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
CC are useful as hybridization probes, in chromosome and gene mapping and in  
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will  
CC also be useful for the preparation of PRO polypeptides, especially by  
CC recombinant techniques

Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;

Query Match 98.2%; Score 1230; DB 3; Length 1238;

Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY	84	CTCAGGATGAGGGGGGAATCTGAGCCCTGGTGGGCGGTTCTTAATCAGCGCTTGCTCTGTCA	143
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OY	144	CTGCTGCCATCTGGAATCTCAGCGCGGTGCGATGACGCGTGTCTGTGAGATCTTC	203
Db	121	CTGCTGCCATCTGGAATCTCAGCGCGGTGCGATGACGCGTGTCTGTGAGATCTTC	180
OY	204	GTCTCTGGCTTAAAGGGGATGCGGGAGAGAGGGAGACAAAGCGCCCGCCGAGCGCT	263
Db	181	GTCTCTGGCTTAAAGGGGATGCGGGAGAGAGGGAGACAAAGCGCCCGCCGAGCGCT	240
OY	284	GGAAAGTCGCGCCCAACGGAGAAAAAGAGACATGTGGGGACAAAGAGACAGAAAGGCAGT	323
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OY	324	GTGGTGTGTCATGGAATAATGTGTCCATTGTCCTTAAAGGTGAGAAAGAGATTCGGGT	383
Db	301	GTGGTGTGTCATGGAATAATGTGTCCATTGTCCTTAAAGGTGAGAAAGAGATTCGGGT	360
OY	384	GACATATAGGACCCCCCTGTGTCTTAATGAGAAACAGGCTCTCCATGTGATGTGACGCCAGCTG	443
Db	361	GACATATAGGACCCCCCTGTGTCTTAATGAGAAACAGGCTCTCCATGTGATGTGACGCCAGCTG	420
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OY	684	GCCGTGTCTTTCATCGGATCAACGACCTTGAGAAAGAGAGGCGCTTGTGTATCTTGTAC	743
Db	661	GCCGTGTCTTTCATCGGATCAACGACCTTGAGAAAGAGAGGCGCTTGTGTATCTTGTAC	720
OY	744	CACCTCCCCCATGCGGACCTTCAACAAGTGGCGGACGCTGTGAGCCCAACAATGCTTACGAC	803
Db	721	CACCTCCCCCATGCGGACCTTCAACAAGTGGCGGACGCTGTGAGCCCAACAATGCTTACGAC	780

QY	804	GAGGAGCACTGCGTGGAGATGTGTGGCTTCGGGCGGCTGTGAACGACGTGGCTTGGCAACC	863
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QY	984	CAGCGAGGGAGCTGTGCCCTCTGTGAAGGGGTGAGAGGCTCAGTGAAGAGGCTGTGTCT	1043
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QY	1044	AACTGAGAAATGGCTTATGAGAGAAATGAAAGTTCCTGGGGGTGTGTCTC	1103
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QY	1104	TGAGGAGACAGATTCAATTACGTGATTTGAGGCCCAATGTCATTTATGTAATTAATACC	1163
Db	1081	TGAGGAGACAGATTCAATTACGTGATTTGAGGCCCAATGTCATTTATGTAATTAATACC	1140
QY	1164	CAGATTGCTCTTCATTAAGCTTGTGCTTGTTCGAAGCTATACAAATAAATCTTTAAG	1223
Db	1141	CAGATTGCTCTTCATTAAGCTTGTGCTTGTTCGAAGCTATACAAATAAATCTTTAAG	1200
QY	1224	TATGTGCACTAGTTAAGTCCAAAAAATAAATAA	1253
Db	1201	TATGTGCACTAGTTAAGTCCAAAAAATAAATAA	1230

RESULT 4	
AA058385	
ID	AA058385 standard; cDNA, 1238 BP.
XX	
AC	AA058385;
XX	
DT	29-JAN-2001 (first entry)
DE	Human PRO1182 nucleotide sequence SEQ ID NO:50.
XX	
XX	Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
KW	Proliferation; tumorigenesis; identification; cancer; cytostatic;
KW	neotrophic; neuroprotective; antiinflammatory; immunosuppressive;
KW	immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
KW	neuronal disorder; glial disorder; astrocytal disorder; angiogenic;
KW	hypochalamic disorder; glandular disorder; macrophagal disorder;
KW	epithelial disorder; stromal disorder; blastocoelec disorder;
KW	inflammatory disorder; immunologic disorder; ss.
OS	Homo sapiens.
XX	
PN	WO200053755-A2.
XX	
PD	14-SEP-2000.
XX	
PF	06-JAN-2000; 2000WO-US000376.
XX	
XX	
PR	08-MAR-1999; 99WO-US005028.
PR	02-JUN-1999; 99WO-US012252.
PR	23-JUN-1999; 99US-0141037P.
PR	07-JUL-1999; 99US-0143048P.
PR	26-JUL-1999; 99US-0145698P.
PR	30-NOV-1999; 99WO-US028313.
PR	20-DEC-1999; 99WO-US030911.
PR	05-JAN-2000; 2000WO-US000219.
XX	
PA	(GETH ) GENENTECH INC.
PI	Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;

PI Watanabe CK, Wood WI;  
 XX MPI: 2000-572270/53.  
 DR P-PSDB; AAB24075.  
 XX  
 PT Thirty PRO polynucleotides encoding PRO polypeptides, useful in the  
 XX treatment, diagnosis and prevention of cancer.  
 PS  
 XX Claim 50; Fig 37; 286pp; English.

The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PRO212, PRO290, PRO41, PRO535, PRO619, PRO17, PRO809, PRO830, PRO848, PRO1005, PRO1009, PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184, PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094, PRO215 OR PRO2198. PRO antagonists can be used to inhibit tumour cell growth. The PRO polypeptides and nucleotides are useful in the treatment, diagnosis and prevention of cancer. The antibodies and other anti-tumour compounds may be used to treat various conditions, including those characterised by overexpression and/or activation of the amplified PRO genes. Exemplary conditions or disorders to be treated with such antibodies and other compounds include benign or malignant tumours (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and neck tumours), leukemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytic, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoele disorders, and inflammatory, angiogenic and immunologic disorders. AACS8242 to AACS9366 represent PCR primers and hybridisation probes used in the isolation of the human PRO sequences. AACS8367 to AACS8396 and AAB24057 to AAB24089 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.

Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;

Query Match 98.2%; Score 1230; DB 3; Length 1238;  
 Best Local Similarity 100.0%; P-Id: 284;  
 Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

24 GCGACGGGACAGAGCGCCGCTGCGCTGAGCGGCTGAGAGTGGTGGTCTCTCCGCG 83  
 1 GCGACGGGACAGAGCGCCGCTGCGCTGAGCGGCTGAGAGTGGTGGTCTCTCCGCG 60  
 84 CTCAGATGAGGGGAAATCTGCGCTGAGCGGCTGAGAGTGGTGGTCTCTCCGCG 143  
 61 CTCAGATGAGGGGAAATCTGCGCTGAGCGGCTGAGAGTGGTGGTCTCTCCGCG 120  
 144 CTGCGCATCTGAGCATCTCTGAGCGGCTGAGAGTGGTGGTCTCTCCGCG 203  
 121 CTGCGCATCTGAGCATCTCTGAGCGGCTGAGAGTGGTGGTCTCTCCGCG 180  
 204 GTCCCTGAGCTCAAAAGGGAGATGCGGAGAGAAAGGAGCAAAAGGCGCGGCGCT 263  
 181 GTCCCTGAGCTCAAAAGGGAGATGCGGAGAGAAAGGAGCAAAAGGCGCGGCGCT 240  
 264 GGAAGAGTGGCGCCCAAGGAGAAAGAGAGACATGGGGGCAAAAGAGCAAAAGGCACT 323  
 241 GGAAGAGTGGCGCCCAAGGAGAAAGAGAGACATGGGGGCAAAAGAGCAAAAGGCACT 300  
 324 GTGGGCTGCTATGAGAAATATGCTGCTCAATGGGCTCAATGAGAAAGAGATTCGGGT 383  
 301 GTGGGCTGCTATGAGAAATATGCTGCTCAATGGGCTCAATGAGAAAGAGATTCGGGT 360  
 384 GACATAGAGACCCCTGCTGCTCAATGAGAAACAGGCTCTCCATGTGAGTCAAGCACTG 443  
 361 GACATAGAGACCCCTGCTGCTCAATGAGAAACAGGCTCTCCATGTGAGTCAAGCACTG 420  
 444 CGCAAGGCTATCGGGGAGATGAGCAACAGGCTCTCTCAAGTGAACAGGAGCTCAAGTTC 503  
 421 CGCAAGGCTATCGGGGAGATGAGCAACAGGCTCTCTCAAGTGAACAGGAGCTCAAGTTC 480  
 504 ATCAAGATGCTGCTGCGGCTGCTGAGAGAGGAGCAAGATCTATCTGCTGAGAG 563

DB 481 ATCAAGATGCTGCTGCGGCTGCTGAGAGAGGAGCAAGATCTATCTGCTGAGAG 540  
 QY 564 GAGAGAGAGGCTATCGGGAGAGCGCCAGAGTCTCTGAGGAGGAGGAGGAGGAGGAGGAGG 623  
 DB 541 GAGAGAGAGGCTATCGGGAGAGCGCCAGAGTCTCTGAGGAGGAGGAGGAGGAGGAGGAGG 600  
 QY 624 ATGCCCAAGAGAGGCTGCTCAATGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 683  
 DB 601 ATGCCCAAGAGAGGCTGCTCAATGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660  
 QY 684 GCCGCTGCTTCAATCGGAGCAACAGCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 743  
 DB 661 GCCGCTGCTTCAATCGGAGCAACAGCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720  
 QY 744 CACTCCCAAGAGGAGGCTTCAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 803  
 DB 721 CACTCCCAAGAGGAGGCTTCAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780  
 QY 804 GAGAGAGAGGCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 863  
 DB 781 GAGAGAGAGGCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840  
 QY 864 ACCATGATCTTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 923  
 DB 841 ACCATGATCTTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900  
 QY 924 CCAATGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 983  
 DB 901 CCAATGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 960  
 QY 984 CAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1043  
 DB 961 CAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1020  
 QY 1044 AAATGAGAAATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1103  
 DB 1021 AAATGAGAAATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080  
 QY 1104 TGAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1163  
 DB 1081 TGAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140  
 QY 1164 CAGAATGCTCTTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1223  
 DB 1141 CAGAATGCTCTTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200  
 QY 1224 TAGTGAGATGATTAAGTCCAAAAA 1253  
 DB 1201 TAGTGAGATGATTAAGTCCAAAAA 1230

RESULT 5  
 AAF44230  
 ID AAF44230 standard; cDNA; 1238 BP.  
 XX AAF44230;  
 AC  
 XX  
 DT 02-APR-2001 (first entry)  
 XX  
 DE Human PRO1182 (UNG96) nucleotide sequence SEQ ID NO:356.  
 XX  
 XX Human; secreted and transmembrane protein; PRO; cytosolic; cell death;  
 KW cancer; chromosomal mapping; gene mapping; tissue typing;  
 KW diagnostic assay; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200073454-A1.  
 XX  
 PD 07-DEC-2000.  
 XX  
 PF 30-MAR-2000; 2000OMO-US008439.



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XX 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0143048P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149396P.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003376.
PR 18-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 12-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
XX
XX (GENTH ) GENENTECH INC.
PA
PI Ashkenazi AJ, Baker KP, Boltsen D, Desnoyers L, Eaton DJ;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,
PI Grimaldi CJ, Gurely AL, Kijavain IU, Napier MA, Pan U, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
XX WPI: 2001-032160/04.
DR P-PSDB; AAB65261.
XX
XX PRO polynucleotides used to produce polypeptides used to target bioactive
XX PT molecules such as toxins, radiolabels or antibodies, to specific cells,
XX PR to cause targeted cell death.
XX
XX
XX Claim 2; Fig 251; 935pp; English.
XX
XX The present invention describes human secreted and transmembrane PRO
XX CC proteins. The PRO proteins have cytosolic activity. The PRO proteins can
XX CC be used for targeted delivery of bioactive molecules, such as toxins,
XX CC radiolabels or antibodies, that cause cell death. PRO nucleotide
XX CC sequences, and their fragments, can be used as hybridisation probes, in
XX CC chromosomal and gene mapping, and in the generation of anti-sense RNA and
XX CC DNA. They may also be used to produce transgenic animals which are used
XX CC to develop and screen therapeutically useful reagents. The PRO nucleotide
XX CC and protein sequence can be used for tissue typing and in treating
XX CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
XX CC AAF44470 represent PCR primers and hybridisation probes used in the
XX CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
XX CC AAB65300 represent human PRO polynucleotide and protein sequences given
XX CC in the exemplification of the present invention
XX
XX Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;
SQ
XX
XX Query Match 98.2%; Score 1230; DB 5; Length 1238;
XX Best Local Similarity 100.0%; Pred. No. 6; 7e-284;
XX Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
XX 24 GCGAGCGGAGAGACGCCCGCTTGCTTACGCGCGCTCTCAGAGATTGGTGTCTGCGTCGG 83
XX |||||
XX 1 GCGAGCGGAGAGACGCCCGCTTGCTTACGCGCGCTCTCAGAGATTGGTGTCTGCGTCGG 60
XX
XX CTCAGAGATGAGGGGGGAAATCTGGGCGCTGTGGGGGCTTATATCAGCGCTGGGCTTCTGTCGA 143
XX |||||
XX 84 CTCAGAGATGAGGGGGGAAATCTGGGCGCTGTGGGGGCTTATATCAGCGCTGGGCTTCTGTCGA 143
XX |||||
XX Db CTCAGAGATGAGGGGGGAAATCTGGGCGCTGTGGGGGCTTATATCAGCGCTGGGCTTCTGTCGA 120
XX |||||
XX 144 CTCGCGCATCTGACATCTCTAGCGCGGCTGGCGGATGAGCGCGCTCTGTGAGATCTCTC 203

```

[illegible]

DB 1201 TAGTCAGTAGTTAAGTCCAAAAA 1230

RESULT 6  
ABL88155  
ID ABL88155 standard; cDNA; 1238 BP.

AC ABL88155;

DT 16-MAY-2002 (first entry)

DE Human PRL1182 cDNA sequence SEQ ID NO:167.

Human; angiogenesis; cardiac; cytosolic; antiangiogenic; hypotensive;  
vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
age-related macular degeneration; arterial restenosis; angina;  
rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
wound healing; chromosome mapping; gene mapping; gene; ss.

OS Homo sapiens.

XX MO200200690-A2.

XX 03-JAN-2002.

PF 20-JUN-2001; 2001WO-US019692.

XX 23-JUN-2000; 2000US-0213637P.

PR 20-JUL-2000; 2000US-0219556P.

PR 25-JUL-2000; 2000US-0220624P.

PR 28-JUL-2000; 2000WO-US020710.

PR 02-AUG-2000; 2000US-0222695P.

PR 17-AUG-2000; 2000US-00643657.

PR 23-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.

PR 07-SEP-2000; 2000US-0230978P.

PR 18-SEP-2000; 2000US-00664610.

PR 18-SEP-2000; 2000US-00665350.

PR 24-OCT-2000; 2000US-0242922P.

PR 08-NOV-2000; 2000US-00709228.

PR 08-NOV-2000; 2000WO-US030952.

PR 10-NOV-2000; 2000WO-US030873.

PR 01-DEC-2000; 2000WO-US032678.

PR 20-DEC-2000; 2000WO-US034956.

PR 22-JAN-2001; 2001US-00767609.

PR 28-FEB-2001; 2001US-00796498.

PR 28-FEB-2001; 2001WO-US006650.

PR 01-MAR-2001; 2001US-00802706.

PR 09-MAR-2001; 2001US-00808689.

PR 14-MAR-2001; 2001US-00816744.

PR 22-MAR-2001; 2001US-00828366.

PR 10-MAY-2001; 2001US-00854208.

PR 10-MAY-2001; 2001US-00854280.

PR 25-MAY-2001; 2001US-00866028.

PR 25-MAY-2001; 2001US-00866034.

PR 25-MAY-2001; 2001WO-US017092.

PR 30-MAY-2001; 2001US-00870574.

PR 30-MAY-2001; 2001WO-US017443.

PR 01-JUN-2001; 2001WO-US017800.

XX (GERTH ) GENENTECH INC.

PA Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,

PI Godowski PJ, Gurney AL, Hillan KJ, Marels SA, Pan J, Paoni NF,

PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,

XX WPI; 2002-090516/12.

DR P-PSDB; ABB84900.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
PR infarction), endothelial or angiogenic disorders in a mammal.

XX Claim 2; Fig 167; 565pp; English.

CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to  
CC ABB85003. The PRO proteins and polynucleotides have cardiac, cytosolic,  
CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic  
CC activities, and can be used in gene therapy. The PRO polynucleotides,  
CC proteins, agonists and antagonists are useful for treating or diagnosing  
CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.  
CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,  
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
CC healing. The PRO polynucleotides have applications in molecular biology,  
CC including use as hybridisation probes, and in chromosome and gene  
CC mapping. ABL88259 to ABL88267 represent primers and probes used in the  
CC exemplification of the present invention

XX Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;

Query Match 98.2%; Score 1230; DB 6; Length 1238;  
Best Local Similarity 100.0%; Pred. No. 6; 7e-284;  
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GCGACGGGCGAGAGCGCCGCTTGCCTAGCGCTGCTCAGAGTGTGCTGCTGCG 83

Db 1 GCGACGGGCGAGAGCGCCGCTTGCCTAGCGCTGCTCAGAGTGTGCTGCTGCG 60

QY 84 CTCAGATGAGGGGGAATCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 143

Db 61 CTCAGATGAGGGGGAATCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120

QY 144 CTGCTGCATCTGAGCATCTGAGCGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 203

Db 121 CTGCTGCATCTGAGCATCTGAGCGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180

QY 204 GTCCCTGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 263

Db 181 GTCCCTGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240

QY 264 GGAAGAGTGGGCGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 323

Db 241 GGAAGAGTGGGCGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300

QY 324 GTGGGTCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 383

Db 301 GTGGGTCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360

QY 384 GACATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 443

Db 361 GACATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420

QY 444 CGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 503

Db 421 CGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480

QY 504 ATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 563

Db 481 ATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540

QY 564 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 623

Db 541 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600

QY 624 ATGCCCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 683

Db 601 ATGCCCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660

```
QY 684 GCCGTGTCCTCATCGGATCAAGCAGCTGGAGAGAGGGGCGCTGTCGTACTCTAC 743
Db 661 GCCGTGTCCTCATCGGATCAAGCAGCTGGAGAGAGGGGCGCTGTCGTACTCTAC 720
QY 744 CACTCCCCCATGCGGACCTTCAACAAGTGGCGACGCGTGAGCCCAACATGCCCTACAC 803
Db 721 CACTCCCCCATGCGGACCTTCAACAAGTGGCGACGCGTGAGCCCAACATGCCCTACAC 780
QY 804 GAGAGAGACTCGTGGAGATGTGTGGCTTGGCGGCGCTGGAACAGATGGCTGCCACAC 863
Db 781 GAGAGAGACTCGTGGAGATGTGTGGCTTGGCGGCGCTGGAACAGATGGCTGCCACAC 840
QY 864 ACCATGTACTCATGTGTGAGTTGACAAAGAGAAATCATGTAGCTCAAGGCTGGGGCTGC 923
Db 841 ACCATGTACTCATGTGTGAGTTGACAAAGAGAAATCATGTAGCTCAAGGCTGGGGCTGC 900
QY 924 CCATTGGGGGGCCCAATGTCCTTCGAGGGTTGGCAGGAGACAGACCCAGCATGTGTC 983
Db 901 CCATTGGGGGGCCCAATGTCCTTCGAGGGTTGGCAGGAGACAGACCCAGCATGTGTC 960
QY 984 CAGCCAGGAGCTGTCTCTGTGAAGGGTGAAGGCTCACTGATGAGGGCTGTGCT 1043
Db 961 CAGCCAGGAGCTGTCTCTGTGAAGGGTGAAGGCTCACTGATGAGGGCTGTGCT 1020
QY 1044 AAACGTGAGAAATGGCTATGCTTAAGAGAAATGAAGTTCCTGGGGCTGTCTC 1103
Db 1021 AAACGTGAGAAATGGCTATGCTTAAGAGAAATGAAGTTCCTGGGGCTGTCTC 1080
QY 1104 TGAAGAGCAGAGTTTCACTTACCTGATTTGAGCCCAATGTCATTATGATTTATACC 1163
Db 1081 TGAAGAGCAGAGTTTCACTTACCTGATTTGAGCCCAATGTCATTATGATTTATACC 1140
QY 1164 CAGAACTCTCTTCCATTAAGCTTGTGCTTTCGCAAGCTATACATTAATCTTTAAG 1223
Db 1141 CAGAACTCTCTTCCATTAAGCTTGTGCTTTCGCAAGCTATACATTAATCTTTAAG 1200
QY 1224 TAGTGCAGTAGTTAGTCCAAAAA 1253
Db 1201 TAGTGCAGTAGTTAGTCCAAAAA 1230

RESULT 7
ABL95644
ID ABL95644 standard; cDNA; 1238 BP.
AC ABL95644;
XX
XX
DT 19-JUL-2002 (first entry)
XX
DE Human angiogenesis related cDNA P101182 SEQ ID NO: 167.
XX
XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiac; cytoskeletal; antiangiogenic; hypotensive; vulnery;
KW antiarteriosclerotic; gene; ss.
XX
OS Homo sapiens.
XX
XX MO200208284-A2.
XX
XX 31-JAN-2002.
XX
XX 09-JUL-2001; 2001WO-US021735.
XX
XX 20-JUL-2000; 2000US-0219556P.
XX 25-JUL-2000; 2000US-0220624P.
XX 25-JUL-2000; 2000US-0220664P.
XX 28-JUL-2000; 2000WO-US020710.
XX 02-AUG-2000; 2000US-0222695P.
XX 17-AUG-2000; 2000US-00643657.
XX 23-AUG-2000; 2000WO-US023522.
XX 24-AUG-2000; 2000WO-US023328.
XX 07-SEP-2000; 2000US-0230978P.
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PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00766498.
PR 01-MAR-2001; 2001WO-US006520.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017443.
PR 20-JUN-2001; 2001WO-US017800.
XX
XX (GETH ) GENENTECH INC.
PA (BAKE) BAKER K P.
PA (FERR) FERRARA N.
PA (GERB) GERBER H.
PA (GERR) GERRITSEN M E.
PA (GODD) GODDARD A.
PA (GODO) GODOWSKI P J.
PA (GURN) GURNEY A L.
PA (HILL) HILLAN K J.
PA (MARS) MARSTERS S A.
PA (PANU) PAN J.
PA (PAON) PAONI N F.
PA (STEP) STEPHAN J F.
PA (WATA) WATANABE C K.
PA (WILL) WILLIAMS P M.
PA (WOOD) WOOD W I.
XX
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
XX Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J,
XX Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,
XX WPI; 2002-171999/22.
XX P-PSDB; ABB95506.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial
XX infarction), endothelial or angiogenic disorders in a mammal.
XX
XX Claim 1; Fig 167; 567pp; English.
XX
XX The present invention provides the protein and coding sequences of human
XX PRO proteins. These are useful for treating or diagnosing a
XX cardiovascular, endothelial or angiogenic disorder, including cardiac
XX hypertrophy, trauma, cancer, age-related macular degeneration,
XX atherosclerosis, hypertension, arterial revascularisation, rheumatoid arthritis,
XX CC angina, myocardial infarction, thrombophlebitis, lymphangitis, tumour
XX angiogenesis (such as breast carcinoma and liver carcinoma) and wound
XX healing. The present sequence is a coding sequence of the invention
XX
XX Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;
XX
XX Query Match 98.2%; Score 1230; DB 6; Length 1238;
XX Best Local Similarity 100.0%; Pred. No. 6.7e-284;
XX Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Db 1 GGGAGGGAGGAGACGCCCGTTCGCTAGCCGCTCTCAGAGGTTGGTGTCTGCTGCTCG 60  
 Qy 84 CTCAGAGTAGAGGGGAAATTTGGCCCTGTGGGCTTTCTAATACGCTTGGCTTCTGCA 143  
 Db 61 CTCAGAGTAGAGGGGAAATTTGGCCCTGTGGGCTTTCTAATACGCTTGGCTTCTGCA 120  
 Qy 144 CTGCTGCCATCTGAGCATCTCAGCGGGTGGGAGTAGACGCTGTCTGTGAGAGTCTCTC 203  
 Db 121 CTGCTGCCATCTGAGCATCTCAGCGGGTGGGAGTAGACGCTGTCTGTGAGAGTCTCTC 180  
 Qy 204 GTCCCTGGCTTCAAAAGGGATGCGGAGAGAAAGGAGACAAAGCGCCCGGAGCGGCT 263  
 Db 181 GTCCCTGGCTTCAAAAGGGATGCGGAGAGAAAGGAGACAAAGCGCCCGGAGCGGCT 240  
 Qy 264 GGAAGAGTCGGGCCCCACGGGAGAAAAAGAGACATGGGGAGCAAGAGCAAGAGGCACT 323  
 Db 241 GGAAGAGTCGGGCCCCACGGGAGAAAAAGAGACATGGGGAGCAAGAGGCAAGGCACT 300  
 Qy 324 GTGGGTGCTCATGAAAAAATTGGTCCATTTGGCTCTAAGGAGAGAAAGGATTTCCGGT 383  
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 Qy 504 ATCAAGAAATGCTGTGCTGCGGTGTGCGGAGACGAGAGCAAGATCTAAGCTGTGTAAG 563  
 Db 481 ATCAAGAAATGCTGTGCTGCGGTGTGCGGAGACGAGAGCAAGATCTAAGCTGTGTAAG 540  
 Qy 564 GAGAGAGAGCCCTACGCGGAGACCCGAGCTGTCTGCGAGGCGCGGGGGAGCACTGAGC 623  
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 Qy 624 ATGCCCAAGAGAGAGGCTGCAATGAGCTGATGAGCCGATACCTGGGCGCAAGCGGGCTG 683  
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 17-JUN-2003 (first entry)  
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 XX Human, secreted and transmembrane protein; cytosolic; anti-HIV;  
 KW virucide; hepatotropic; antiinflammatory; neuroprotective; gene therapy;  
 KW PBO; pharmaceutical; diagnostic; biosensor; bioindicator; malignancy;  
 KW cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; leukaemia;  
 KW lymphoma; hepatitis B; multiple sclerosis; Crohn's disease;  
 KW drug screening; gene; ss.  
 XX Homo sapiens.  
 OS  
 PN US2003003531-A1.  
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 PD 02-JAN-2003.  
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 PF 19-NOV-2001, 2001US-00989734.  
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 PR 16-JUN-1997; 97US-0049787P.  
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 PR 12-NOV-1997; 97US-0065186P.  
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DT 22-APR-2003 (first entry)  
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DE Human secreted/transmembrane protein cDNA, #144.  
XX  
KW Human; gene; ss; PRO; secreted; transmembrane; pharmaceutical;  
KW diagnostic; biosensor; bioindicator; tumour; therapeutic; gene therapy;  
KW tumour-associated antigenic target; TAT; ADPPI;  
KW antibody-dependent enzyme mediated; prodrug therapy; cytostatic.  
OS Homo sapiens.  
XX  
PN US2003027162-A1.  
XX  
PD 06-FEB-2003.  
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PF 15-NOV-2001; 2001US-00997428.  
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PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
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PR 02-MAR-2000; 2000WO-US005004.  
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XX ACD4367;  
XX 10-SEP-2003 (first entry)  
XX cDNA encoding human PRO1182 polypeptide.  
XX Human; PRO polypeptide; secreted protein; transmembrane protein;  
XX genetic disorder; antibacterial; immunosuppressive; transgenic;  
XX gene therapy; gene; ss.  
XX Homo sapiens.  
XX OS  
XX US2002127576-A1.  
XX 12-SEP-2002.  
XX 14-NOV-2001; 2001US-00991073.  
XX 16-JUN-1997; 97US-0049787P.  
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KM Human; Gene; ss; PRO; secreted; transmembrane; signal peptide;  
KW pharmaceutical; diagnostic; biosensor; bioindicator; tumour therapeutic;  
KW colon cancer; lung cancer; breast cancer; cancer; gene therapy.  
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XX US2002142961-A1.  
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PD 03-OCT-2002.  
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PF 19-NOV-2001; 2001US-00989721.  
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XX  
XX (GENTH ) GENENTECH INC.  
XX  
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XX Ferrara N<sup>5</sup>, Fong S<sup>6</sup>, Gerber H<sup>7</sup>, Gerritsen ME<sup>8</sup>, Goddard A<sup>9</sup>, Godowski PJ,  
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XX Zhang Z<sup>20</sup>,  
XX  
XX WPI, 2003-155950/15.  
XX P-PSDB; ABUS9007.  
XX  
XX New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184,  
XX PRO361 or PRO846) useful as targets for therapeutic intervention in  
XX cancers (e.g. lung or breast cancers), or for diagnosing these cancers.  
XX  
XX Claim 2; Fig 251; 647P; English.  
XX  
XX The invention discloses isolated PRO secreted/transmembrane polypeptides  
XX comprising a sequence without signal peptide and the nucleic acid  
XX encoding them. The polypeptides can be used to raise antibodies that  
XX specifically bind to the PRO polypeptide, for linking a bioactive  
XX molecule to a cell expressing a PRO protein and for modulating at least  
XX one biological activity of a cell. The PRO polypeptides or  
XX polynucleotides are also useful as pharmaceuticals, diagnostics,  
XX biosensors or bioeffectors, for detecting or treating e.g. tumours in  
XX mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or  
XX rabbits, as targets for therapeutic intervention in certain cancers (e.g.  
XX colon, lung or breast cancers) and diagnostic determination of the  
XX presence of these cancers. The PRO polypeptides are also useful as  
XX molecular weight markers or for chromosome identification. The PRO genes  
XX are useful as hybridisation probes or for screening libraries of human  
XX cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene  
XX therapy, particularly for replacing a defective gene. The sequences  
XX presented in ABX79290-ABX79675 are the genes encoding, the primers  
XX amplifying and the probes detecting the PRO polynucleotides of the  
XX invention. Note: The sequence data for this patent is also available in  
XX electronic format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)  
XX  
XX Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;



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KW chromosome mapping; gene mapping; transgenic animal; knock-out animal;  
KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;  
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Job time : 930 secs

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Run on: December 16, 2004, 07:21:34 ; Search time 8739 Seconds

(without alignments)  
6780,409 Million cell updates/sec

Title: US-09-806-277A-13

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Searched: 4526729 seqs, 23644849745 residues

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Minimum DB seq length: 0  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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7	1157.6	92.4	1417	9	BC009951 Homo sapi
8	1132.4	90.4	1341	6	BD103302 Novel col
9	978.4	78.1	1269	6	BD103330 Novel col
10	978.4	78.1	1269	6	BD103331 Novel col
11	950.6	75.9	1139	6	BD103303 Novel col
12	877	70.0	1067	6	BD103305 Novel col
13	834.4	66.6	1197	6	BD103329 Novel col
14	832.2	66.4	1067	6	BD103306 Novel col
15	813	64.9	813	6	BD103332 Novel col
16	805.6	63.3	995	6	BD103304 Novel col
17	733.4	58.5	139357	9	AC010907 Homo sapi
18	686.6	54.8	735	6	BD103333 Novel col
19	686.2	54.8	1522	6	BD103307 Novel col

20	659	52.6	741	6	BD103340 Novel col
21	659	52.6	741	6	BD103341 Novel col
22	641.8	51.2	813	6	BD103338 Novel col
23	613	48.9	663	6	BD103336 Novel col
24	580.4	46.3	708	6	CQ716215 Sequence
25	568.2	45.3	663	6	BD103337 Novel col
26	545.2	43.5	669	6	BD103339 Novel col
27	541.6	43.2	591	6	BD103335 Novel col
28	477	38.1	477	6	BD103334 Novel col
29	458.6	36.6	1272	5	BC056052 Xenopus l
30	391.4	31.2	619	6	BD103308 Novel col
31	323.8	25.8	175475	2	AC123631 Mus muscu
32	322.2	25.7	246539	2	AC125638 Rattus no
33	251.6	20.1	867	10	AB016429 Mus muscu
34	247.6	19.8	1016	6	CQ767629 Sequence
35	247.6	19.8	1016	6	AX376032 Sequence
36	247.6	19.8	1016	6	AY359038 Homo sapi
37	247.6	19.8	1594	6	CQ719085 Sequence
38	246	19.6	1594	9	AB002631 Homo sapi
39	246	19.6	1595	6	E29008 Novel colle
40	246	19.6	1686	6	AX959723 Sequence
41	226.4	18.1	212049	5	BX005484 Zebrafish
42	221	17.6	273	11	G24618 human STS W
43	212.4	17.0	321	6	AX408538 Sequence
44	160.2	12.8	234922	2	AC097055 Rattus no
45	157	12.5	141262	9	AC080033 Homo sapi

## ALIGNMENTS

RESULT 1	AR252616	Sequence 356 from patent US 6478825.	1238 bp	DNA	linear	PAT 20-DEC-2002
LOCUS	AR252616					
DEFINITION	Sequence 356 from patent US 6478825.					
ACCESSION	AR252616					
VERSION	AR252616.1	GI:27300524				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 1238)					
AUTHORS	Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.					
TITLE	Implant, method of making same and use of the implant for the					
JOURNAL	treatment of bone defects					
FEATURES	Patent: US 6478825-A 356 12-NOV-2002;					
source	Location/Qualifiers					
	1..1238					
ORIGIN	/organism="unknown"					
	/mol_type="genomic DNA"					
Query Match	98.2%; Score 1230; DB 6; Length 1238;					
Best Local Similarity	100.0%; Pred. No. 4.5e-208;					
Matches 1230; Conservative	0; Mismatches 0; Indels 0; Gaps 0;					
QY	24 GCGACGGCGAGAGCGCCCGCTTCGCTGACCGCTGCTGAGAGTTGCTCTGCTCGG 83					
DB	1 GCGACGGCGAGAGCGCCCGCTTCGCTGACCGCTGAGAGTTGCTCTGCTCGG 60					
QY	84 CTCGAGATGAGGGGGAATCTGGCCCTGGTGGCGCTTCAATCAGCGCTTCCTGCA 143					
DB	61 CTCGAGATGAGGGGGAATCTGGCCCTGGTGGCGCTTCAATCAGCGCTTCCTGCA 120					
QY	144 CTGCTGCATCTGACATCTCAGCGGCTGGCAGTACGCTGCTGTCAGATCTTC 203					
DB	121 CTGCTGCATCTGACATCTCAGCGGCTGGCAGTACGCTGCTGTCAGATCTTC 180					
QY	204 GTTCCTGCTCTCAAGGGGATGCGGAGAGAAAGGAGCAAAAGGCGCCCGGAGCGCT 263					
DB	181 GTTCCTGCTCTCAAGGGGATGCGGAGAGAAAGGAGCAAAAGGCGCCCGGAGCGCT 240					
QY	264 GGAAGATGCGGCCCGCAGCGAGAAAAAGAGACATGGGGGCAAAAGAGGAGCACT 323					

Db	2.1	GGAAAGTCGGCCCAACGGGAGAAAAAGGAGCATGTGGGGACAAAGACAGAAAGCAGT	300
QY	3.24	GTGGGTCTGTCATGGAAAAATTTGGTCCCATTTGGCTTAAAGGTGAGAAAGAGATTCCGGT	383
Db	3.01	GTGGGTCTGTCATGGAAAAATTTGGTCCCATTTGGCTTAAAGGTGAGAAAGAGATTCCGGT	360
QY	3.84	GACATAGGACCCCTGTGTCCTTAATGGAGAACAGGCTCTCCCATGTGAGTGCAGCCAGCTG	443
Db	3.61	GACATAGGACCCCTGTGTCCTTAATGGAGAACAGGCTCTCCCATGTGAGTGCAGCCAGCTG	420
QY	4.44	CGCAAGCCATTCGGGAGATGGAGCAACCAAGTCTCTCACTGACCCAGCGAGCTCAAGTTC	503
Db	4.21	CGCAAGCCATTCGGGAGATGGAGCAACCAAGTCTCTCACTGACCCAGCGAGCTCAAGTTC	480
QY	5.04	ATCAAGAAATGCTGTGCGCGGTGTGGCGCAGACGGAGACAGAAATCTACTGTGGTGGAG	563
Db	4.81	ATCAAGAAATGCTGTGCGCGGTGTGGCGCAGAGCGAGACAGAAATCTACTGTGGTGGAG	540
QY	5.64	GAGAGAAAGCGTATGCGGAGCGCCAGCTGTCTCCAGAGGCGCGGGGGGACGCTGAGC	623
Db	5.41	GAGAGAAAGCGTATGCGGAGCGCCAGCTGTCTCCAGAGGCGCGGGGGGACGCTGAGC	600
QY	6.24	ATGCCCAAGAGACGAGGCTGCCAATAGGCTGATATGTCGCGATACCTTGCGCGACCGGCTG	683
Db	6.01	ATGCCCAAGAGACGAGGCTGCCAATAGGCTGATATGTCGCGCGATACCTTGCGCGACCGGCTG	660
QY	6.84	GCCCGTGTCTTCATGSGGATCAACGACCTGGAGAGAGAGGGGCGCTTGATGTATCTGTAC	743
Db	6.61	GCCCGTGTCTTCATGSGGATCAACGACCTGGAGAGAGAGGGGCGCTTGATGTATCTGTAC	720
QY	7.44	CATCTCCCCCATGCGGACCTTCAACAAGTGGCGGACGGGTGAGCCCAATATGCTTACGAC	803
Db	7.21	CATCTCCCCCATGCGGACCTTCAACAAGTGGCGGACGGGTGAGCCCAATATGCTTACGAC	780
QY	8.04	GAGGAGAGCTGCTGGAATGATGGTGGCTCGGGCGGCTGGAAACGATGTGGCTGCCACAC	863
Db	7.81	GAGGAGAGCTGCTGGAATGATGGTGGCTCGGGCGGCTGGAAACGATGTGGCTGCCACAC	840
QY	8.64	ACCATGTACTTCATGTGTGAGTTTGACAAGAAGAACATGTAGCTTCAGGCTGGGGCTGC	923
Db	8.41	ACCATGTACTTCATGTGTGAGTTTGACAAGAAGAACATGTAGCTTCAGGCTGGGGCTGC	900
QY	9.24	CCATTGGGGGGCCCACATGTCCCTCGCAGAGGTTTGGAGGGACAGAGCCCAAGCATGTGTC	983
Db	9.01	CCATTGGGGGGCCCACATGTCCCTCGCAGAGGTTTGGAGGGACAGAGCCCAAGCATGTGTC	960
QY	9.84	CAGCCAGGAGACTGTCCCTCTGTGGAAGGATGAGAGGCTCACTGAGTGAAGGGCTGTGCT	1043
Db	9.61	CAGCCAGGAGACTGTCCCTCTGTGGAAGGATGAGAGGCTCACTGAGTGAAGGGCTGTGCT	1020
QY	10.44	AAACTGAGAAAAATGGCTTATGTGTTAAGGAAAAATGAAAGTTCCTGGGGTGTGTCTC	1103
Db	10.21	AAACTGAGAAAAATGGCTTATGTGTTAAGGAAAAATGAAAGTTCCTGGGGTGTGTCTC	1080
QY	11.04	TGAAGAAGCAGAGTTTCATCTACCTGATATGTAGAGCCCAATGTCAATATGTAATTAATAC	1163
Db	10.81	TGAAGAAGCAGAGTTTCATCTACCTGATATGTAGAGCCCAATGTCAATATGTAATTAATAC	1140
QY	11.64	CAGAAATGCTCTTCCATTAAGCTTGTGCTTTGTCCAAAGCTTACAAATTAATCTTTAAG	1223
Db	11.41	CAGAAATGCTCTTCCATTAAGCTTGTGCTTTGTCCAAAGCTTACAAATTAATCTTTAAG	1200
QY	12.24	TATGTGAGTATGTAAGTCCAAAAAATTTTAA	1253
Db	12.01	TATGTGAGTATGTAAGTCCAAAAAATTTTAA	1230

RESULT 2			
AX403469			
LOCUS	AX403469	1238 bp	DNA
DEFINITION	Sequence	356 from Patent WO0073454.	linear
ACCESSION	AX403469		

VERSION	AX403469.1	GI:21436970
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.	
AUTHORS	1 Ashkenazi, A.J., Baker, K.P., Botstein, D., Denny, L., Eaton, D., Ferrara, N., Gerber, H., Gertzi, M., Goddard, A., Godowski, P., Grimaldi, C.J., Gurney, A.L., Kjelavain, I., Napier, M.A., Pan, J., Paoli, N.F., Roy, M., Stewart, T.A., Tuma, D., Watanabe, C.K., Williams, P., Wood, W.I. and Zhang, Z.	
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same	
JOURNAL	Patent: WO 973454-A 356 07-DEC-2000;	
FEATURES	Genentech Inc. (US)	
source	Location/Qualifiers	
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	/mol_type="unassigned DNA"	
	/db_xref="taxon:9606"	
ORIGIN		
Query Match	98.2%;	Score 1230; DB 6; Length 1238;
Best Local Similarity	100.0%;	Pred. No. 4.5e-208;
Matches 1230; Conservative	0;	Mismatches 0; Indels 0; Gaps 0
QY	24	GCGACGGGCAAGACGCCCCCTTCCCTACGCGCGCTACAGAGTGGTCTCTGCTCGG 83
DB	1	GCGACGGGCAAGACGCCCCCTTCCCTACGCGCGCTACAGAGTGGTCTCTGCTCGG 60
QY	84	CTCAGAGTAGAGGGGGAATCTGACCTTGATGGGCGTTCTAATCAGCCTGACCTTCTGTCA 143
DB	61	CTCAGAGTAGAGGGGGAATCTGACCTTGATGGGCGTTCTAATCAGCCTGACCTTCTGTCA 120
QY	144	CTGCTGCCATCTGACATCTCTACGCGGCTGGCGATGACGCGCTGCTCTGTGCAATCTTC 203
DB	121	CTGCTGCCATCTGACATCTCTACGCGGCTGGCGATGACGCGCTGCTCTGTGCAATCTTC 180
QY	204	GTCCCTGGCTCCAAGGGGATGCGGGAGAGAAAGGAGCAAAAGGCGCCCCGGACGGGCT 263
DB	181	GTCCCTGGCTCCAAGGGGATGCGGGAGAGAAAGGAGCAAAAGGCGCCCCGGACGGGCT 240
QY	264	GGAAGAGTCGGCCCCACGGAGAAAAAAGAGACATGGGGGACAAAGACAGAAAGCAGT 323
DB	241	GGAAGAGTCGGCCCCACGGAGAAAAAAGAGACATGGGGGACAAAGACAGAAAGCAGT 300
QY	324	GTGGGTGCTATGAGAAAAATTTGGTCCATTGGCTCTAAAGGTGAGAAAGAGATTCGGGT 383
DB	301	GTGGGTGCTATGAGAAAAATTTGGTCCATTGGCTCTAAAGGTGAGAAAGAGATTCGGGT 360
QY	384	GACATAGGACCCCTGGTGTCTTAATGAGAAACCAAGGCTCCCATGATGATGACGACGCTG 443
DB	361	GACATAGGACCCCTGGTGTCTTAATGAGAAACCAAGGCTCCCATGATGATGACGACGCTG 420
QY	444	CGCAAGGCTATCGGGAGATGAGCAACCAAGGCTTCTACGCTGACCAAGGAGCTCAAGTTT 503
DB	421	CGCAAGGCTATCGGGAGATGAGCAACCAAGGCTTCTACGCTGACCAAGGAGCTCAAGTTT 480
QY	504	ATCAAGAAATGTGTGCGCGGTGTGCGGAGACGAGACGAGCAAGATCTACCTGTGGTAG 563
DB	481	ATCAAGAAATGTGTGCGCGGTGTGCGGAGACGAGACGAGCAAGATCTACCTGTGGTAG 540
QY	564	GAGAGAAAGCGCTTACGCGAGACGCCAGTGTCTTGCAAGGGCGCGGGGGACAGCTGAGC 623
DB	541	GAGAGAAAGCGCTTACGCGAGACGCCAGTGTCTTGCAAGGGCGCGGGGGACAGCTGAGC 600
QY	624	ATGCCCAAGACGAGGCTGCGCAATGGCTGATGGCCGATATCTGGCGCAAGCGGCGTGG 683
DB	601	ATGCCCAAGACGAGGCTGCGCAATGGCTGATGGCCGATATCTGGCGCAAGCGGCGTGG 660
QY	684	GCCGCTGCTTCAATCGGATCAAGACTGAGAAAGAGGAGGCGGCTTGTGATCTTAC 743

[illegible]

RESULT	3
AX454582	
LOCUS	AX454582
DEFINITION	Sequence 167 from Patent WO0208284.
ACCESSION	AX454582
VERSION	AX454582.1 GI:21713915
KEYWORDS	.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE	AUTHORS	TITLE	JOURNAL
1	Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, D., Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I. and Ye, W.	Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis	Patent: NO 0208284-A 167 31-JAN-2002;
	Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone (US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard, Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ; Hillan, Kenneth J. (US) ; Marsters, Scott A. (US) ; Pan, James (US) ; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ; Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William I. (US)		

FEATURES	source	location/Qualifiers
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		/organism="Homo sapiens"
		/mol_type="unassigned DNA"
		/db_xref="taxon:9606"
ORIGIN		
Query Match	98.2%	Score 1230; DB 6; Length 1238;

Best Local Similarity 100.0%; Pred. No. 4,5e-208;		
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	24	GCAGCGGSCAGAGACGCCCCGTTGCGCTTAAGCGCGTGTCTCAAGAGTTGGTGTCTTGCGCTGCG
DB	1	GCAGCGGSCAGAGACGCCCCGTTGCGCTTAAGCGCGTGTCTCAAGAGTTGGTGTCTTGCGCTGCG
QY	84	CTCAGAGTGAAGGGGGAATCTTGCCCCCTGTGTGGGCGTTCTAATCAACCTTGCCCTTCTGTCA
DB	61	CTCAGAGTGAAGGGGGAATCTTGCCCCCTGTGTGGGCGTTCTAATCAACCTTGCCCTTCTGTCA
QY	144	CTGCTGCATCTGAGACATCTCAAGCCGGCTTGCGCATGACGCGCTCTGTGCAATCTCTC
DB	121	CTGCTGCATCTGAGACATCTCAAGCCGGCTTGCGCATGACGCGCTCTGTGCAATCTCTC
QY	204	GTCCCTGGCCTCAAAAGGGAGTGCGGAGAGAGAGGAGACAAGGCGCCCCGGACGCGCTT
DB	181	GTCCCTGGCCTCAAAAGGGAGTGCGGAGAGAGAGGAGACAAGGCGCCCCGGACGCGCTT
QY	264	GGAAGAGTCCGGCCCCCAGGAGAGAAAAAGAGACATGGGGGGAACAAGGACAGAAAGGCACT
DB	241	GGAAGAGTCCGGCCCCCAGGAGAGAAAAAGAGACATGGGGGGAACAAGGACAGAAAGGCACT
QY	324	GTGGGTGTGTCATGGAAAAATTGTCCTCATTTGGGCTCTAAAGGTGAGAAAGAGATTCGGGT
DB	301	GTGGGTGTGTCATGGAAAAATTGTCCTCATTTGGGCTCTAAAGGTGAGAAAGAGATTCGGGT
QY	384	GACATAGAGACCCCCCTGGTGTCTTAATGAGAACAGAGCCTCCCATGTGATGACCGACGTG
DB	361	GACATAGAGACCCCCCTGGTGTCTTAATGAGAACAGAGCCTCCCATGTGATGACCGACGTG
QY	444	CGCAAGGCATCGGGGAGATGAGACACAGGTCTCTCACTGACACAGGAGCTCAATTTTC
DB	421	CGCAAGGCATCGGGGAGATGAGACACAGGTCTCTCACTGACACAGGAGCTCAAGTTTC
QY	504	ATCAAGATGTGTGCGCGGGTGTGCGGGAGACGGAGACAGATCTAATCTGTGGTGAAG
DB	481	ATCAAGATGTGTGCGCGGGTGTGCGGGAGACGGAGACAGATCTAATCTGTGGTGAAG
QY	564	GAGAGAGAGCGCTACGCGGACGCGCCAGTGTCTTGCCAGAGGCGCGGGGGACAGCTGAGC
DB	541	GAGAGAGAGCGCTACGCGGACGCGCCAGTGTCTTGCCAGAGGCGCGGGGGACAGCTGAGC
QY	624	ATGCCCCAAGAGCAGAGGCTGCCAATGCGCTGTAGTGCCTGATCTTGCGCGAAGCGGCGCTG
DB	601	ATGCCCCAAGAGCAGAGGCTGCCAATGCGCTGTAGTGCCTGATCTTGCGCGAAGCGGCGCTG
QY	684	GCCGTGTCTTCAATCGGCATCTAAGACTTGAGACTTGAGAGAGGGCGGCTTCGTGTACTCTAGC
DB	661	GCCGTGTCTTCAATCGGCATCTAAGACTTGAGACTTGAGAGAGGGCGGCTTCGTGTACTCTAGC
QY	744	CACATCCCCCATATGCGGACCTTCAACAGATGGGCGCAGCGGTGAGCCCAATATGCTTACAGC
DB	721	CACATCCCCCATATGCGGACCTTCAACAGATGGGCGCAGCGGTGAGCCCAATATGCTTACAGC
QY	804	GAGGAGGACTGCGTGAAGATGTTGAGCTTCGGGCGGCTGGAACGAGCTGTGCTGCCACCC
DB	781	GAGGAGGACTGCGTGAAGATGTTGAGCTTCGGGCGGCTGGAACGAGCTGTGCTGCCACCC
QY	864	ACCATGTATCTTCAATGTGTGAGTTTGAACAAGAGAACATGTGAGGCTCAAGGCTTGGGGCTGC
DB	841	ACCATGTATCTTCAATGTGTGAGTTTGAACAAGAGAACATGTGAGGCTCAAGGCTTGGGGCTGC
QY	924	CCATTTGGGGGGCCCCACATGTCCCTGACAGGGTTGGACAAGGACAGAGCCACAGACATATGTGC
DB	901	CCATTTGGGGGGCCCCACATGTCCCTGACAGGGTTGGACAAGGACAGAGCCACAGACATATGTGC
QY	984	CAGCCAGGAGACTGTCCCTCTGTGAGAGGGTGAAGGCTCACTGAGTGAAGGCGCTGTGTCT
DB	961	CAGCCAGGAGACTGTCCCTCTGTGAGAGGGTGAAGGCTCACTGAGTGAAGGCGCTGTGTCT
QY	1044	AAACTGAGAAAATGGCTTATGCTTAAAGAGAAAATGAAAAGTTCCTGGGGTGTCTGTCTC

Db 1021 AAAGTGAAGAAATGCGCTATGCTTAAGAGAAATGAAAGTGTCTCGGGGTGCTGTCTC 1080

Qy 1104 TGAAGAAGAGAGTTTCTATCTATGTTAGTACCCCATGTCATTAATTAATTTACC 1163

Db 1081 TGAAGAAGAGAGTTTCTATCTATGTTAGTACCCCATGTCATTAATTAATTTACC 1140

Qy 1164 CAGAAATGCTCTCCATTAAGCTTGTGCTTGTCCAGCTATACATTAATTTTAAG 1223

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Qy 1224 TAGTCAGTAGTTAAGTCCAAAAA 1253

Db 1201 TAGTCAGTAGTTAAGTCCAAAAA 1230

RESULT 4

AX491060 1238 bp DNA linear PAT 16-AUG-2002

LOCUS Sequence 167 from Patent WO200690.

DEFINITION AX491060

ACCESSION AX491060

VERSION AX491060.1 GI:22323867

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Baker, K.P., Ferrara, N., Gerber, H., Gertlisen, M.E., Goddard, A., Godwin, K., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J., Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I. and Ye, W.

TITLE Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis

JOURNAL Patent: WO 0200690-A 167 03-JAN-2002;

FEATURES

Source Location/Qualifiers

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/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

ORIGIN

Query Match 98.2%; Score 1230; DB 6; Length 1238;

Best Local Similarity 100.0%; Pred. No. 4.5e-208;

Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 GCGACGGGACAGAGCGCCGCTTGGCTAGCGCGCTAGAGAGTTGGTCTGCTGCG 83

Db 1 GCGACGGGACAGAGCGCCGCTTGGCTAGCGCGCTAGAGAGTTGGTCTGCTGCG 60

Qy 84 CTCAGATGAGGGGAAATCTGAGCCTGTGAGCGTTCTAATCAGCCTTCTCTGCA 143

Db 61 CTCAGATGAGGGGAAATCTGAGCCTGTGAGCGTTCTAATCAGCCTTCTCTGCA 120

Qy 144 CTGCTGCGATCTGACATCTCTAGCGCGCTGAGCGAGTACGCGTCTGCTGCAATCTC 203

Db 121 CTGCTGCGATCTGACATCTCTAGCGCGCTGAGCGAGTACGCGTCTGCTGCAATCTC 180

Qy 204 GTCCCTGGCTCAAAAGGGAGATGCGGGAGAGAAAGGAGCAAAAGCGCCCGGAGCGGCT 263

Db 181 GTCCCTGGCTCAAAAGGGAGATGCGGGAGAGAAAGGAGCAAAAGCGCCCGGAGCGGCT 240

Qy 264 GAAAGAGTGGCGCCCAAGGAGAAAGAGAGCAATGGGGAGCAAAAGAGAGAGAGT 323

Db 241 GAAAGAGTGGCGCCCAAGGAGAAAGAGAGCAATGGGGAGCAAAAGAGAGAGT 300

Qy 324 GTGGGTCTCATGAAAAATTTGTTCCATTGGCTCTTAAAGTGAAGAGAGATTCGGT 383

Db 301 GTGGGTCTCATGAAAAATTTGTTCCATTGGCTCTTAAAGTGAAGAGAGATTCGGT 360

Qy 384 GACATAGAGACCCCGTGTCTTAATGAGAGAACAGGCGCTCCCATGATGAGAGCAGCTG 443

Db 361 GACATAGAGACCCCGTGTCTTAATGAGAGAACAGGCGCTCCCATGATGAGAGCAGCTG 420

Qy 444 CGCAAGGCCATCGGGAGATGAGCAACCAAGTCTCTTACGCTGACCAAGGAGCTCAAGTTC 503

Db 421 CGCAAGGCCATCGGGAGATGAGCAACCAAGTCTCTTACGCTGACCAAGGAGCTCAAGTTC 480

Qy 504 ATCAAGATCTGTCGCGGTGTGCGGAGACGAGAGCAAGATCTTCTGCTGTTAAG 563

Db 481 ATCAAGATCTGTCGCGGTGTGCGGAGACGAGAGCAAGATCTTCTGCTGTTAAG 540

Qy 564 GAGGAGAGGCTTACGCGACGCCAGCTGTCTTCCAGGAGCGGGGAGACGCTGAGC 623

Db 541 GAGGAGAGGCTTACGCGACGCCAGCTGTCTTCCAGGAGCGGGGAGACGCTGAGC 600

Qy 624 ATGCCAAGAGACAGAGCTGCGCAATGAGCTGATGAGCGGAGCAATCTGAGCGCAAGCGGCTG 683

Db 601 ATGCCAAGAGACAGAGCTGCGCAATGAGCTGATGAGCGGAGCAATCTGAGCGCAAGCGGCTG 660

Qy 684 GCCCGTCTTCAATCGGATCAACGACCTGAGAGAGAGGAGCGCTTCTGTACTGAC 743

Db 661 GCCCGTCTTCAATCGGATCAACGACCTGAGAGAGAGGAGCGCTTCTGTACTGAC 720

Qy 744 CACTCCCCATGCGGACCTTCAACAGTGGCGAGCGGTGAGCCCAATGCTTACGAC 803

Db 721 CACTCCCCATGCGGACCTTCAACAGTGGCGAGCGGTGAGCCCAATGCTTACGAC 780

Qy 804 GAGGAGAGCTGCGGAGATGAGTGGGCTGCGGGGCTGGAACAGAGCTGCGCAAGC 863

Db 781 GAGGAGAGCTGCGGAGATGAGTGGGCTGCGGGGCTGGAACAGAGCTGCGCAAGC 840

Qy 864 ACCATGACTTCAATGAGTGAATTTGACAGAGAGACATGAGCTTCAAGCTGAGGCTGCG 923

Db 841 ACCATGACTTCAATGAGTGAATTTGACAGAGAGACATGAGCTTCAAGCTGAGGCTGCG 900

Qy 924 CCAATGGGGGCCCCCATGATGCTTCTGAGGCTTGGCAGAGGACAGAGCCCAACATGATGTC 983

Db 901 CCAATGGGGGCCCCCATGATGCTTCTGAGGCTTGGCAGAGGACAGAGCCCAACATGATGTC 960

Qy 984 CAGCGAGGAGAGCTGCTCCCTGTGAGAGGCTGAGGCTCACTGATGAGAGGCTGTTGCT 1043

Db 961 CAGCGAGGAGAGCTGCTCCCTGTGAGAGGCTGAGGCTCACTGATGAGAGGCTGTTGCT 1020

Qy 1044 AAATGAGAAATGCGCTATGCTTAAAGAGAAATGAAAGTCTTCTGAGGCTGCTGCTC 1103

Db 1021 AAATGAGAAATGCGCTATGCTTAAAGAGAAATGAAAGTCTTCTGAGGCTGCTGCTC 1080

Qy 1104 TGAAGAAGAGAGTTTCTATCTGATGTTAGTACCCCAATGATTAATTAATTAAC 1163

Db 1081 TGAAGAAGAGAGTTTCTATCTGATGTTAGTACCCCAATGATTAATTAATTAAC 1140

Qy 1164 CAGAAATGCTCTTCAATTAAGCTTGTGCTTGTCCAGCTATACATTAATTTTAAG 1223

Db 1141 CAGAAATGCTCTTCAATTAAGCTTGTGCTTGTCCAGCTATACATTAATTTTAAG 1200

Qy 1224 TAGTCAGTAGTTAAGTCCAAAAA 1253

Db 1201 TAGTCAGTAGTTAAGTCCAAAAA 1230

RESULT 5

AY358439 1238 bp mRNA linear PRI 03-OCT-2003

LOCUS Homo sapiens clone DNA59848 RGNL596 (UNQ596) mRNA, complete cds.

DEFINITION AY358439

ACCESSION AY358439

VERSION AY358439.1 GI:37382002

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Chark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B., Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P.E.,



Helde, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S.,  
 Lee, J., Lawler, L., Liao, D., Mark, M., Robbie, E., Sanchez, C.,  
 Schoenfeld, J., Seehagitz, S., Simmons, L., Singh, J., Smith, V.,  
 Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wiand, D., Woods, K.,  
 Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z.,  
 Goddard, A., Wood, M.I., and Godowski, P.  
 The Secreted Protein Discovery Initiative (SPDI), a Large-Scale  
 Effort to Identify Novel Human Secreted and Transmembrane Proteins:  
 A Bioinformatics Assessment  
 Genome Res. 13 (10), 2265-2270 (2003)

JOURNAL PUBMED 12975309  
 REFERENCE 2 (bases 1 to 1238)  
 AUTHORS Clark, H.F.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,  
 Inc., 1 DNA Way, South San Francisco, CA 94080, USA

FEATURES  
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 REFERENCE 1 (bases 1 to 1248)  
 AUTHORS Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D.,  
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
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TITLE  
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AUTHORS  
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JOURNAL  
TITLE  
JOURNAL

REMARK  
COMMENT

Scheetz, T.E., Brownstein, M.J., Uedlin, T.B., Toshiyuki, S.,  
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Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E.,  
Scherer, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

2 (bases 1 to 1248)  
Strausberg, R.  
Direct Submission  
Submitted (03-NOV-2000) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>  
On Aug 20, 2003 this sequence version replaced gi:12652660.  
Contact: MGC help desk  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
DNA Sequencing by: Institute for Systems Biology  
<http://www.systemsbio.org>  
contact: [amadan@systemsbio.org](mailto:amadan@systemsbio.org)  
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha  
Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>  
Series: IRAL Plate: 7 Row: 9 Column: 20  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 13128971.

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SOURCE

gene

CDS

ORIGIN

Query Match 97.8%; Score 1225.8; DB 9; Length 1248;  
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Matches 1230; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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VERSION	BC009951.2	GI:33871813	
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SOURCE	Homo sapiens (human)		
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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
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	Schmerer,A., Schein,J.E., Jones,S.J., and Matra,M.A.		
	Generation and initial analysis of more than 15,000 full-length		
	human and mouse cDNA sequences		
	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
	2 (bases 1 to 1417)		
JOURNAL	Strauberg,R.		
PUBMED	Direct Submission		
REFERENCE	Submitted (02-JUN-2001) National Institutes of Health, Mammalian		
AUTHORS	Gene Collection (MGC), Cancer Genomics Office, National Cancer		
JOURNAL	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,		
	USA		
	NIH-MGC Project URL: http://mgc.nci.nih.gov		
	On Aug 19, 2003 this sequence version replaced gi:14714411.		
REMARK	Contact: MGC help desk		
COMMENT	Email: cgabbs@email.nih.gov		
	Tissue Procurement: ATCC		
	cDNA Library Preparation: Rubin Laboratory		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: National Institutes of Health Intramural		
	Sequencing Center (NISC),		
	Gaithersburg, Maryland;		
	Web site: http://www.nisc.nih.gov/		
	Contact: nisc.mgc@nih.gov		
	Akhmetov,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B.,		
	Blakesley,R.W., Bouffard,G.G., Breun,K., Brinkley,C., Brooks,S.,		
	Dierker,N.L., Grant,S., Guan,X., Gupta,U., Haghighi,P.,		
	Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Latic,P., Legaspi,R.,		
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Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>

Series: IRAL Plate: 20 Row: f Column: 22

This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

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DEFINITION Novel collection.
ACCESSION BD103302
VERSION   BD103302.1 GI:22648876
KEYWORDS  WO 0181401-A/1.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1341)
AUTHORS  Wakamiya,N., Keshi,H., Otani,K., Sakamoto,T. and Kishi,Y.

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TITLE Novel collection
JOURNAL Patent: WO 0181401-A 1 01-NOV-2001;
FUSO PHARMACEUTICAL INDUSTRIES LTD, NOBUTAKA WAKAMIYA, HIROYUKI
KESHI, KATSUKI OTANI, TAKASHI SARAKOTO, YUICHIRO KISHI
COMMENT OS Homo sapiens (human)
PN WO 0181401-A/1
PF 01-NOV-2001
PR 23-APR-2001 WO 2001JP003468
PI NOBUTAKA WAKAMIYA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI PI
SAKAMOTO,
PI YUICHIRO KISHI
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 Matches 1139; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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REFERENCE 1 (bases 1 to 1269)  
AUTHORS Wakamiya,N., Keshi,H., Otani,K., Sakamoto,T. and Kishi,Y.  
TITLE Novel collection  
JOURNAL Patent: WO 0181401-A 29 01-NOV-2001;  
FUSO PHARMACEUTICAL INDUSTRIES LTD,NOBUTAKA WAKAMIYA,HIROYUKI  
KESHI, KATSUKI OTANI,TAKASHI SAKAMOTO,YUICHIRO KISHI  
OS Homo sapiens (human)  
COMMENT OS WO 0181401-A/29  
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PF 23-APR-2001 WO 2001JP003468  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 REFERENCE 1 (bases 1 to 1269)  
 AUTHORS Wakamiya,N., Keshi,H., Ocani,K., Sakamoto,T. and Kishi,Y.  
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 JOURNAL Patent: WO 0181401-A 30 01-NOV-2001;  
 FUSO PHARMACEUTICAL INDUSTRIES LTD,NOBUTAKA WAKAMIYA,HIROYUKI  
 KESHI, KATSUKI OTANI,TAKASHI SAKAMOTO,YOICHIRO KISHI  
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 PI YOICHIRO KISHI  
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 REFERENCE 1 (bases 1 to 1139)  
 AUTHORS Wakamiya,N., Keshi,H., Ocani,K., Sakamoto,T. and Kishi,Y.  
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Wakamaya,N., Keshi,H., Otani,K., Sakamoto,T. and Kishi,Y.				
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FUSO PHARMACEUTICAL INDUSTRIES LTD, NOBUTAKA WAKAMAYA, HIROYUKI				
KESHI, KATSUOKI OTANI, TAKASHI SAKAMOTO, YUCHIRO KISHI				
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REFERENCE 1 (bases 1 to 1067)  
AUTHORS Wakamiya,N., Keshi,H., Otani,K., Sakamoto,T. and Kishi,Y.  
TITLE Novel collectin  
JOURNAL Patent: WO 0181401-A 5 01-NOV-2001;  
FUSO PHARMACEUTICAL INDUSTRIES LTD, NOBUTAKA WAKAMIYA, HIROYUKI  
KESHI, KATSUKI OTANI, TAKASHI SAKAMOTO, YUICHIRO KISHI  
COMMENT OS Homo sapiens (human)  
PN WO 0181401-A/5  
PD 01-NOV-2001  
PF 23-APR-2001 WO 2001JP003468  
PR 21-APR-2000 JP 00P 120358  
PI NOBUTAKA WAKAMIYA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI PI  
SAKAMOTO.  
PI YUICHIRO KISHI  
PC C07K14/47,C12N15/12,C12P21/02,A01K67/027,C07K16/18,G01N33/53  
CC Novel collectin  
FH Key Location/Qualifiers  
FT CDS (141)..(803).  
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ACCESSION BD103332  
VERSION BD103332.1 GI:22648906  
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REFERENCE 1 (bases 1 to 813)  
AUTHORS Wakamiya,N., Keshi,H., Otani,K., Sakamoto,T. and Kishi,Y.  
TITLE Novel collectin  
JOURNAL Patent: WO 0181401-A 31 01-NOV-2001;  
FUSO PHARMACEUTICAL INDUSTRIES LTD, NOBUTAKA WAKAMIYA, HIROYUKI  
KESHI, KATSUKI OTANI, TAKASHI SAKAMOTO, YUICHIRO KISHI  
COMMENT OS Homo sapiens (human)  
PN WO 0181401-A/31  
PD 01-NOV-2001  
PF 23-APR-2001 WO 2001JP003468  
PR 21-APR-2000 JP 00P 120358  
PI NOBUTAKA WAKAMIYA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI PI  
SAKAMOTO,  
PI YUICHIRO KISHI

Search completed: December 16, 2004, 19:01:41  
Job time : 8745 secs

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## FEATURES

source

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Query Match 64.9%; Score 813; DB 6; Length 813;  
Best Local Similarity 100.0%; Pred. No. 3.8e-134; Mismatches 0; Indels 0; Gaps 0;  
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ACCESSION					
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VERSION					
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ORGANISM					
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
REFERENCE					
AUTHORS					
Li, W.B., Gruber, C., Jeesee, J. and Polayes, D.					
Full-length cDNA libraries and normalization					
Unpublished					
CONTACT					
Contact: Peng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600					
Paradey Avenue					
2 (bases 1 to 1252)					
REFERENCE					
AUTHORS					
Genoscope.					
Direct Submission					
Submitted (20-JUN-2004) Genoscope - Centre National de Sequencage					
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqret@genoscope.cns.fr					
- Web: www.genoscope.cns.fr)					
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primers					
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was normalized. Library was constructed by Life Technologies, a					
division of Invitrogen.					
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VERSION CR599770.1 GI:50480577
KEYWORDS HTC; CNSLT_cDNA.
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AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact: Feng Liang Email: fliang@life.techn.com URL:
http://fulllength.livtrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
Genoscope.
2 (bases 1 to 1150)
REFERENCE Direct Submission
AUTHORS Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
TITLE BP 191 9106 EVR cedex - FRANCE (E-mail: seque@genoscope.cns.fr)
JOURNAL - Web : www.genoscope.cns.fr
COMMENT 1st strand cDNA was primed with a NotI-oligo(47) primer. Five prime
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
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REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
NIH-MGC <http://mgi.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
[found through the I.M.A.G.E. Consortium/LLNL at:](http://image.llnl.gov)  
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Location/Qualifiers

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source

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Note: this is a NIH\_MGC Library."

## ORIGIN

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469 ACCAGTCTCTACGTGACACAGCAGCTCAAGTATCATCAAGATGCTGCGCGGTGTC 528  
61 ACCAGTCTCTACGTGACACAGCAGCTCAAGTATCATCAAGATGCTGCGCGGTGTC 120  
529 GCGAGACGAGAGCAAGATCTACCTGCTGTGTAAGAGAGAGGAGGCTTACGCGAGCGCC 588  
121 GCGAGACGAGAGCAAGATCTACCTGCTGTGTAAGAGAGAGGAGGCTTACGCGAGCGCC 180  
589 AGCTGTCTCTGCGAGGCGCGGGGAGCAGCTGAGATGCCCAAGAGCAGAGCTGCCAATG 648  
181 AGCTGTCTCTGCGAGGCGCGGGGAGCAGCTGAGATGCCCAAGAGCAGAGCTGCCAATG 240  
649 GCGTATGCGCCCATACCTGTGGGCAAGCGGCTGCGCGCTCTTTCATCGGCATCAACG 708  
241 GCGTATGCGCCCATACCTGTGGGCAAGCGGCTGCGCGCTCTTTCATCGGCATCAACG 300  
709 ACCTGAGAGAGAGGCGCGCTTGTGTACTGACCACTCCCGCATGGGAGACCTTCAACA 768  
301 ACCTGAGAGAGAGGCGCGCTTGTGTACTGACCACTCCCGCATGGGAGACCTTCAACA 360  
769 AGTGCGCAGCGGCTGAGCCCAATGCTTACGAGAGAGAGAGCTGCGTGAAGATGATG 828  
361 AGTGCGCAGCGGCTGAGCCCAATGCTTACGAGAGAGAGAGCTGCGTGAAGATGATG 420  
829 CCTGGGGGGGCTGGAACAAGCTGGGCTGCAACACCATGTAATTTATGTGTGATTG 888  
421 CCTGGGGGGGCTGGAACAAGCTGGGCTGCAACACCATGTAATTTATGTGTGATTG 480

QY 889 ACAAGAGAAATGATGAGGCTCAGGCTGGGCGCTGCCATTGGGGGCCCCACATGTCCTG 948  
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QY 949 CAGGTTGGCAGGAGCAGAGCCCAACATGTTGCCAGGCGAGAGCTGCTCTGTGA 1008  
DB 541 CAGGTTGGCAGGAGCAGAGCCCAACATGTTGCCAGGCGAGAGCTGCTCTGTGA 600  
QY 1009 AGGTTGAGGCTCAGTGAATGAGGCGTGTGTCTAACTGAGAAATGGGCTATGCTTA 1068  
DB 601 AGGTTGAGGCTCAGTGAATGAGGCGTGTGTCTAACTGAGAAATGGGCTATGCTTA 660  
QY 1069 AGAGAAATGAATGAATGTTCTCGGGGCTGTCTCTGAAGAAGCAGAGTTTCAATACCTG 1128  
DB 661 AGAGAAATGAATGAATGTTCTCGGGGCTGTCTCTGAAGAAGCAGAGTTTCAATACCTG 720  
QY 1129 TATTTAGCCCCAATGCTATTAATTAATTAATACCC 1164  
DB 721 TATTTAGCCCCAATGCTATTAATTAATTAATACCC 756

RESULT 6  
BQ927000 962 bp mRNA linear EST 20-AUG-2002  
LOCUS BQ927000 5', mRNA sequence.  
DEFINITION AGENCOURT 8804355 NIH\_MGC\_47 Homo sapiens CDNA clone IMAGE:6377965  
ACCESSION BQ927000.1 GI:22342031  
VERSION BQ927000  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

NIH-MGC <http://mgi.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: L10M2562 row: j column: 14  
High quality sequence stop: 616.  
Location/Qualifiers

FEATURES  
source

1. 962  
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/clone="IMAGE:6377965"  
/tissue\_type="neuroblastoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_47"  
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:  
ECORI; CDNA made by oligo-dt priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 54.0%; Score 676; DB 5; Length 962;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GCGCAGCAGCGGAGAGCGCCGCTTGCCTAGCGGCTGCTCAGAGATGTGTCTGCG 78







QY 96 GGAATCTGGCCCTGGTGGGGCTTCTATCAGCCCTGCTCTCTCACTGCTCCATCT 155  
DB 61 GGGATCTGGCCCTGGTGGGGCTTCTATCAGCCCTGCTCTCTCACTGCTCCATCT 120  
QY 156 GGAATCTCTCAGCCGCTGGGATGACCGCTGCTCTGTCAGATCTCTGCTGCTGCTGCTC 215  
DB 121 GGAATCTCTCAGCCGCTGGGATGACCGCTGCTCTGTCAGATCTCTGCTGCTGCTGCTC 180  
QY 216 AAGGGGATGCGGGAG 275  
DB 181 AAGGGGATGCGGGAG 240  
QY 276 CCCACGGGAG 335  
DB 241 CCCACGGGAG 300  
QY 336 GGAATAATTTGCTCCATTTGCTCTAAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 395  
DB 301 GGAATAATTTGCTCCATTTGCTCTAAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 360  
QY 396 CTTGCTCTAATGAG 455  
DB 361 CTTGCTCTAATGAG 420  
QY 456 GGGGAGATGAG 515  
DB 421 GGGGAGATGAG 480  
QY 516 GTCCGCTGCTGCGGAG 575  
DB 481 GTCCGCTGCTGCGGAG 540  
QY 576 TACCGGAG 635  
DB 541 TACCGGAG 600  
QY 636 GAGGCTGCCAATGAGCTGATG 657  
DB 601 GAGGCTGCCAATGAGCTGATG 622

RESULT 10  
BE262656 644 bp mRNA linear EST 26-OCT-2000  
LOCUS 6011514651 NIH\_MGC\_19 Homo sapiens cDNA clone IMAGE:3507377 5',  
DEFINITION mRNA sequence.  
ACCESSION BE262656  
VERSION BE262656.1 GI:9135855  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 644)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/BLNL at: image.lnml.gov  
Plate: L10M187 row: b column: 18  
High quality sequence start: 14  
High quality sequence stop: 643.  
Location/Qualifiers  
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/tissue\_type="neuroblastoma"  
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/clone\_lib="NIH\_MGC\_19"  
/notes="Organ: Brain; Vector: pOT7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCAAGAG(G). Library constructed by Ling Hong  
in the Laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

Query Match 49.6%; Score 622; DB 2; Length 644;  
Best Local Similarity 100.0%; Pred. No. 1.3e-305;  
Matches 622; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 GCGGAGCAG 75  
DB 23 GCGGAGCAG 82  
QY 76 TGCTGCTCAGAGATGAG 135  
DB 83 TGCTGCTCAGAGATGAG 142  
QY 136 TGCTGCTCAGAGATGAG 195  
DB 143 TGCTGCTCAGAGATGAG 202  
QY 196 AGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 255  
DB 203 AGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 262  
QY 256 GAGGCTGAG 315  
DB 263 GAGGCTGAG 322  
QY 316 AAGGCAATGAG 375  
DB 323 AAGGCAATGAG 382  
QY 376 ATTCCGCTGAGATGAG 435  
DB 383 ATTCCGCTGAGATGAG 442  
QY 436 GCCAGCTGCGCAAG 495  
DB 443 GCCAGCTGCGCAAG 502  
QY 496 TCAGATTCATCAAG 555  
DB 503 TCAGATTCATCAAG 562  
QY 556 TGGTGAAG 615  
DB 563 TGGTGAAG 622  
QY 616 CGCTGAGCATGCGCAAG 637  
DB 623 CGCTGAGCATGCGCAAG 644

RESULT 11  
BE382845 723 bp mRNA linear EST 21-JUL-2000  
LOCUS 6012977141 NIH\_MGC\_19 Homo sapiens cDNA clone IMAGE:3627794 5',  
DEFINITION mRNA sequence.  
ACCESSION BE382845  
VERSION BE382845.1 GI:9328210  
KEYWORDS EST.  
SOURCE Homo sapiens (human)



Qy	196	AGATCTCTCTCCCTGGCCCTCAAGGGGATGCGGGAGAAAGGAGACAAAGCGCCCG	255
Db	181	AGATCTCTCTCTCTGGCCTCAAGGGGATGCGGGAGAAAGGAGACAAAGCGCCCG	240
Qy	256	GACGCGCTTGAAAGAGTCGGCCCAACGGAGAAAAGAGACATGGGGGACAAAGACAGA	315
Db	241	GACGCGCTTGAAAGAGTCGGCCCAACGGAGAAAAGAGACATGGGGGACAAAGACAGA	300
Qy	316	AAGCGAGTGTGGGTGTCATGGAATAATGGTCCCATTTGGCTTAAAGTGAAGAAAGAG	375
Db	301	AAGCGAGTGTGGGTGTCATGGAATAATGGTCCCATTTGGCTTAAAGTGAAGAAAGAG	360
Qy	376	ATTCCGGTGCATAGGACCCCTCTGTCCTAAATGAGAACGAGGCTCCATGTGAGTGCA	435
Db	361	ATTCCGGTGCATAGGACCCCTCTGTCCTAAATGAGAACGAGGCTCCCATGTGAGTGCA	420
Qy	436	GCCAGCTGGCGCAAGGCTCATGGGGAGATGGAACACAGGTCTTCACCTGACCAAGGAGC	495
Db	421	GCCAGCTGGCGCAAGGCTCATGGGGAGATGGAACACAGGTCTTCACCTGACCAAGGAGC	480
Qy	496	TCAAGTTCATCAAGAATGCTGTGCGCGGATGTCGCGAGACGGAAGGAGAAGATCTACCTGC	555
Db	481	TCAAGTTCATCAAGAATGCTGTGCGCGGATGTCGCGGATGTCGCGAGACGGAAGGAGAAGATCTACCTGC	540
Qy	556	TGATGAAGAGAGAAAGCGCTACGCGAGACGCCCACTGTCTGCGAAGGCCCGCGGGGCA	615
Db	541	TGATGAAGAGAGAAAGCGCTACGCGAGACGCCCACTGTCTGCGAAGGCCCGCGGGGCA	600
Qy	616	CGCTGAGCATGCC	628
Db	601	CGCTGAGCATGCC	613

RESULT 13	BE382433	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
	BE382433	601297261p1	NIH_MGC_19 Homo sapiens CDNA clone IMAGE:3627375 5',	683 bp	mRNA	linear	EST 21-JUL-2000						
			mRNA sequence.	BE382433			GI:9327798						
			EST.					Homo sapiens (human)					
								Homo sapiens					
								Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
								Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
								1 (bases 1 to 683)					
								NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .					
								National Institutes of Health, Mammalian Gene Collection (MGC)					
								Unpublished (1999)					
								Contact: Robert Strausberg, Ph.D.					
								Email: <a href="mailto:cgabbs-r@mail.nih.gov">cgabbs-r@mail.nih.gov</a>					
								Tissue Procurement: ATCC					
								CDNA Library Preparation: Ling Hong/Rubin Laboratory					
								CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)					
								DNA Sequencing by: Incyte Genomics, Inc.					
								Clone distribution: MGC clone distribution information can be					
								found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">image.llnl.gov</a>					
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								High quality sequence stop: 595.					

**FEATURES**  
**Source**

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/clone_1ib="N1H MCC 19"
/note="Organ: brain; Vector: pOT37; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming; EcoRI sites using the following 5' cloned into EcoRI/XhoI sites using the following 5' adaptor: GCGCAGCAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of

```

ORIGIN

Query Match	47.7%;	Score 598;	DB 2;	Length 683;
Best Local Similarity	100.0%;	Pred. No. 2.3e-293;		
Matches 598;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC Library."

[illegible]

RESULT 14				
BE313199				
LOCUS	BE313199	715 bp	mrna	linear
DEFINITION	601149012P1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE3501747 5',			
ACCESSION	BE313199			
VERSION	BE313199.1			
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
1 (bases 1 to 715)  
REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC).  
JOURNAL Unpublished. (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.

Tissue Procurement: ATCC  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MCC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
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High quality sequence stop: 643.  
Location/Qualifiers

## FEATURES

Source

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/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC library."

## ORIGIN

Query Match 47.3%; Score 593; DB 2; Length 715;  
Best Local Similarity 100.0%; Pred. No. 8.2e-291;  
Matches 593; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

36 ACGCCCTTGGCCCTAGGCGGCTCAGAGTGTGCTTCCCTGCGCTCAGATGAGG 95  
1 ACGCCCTTGGCCCTAGGCGGCTCAGAGTGTGCTTCCCTGCGCTCAGATGAGG 60  
96 GGAATCTGCGCCTGTGGCGCTTCTAATCAGCTGCGCTTCTGCTCACTGCTGCATCT 155  
61 GGAATCTGCGCCTGTGGCGCTTCTAATCAGCTGCGCTTCTGCTCACTGCTGCATCT 120  
156 GGAATCTGCGCCTGTGGCGCTTCTAATCAGCTGCGCTTCTGCTCACTGCTGCATCT 215  
121 GGAATCTGCGCCTGTGGCGCTTCTAATCAGCTGCGCTTCTGCTCACTGCTGCATCT 180  
216 AAGGGGATGGGGAG 275  
181 AAGGGGATGGGGAG 240  
276 CCCACGGAG 335  
241 CCCACGGAG 300  
336 GGAATCTGCGCCTGTGGCGCTTCTAATCAGCTGCGCTTCTGCTCACTGCTGCATCT 395  
301 GGAATCTGCGCCTGTGGCGCTTCTAATCAGCTGCGCTTCTGCTCACTGCTGCATCT 360  
396 CCTGTCTTAATGAGAACCAAGGCTTCCATGTGATGATGATGATGATGATGATGATG 455  
361 CCTGTCTTAATGAGAACCAAGGCTTCCATGTGATGATGATGATGATGATGATGATG 420  
456 GGGGATGAGCAACCAAGGCTTCTAATCAGCTGCGCTTCTGCTCACTGCTGCATCT 515  
421 GGGGATGAGCAACCAAGGCTTCTAATCAGCTGCGCTTCTGCTCACTGCTGCATCT 480  
516 GTCGCGGTGTGCGCGAGACGAGAGCAAGATCTAATCTGCTGTGTAAGAGAGAGAGAG 575  
481 GTCGCGGTGTGCGCGAGACGAGAGCAAGATCTAATCTGCTGTGTAAGAGAGAGAGAG 540  
576 TACCGGAGCGCCCAAGCTGTCTGCGAGGCGCGCGGGGCAAGCTGAGCATGCC 628  
541 TACCGGAGCGCCCAAGCTGTCTGCGAGGCGCGCGGGGCAAGCTGAGCATGCC 593

RESULT 15  
BF311185 702 bp mRNA linear EST 21-NOV-2000  
LOCUS BF311185 601898434P1 NIH\_MGC\_19 Homo sapiens cDNA clone IMAGE:4127577 5',  
DEFINITION mRNA sequence.  
ACCESSION BF311185

VERSION BF311185.1 GI:1125873  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
1 (bases 1 to 702)  
TITLE NIH-MGC http://mgi.nci.nih.gov/  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-rcmail.nih.gov  
Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
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High quality sequence stop: 695.  
Location/Qualifiers

## FEATURES

Source

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## ORIGIN

Query Match 46.9%; Score 588; DB 2; Length 702;  
Best Local Similarity 100.0%; Pred. No. 2.9e-288;  
Matches 588; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

16 GCGGCGCAG 75  
1 GCGGCGCAG 60  
76 TGCCGCGCTCAGAGATGAG 135  
61 TGCCGCGCTCAGAGATGAG 120  
136 TCCTGTCACTGCTCAGATCTGAGATCTCAGCGGCTGCGATGAGCGCTTCTGTGTC 195  
121 TCCTGTCACTGCTCAGATCTGAGATCTCAGCGGCTGCGATGAGCGCTTCTGTGTC 180  
196 AGATCTGCTGCTGCGCTTCAAAGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 255  
181 AGATCTGCTGCTGCGCTTCAAAGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
256 GACGCGCTGAG 315  
241 GACGCGCTGAG 300  
316 AAGGCAAGTGTGGTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 375  
301 AAGGCAAGTGTGGTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360  
376 ATTCGCGGATGAG 435  
361 ATTCGCGGATGAG 420  
436 GCCAGTGGCGCAAGGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 495

Db 421 GCCAGCTGCCAAGGCCATCGGGAGATGACAAACAAGTCTTCAAGCTGACGCGAGC 480  
QY 496 TCAAGTTCATCAGAGATGCTGTGCGCGGTGTGCGGAGACGAGAGCAAGATCTACCTGC 555  
Db 481 TCAAGTTCATCAGAGATGCTGTGCGCGGTGTGCGGAGACGAGAGCAAGATCTACCTGC 540  
QY 556 TGGTGAAGAGAGAGAGCGCTACCGGAGACGCCCAAGCTGTCTGCGCAGG 603  
Db 541 TGGTGAAGAGAGAGAGCGCTACCGGAGACGCCCAAGCTGTCTGCGCAGG 588

Search completed: December 17, 2004, 03:37:43  
Job time : 6193 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

# OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 17, 2004, 11:20:00 ; Search time 3865 Seconds  
(without alignments)  
2555.024 Million cell updates/sec

Title: US-09-806-277A-6

Perfect score: 271

Sequence: 1 MRGUALVGVLSIAFLSL.....NDVACHTMYMCEFDKENM 271

## Scoring table:

OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Word size: 1

Total number of hits satisfying chosen parameters: 65644297

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

## Command line parameters:

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-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45  
-DOCLALIGN=200 -THR.SCORB=quality -THR.MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc  
-NOR=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000  
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## Database :

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4: gb\_est3:\*  
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6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_g981:\*  
9: gb\_g982:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	271	100.0	1252	3	CR604552 full-length
2	271	100.0	1397	3	CR612268 full-length
3	208	75.8	894	5	BU147034 AGENCOURT
4	205	75.6	1150	3	CR599770. full-length
5	202	74.5	962	3	BQ927000 AGENCOURT
6	195	72.0	1083	5	BX427124 AGENCOURT
7	190	70.1	672	2	BF206254 AGENCOURT
8	189	69.7	640	2	BE383325 AGENCOURT
9	188	69.4	723	2	BE382845 AGENCOURT

10	182	67.2	644	2	BE262656
11	181	66.8	683	2	BE382433
12	180	66.4	715	2	BE313199
13	179	66.1	613	2	BF312666
14	175	64.6	654	2	BE312923
15	175	64.6	1012	2	BE260904
16	172	63.5	737	2	BE313410
17	172	63.5	767	2	BE260355
18	171	63.1	702	2	BF311185
19	168	62.0	788	2	BF311981
20	164	60.5	962	5	BQ069775
21	162	59.8	542	2	BE313758
22	159	58.7	537	2	BE261686
23	157	57.9	525	2	BE261369
24	136	50.2	769	2	BE312920
25	123	45.4	538	2	BE312003
26	119	43.9	823	4	BF198782
27	119	43.9	916	2	BF316717
28	114	42.1	893	2	BF314316
29	113	41.7	1078	2	BF333394
30	109	40.2	892	2	BF314275
31	109	40.2	1094	2	BM547424
32	104	38.4	665	2	BF317432
33	104	38.4	1321	2	BF316150
34	95	35.1	626	2	BF316496
35	95	35.1	728	2	BE260359
36	94	34.7	642	1	AV655586
37	87	32.1	948	2	BF206235
38	83	30.6	273	5	BK099011
39	83	30.6	1195	2	BF316270
40	81	29.9	969	5	BK427123
41	75	27.7	924	4	BF198572
42	74	27.3	1071	5	BK394624
43	71	26.2	851	6	CB992054
44	70	25.8	619	4	BF199068
45	67	24.7	642	2	BF311988

## ALIGNMENTS

RESULT 1  
CR604552  
LOCUS  
DEFINITION  
full-length cDNA clone CS0DC024Y19 of Neuroblastoma Cot  
25-normalized of Homo sapiens (human).  
ACCESSION  
CR604552  
VERSION  
CR604552.1 GI:50485359  
KEYWORDS  
HTC; CNSL; cDNA.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE  
Li M.B., Gruber C., Jessee J. and Polayes D.  
Full-length cDNA libraries and normalization  
Unpublished  
Contact: Feng Liang Email: fliang@lifetech.com URL:  
http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Faraday Avenue  
2 (bases 1 to 1252)  
REFERENCE  
Genoscope.  
Direct Submission  
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 Evry cedex - FRANCE (E-mail: seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with NotI and cloned  
into the NotI and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
FEATURES  
location/Qualifiers  
1..1252  
/organism="Homo sapiens"





QY 121 AAlaIleGIyGluMetAspAsnGlnValSerGlnLeuThrSerGlnLeuLeuPheIleIys 140  
Db 452 GCCATCGGGAGATGGACACCAAGGTCTCTCGCTGACGACGAGCTCAAGTTCATCAAG 511  
QY 141 AAsnAlaValAlaGluValArgGluThrGluSerIleIleTyrLeuLeuValIleGluGlu 160  
Db 512 AATGCTGTGCGCGGTGTGCGCGAGACGAGACCAAGATCTTACTCTGCTGTGAAGAGAG 571  
QY 161 LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyArgGlyTyrThrLeuSerMetPro 180  
Db 572 AAGCGCTACGGCGAGACCCAGCTGTCTGTCCAGCGGCGCGGCGGACCGCTGAGATGCC 631  
QY 181 LysAspGluAlaAlaAsnGlyLeuMetAlaAlaTyrLeuAlaGlnAlaGlyLeuAlaArg 200  
Db 632 AAGGACGAGGCTGCGCAATGGCTGTATGGCCGCTCTGCGCAGCCGCGCTGCGCT 691  
QY 201 ValPheIleGlyIleAsnAspLeuGluIleYsgIuGlyAlaPheValTyrSerAspHisSer 220  
Db 692 GTCTTCATCGGCATACAGACCTGAGAGAGAGGCGGCTTCTGTACTGTGACCATCTCC 751  
QY 221 ProMetArgThrPheAsnLysTyrArgSerGlyGluProAsnAsnAlaTyrAspGluGlu 240  
Db 752 CCCATGCGGACCTTCAACAGTAGGCGCAGCGGTGAGCCCAACATGCTTACGAGAGAG 811  
QY 241 AspCysValGluMetValAlaSerGlyTyrPheAspValAlaCysHisThrThrMet 260  
Db 812 GACTGCGTGAGATGTGTGGCTCGCGCGCTGGAGACGATGGCTGCGCACACCATG 871  
QY 261 TyrPheMetCysGluPheAspLysGluAsnMet 271  
Db 872 TACTTCATGTGTGAGTTTGACAGAGAGACATG 904

RESULT 3  
BUI47034 894 bp mRNA linear EST 03-SEP-2002  
LOCUS BUI47034  
DEFINITION AGENCOURT\_8736281 NIH\_MGC\_47 Homo sapiens cDNA clone IMAGE:6338772  
5', mRNA sequence.  
ACCESSION BUI47034  
VERSION BUI47034.1 GI:22660566  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 894)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-rcmail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
Cloned through the I.M.A.G.E. Consortium distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
http://image.llnl.gov  
Plate: LNCM2532 row: 1 column: 13  
High quality sequence stop: 621.  
Location/Qualifiers  
1. 894  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6338772"  
/tissue\_type="neuroblastoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_47"  
/note="Organ: brain; Vector: pOTB7, site\_1: XhoI, site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGACGAG(G). Size-selected >500bp for average

Insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

ORIGIN  
Alignment Scores:  
Pred. No.: 4.2e-190 Length: 894  
Score: 208.00 Matches: 242  
Percent Similarity: 99.18% Conservative: 0  
Best Local Similarity: 99.18% Mismatches: 1  
Query Match: 76.75% Indels: 2  
DB: Gaps: 0  
US-09-806-277A-6 (1-271) x BUI47034 (1-894)

QY 1 MetArgGlyAsnLeuAlaLeuValGlyValLeuIleSerIleuAlaPheLeuSerLeuLeu 20  
Db 72 ATGAGGGGGAATCTGGCCCTGTGGGCTTAAATCAAGCTTGCCCTTCTCTCACTGCTG 131  
QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
Db 132 CCATCTGGACATCTCTCAAGCCGCGGTGCGATGACCGCTGCTGTGTGACAGATCCTGCTCCT 191  
QY 41 GlyLeuLysGlyAspAlaGlyGluLysGlyAspLysGlyAlaProGlyValArgProGlyValArg 60  
Db 192 GGCCTCAAGGGGAGATGGCGGAGAGAGAGAGACAAAGCGCCCGGACCGGCTGGAGAGA 251  
QY 61 ValGlyProThrGlyGluLysGlyAspMetGlyAspLysGlyIleLysGlySerValGly 80  
Db 252 GTCCGCCCGGACGGAGAGAGAGAGACATGGGGAGACAAAGACAGAGAGAGAGAGAGAG 311  
QY 81 ArgHisGlyLysIleGlyProIleGlySerIleGlyLysGlyLysGlyAspSerGlyAspIle 100  
Db 312 CGTATGGAGAAATTTGGTCCATTTGGCTCTTAAAGTGAGAGAGAGATTCGGTGACATTA 371  
QY 101 GlyProProGlyProAsnGlyGluProGlyLeuProCysGlyCysSerGlnLeuValArgLys 120  
Db 372 GGACCCCTGTGTCTTAATGAGAGACAGGCTCCCATGTGTGTGACAGCCACTCGGCAAG 431  
QY 121 AAlaIleGIyGluMetAspAsnGlnValSerGlnLeuThrSerGlnLeuLeuPheIleIys 140  
Db 432 GCCATCGGGAGATGGACACCAAGGTCTCTGACTGACGACGAGCTCAATTCAATCAAG 491  
QY 141 AAsnAlaValAlaGluValArgGluThrGluSerIleIleTyrLeuLeuValIleGluGlu 160  
Db 492 AATGCTGTGCGCGGTGTGCGCGAGACGAGACCAAGATCTTACTCTGCTGTGAAGAGAG 551  
QY 161 LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyArgGlyTyrThrLeuSerMetPro 180  
Db 552 AAGCGCTACGGCGAGCGCCAGCTGTCTGCGCAGGGCGCGGCGGCGCAGCTGAGATGCC 611  
QY 181 LysAspGluAlaAlaAsnGlyLeuMetAlaAlaTyrLeuAlaGlnAlaGlyLeuAlaArg 200  
Db 612 AAGACGAGGCTGCGCAATGGCTGTATGGCCCAATACCTGTGGCAGAGCGGCTGGCCGT 671  
QY 201 ValPheIleGlyIleAsnAspLeuGluLysGluGlyAlaPheValTyrSerAspHisSer 220  
Db 672 GTCTTCATCGGCATACAGACCTGNA-GAAGAGGGGCGCTTGTGTACTGTGACCATCTC 730  
QY 220 rProMetArgThrPheAsnLysTyrArgSerGlyGluProAsnAsnAlaTyrAspGluGlu 240  
Db 731 CCCCATGCGGACCTTCAACAGTAGGCGGAGCGGAGCCCAACATGTCTTACGAGAGAGA 790  
QY 240 uAspCysVal 243  
Db 791 GGACTGCGTG 800  
RESULT 4  
CR599770 1150 bp mRNA linear HTC 21-JUL-2004  
LOCUS CR599770  
DEFINITION full-length cDNA clone CS0DC018Y07 of Neuroblastoma C6c

[illegible]

QY	207	AsplenigluysgijugjyvalaphavaltyrseaphisierPrometacgthrPheAsn	226
Db	643	GACCTGGAGNAGGAGGGCGGCTTGTTACTCTGACCACTCCCGACGACCTTACAC	702
QY	227	LystrTPATgSerGjygiuPProAsnAsnAlATyrAspGluGluMetCyValGluMetVal	246
Db	703	AAATGGCGCAGCGGTGAGCCCAACATGCTCTAGACGAGGAGCATGCTGGAGATGCTG	762
QY	247	AlAsertGjygiyTTPanAapValAlACyGhiGthrThrmetyrrPheMetCyGluPhe	266
Db	763	GCCCTGGCGGCTGTGAACGACGTGGCTGCACACCACTGATCTTCATGTGTGAGTTT	822
QY	267	AsplysgluAsnMet	271
Db	823	GACNAGGAGNACATG	837
RESULT 5			
BQ927000		962 bp	mRNA linear EST 20-AUG-2002
LOCUS			
DEFINITION	AGENCOURT 8804355 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:6377965		
ACCESSION	5', mRNA sequence.		
KEYWORDS	BQ927000		
SOURCE	BQ927000.1 GI:22342031		
ORGANISM	EST.		
	Homo sapiens (human)		
	Homo sapiens		
	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 962)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgabbs-remail.nih.gov		
	Tissue Procurement: ATCC		
	cDNA Library Preparation: Rubin Laboratory		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNL at:		
	http://image.llnl.gov		
	Plate: LNCM562 row: j column: 14		
	High quality sequence stop: 616.		
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	/tissue_type="neuroblastoma, cell line"		
	/lab_host="DH10B (phage-resistant)"		
	/clone_idb="NIH_MGC_47"		
	/note="Organ: brain; Vector: pOT17, Site 1: XhoI, Site 2:		
	EcoRI, cDNA made by oligo-dT priming. Directionally		
	cloned into EcoRI/XhoI sites using the following 5'		
	adaptor: GGCACGAG(G). Size-selected >500bp for average		
	insert size 1.8kb. Library constructed by Ling Hong in		
	the laboratory of Gerald M. Rubin (University of		
	California, Berkeley) using ZAP-cDNA synthesis kit		
	(Stratagene) and Superscript II RT (Life Technologies).		
	Note: this is a NIH_MGC Library."		
ORIGIN			
Alignment Scores:			
Pred. No.:	2.8e-184	Length:	962
Score:	202.00	Matches:	202
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	74.54%	Indels:	0
DB:	5	Gaps:	0

QY 1 MetArgGlyAenLeuAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeu 20  
DB 72 ATGAGGGGGAATCTGCGCTGGTGGGCGCTTCTAATCAGCTGCGCTTCTGCACTGCTG 131  
QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCySerValGlnIleLeuValPro 40  
DB 132 CCATTTGGACATCTCTCAGCGCGCTGGCCATGACGCTGCTCTGTGCAGATCTCTGCTCC 191  
QY 41 GlyLeuValGlyAspAlaGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 60  
DB 192 GGCCTCAAGGGGAGATGCGGAG 251  
QY 61 ValGlyProThrGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 80  
DB 252 GTCCGCCCCACCGGAG 311  
QY 81 ArgHisGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 100  
DB 312 CGTCAATGGAGAAATTTGGTCCATTTGGCTTAAAGGTGAGAAAGAGATTTCCGATGACATA 371  
QY 101 GlyProProGlyProAsnGlyGluProGlyLeuProGlyValGlyValGlyValGlyVal 120  
DB 372 GGACCCCTGCTGCTAATGAG 431  
QY 121 AlaIleGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 140  
DB 432 GCCATCGGAGAGATGAG 491  
QY 141 AsnAlaValAlaGlyValAlaGlyValGlyValGlyValGlyValGlyValGlyValGly 160  
DB 492 AATGCTGTGCGCGGTGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 551  
QY 161 LysArgGlyValAlaAspAlaGlyValGlyValGlyValGlyValGlyValGlyValGly 180  
DB 552 AAGCCTTACGCGGAG 611  
QY 181 LysAspGlyValAlaAsnGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 200  
DB 612 AAGGAG 671  
QY 201 ValPhe 202  
DB 672 GTCTTT 677  
RESULT 6  
LOCUS BX427124 1083 bp mRNA linear EST 04-MAY-2004  
DEFINITION BX427124 Homo sapiens FETAL LIVER Homo sapiens cDNA clone  
CSQDM008Y18 5-PRIME, mRNA sequence.  
ACCESSION BX427124  
VERSION BX427124.2 GI:47002248  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1083)  
AUTHORS L.J.W.B., Gruber,C., Jeessee,J. and Polayes,D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT Contact: Genoscope - Centre National de Sequencage  
Genoscope - Centre National de Sequencage  
BP 191 91006 Evry cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-Oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library  
was not normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
This sequence belongs to sequence cluster 1719.f  
For more information about this cluster, see

http://www.genoscope.cns.fr/cdna7s-CSQDM008DP09QP1k-1719.f.  
FEATURES  
Location/Qualifiers  
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/clone="CSQDM008Y18"  
/tissue\_type="FETAL LIVER"  
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/note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA  
was primed with a NotI-Oligo(dT) primer. Five prime end  
enriched, double-strand cDNA was digested with Not I and  
cloned into the Not I and EcoRV sites of the pCMVSPORT 6  
vector. Library was not normalized."  
ORIGIN  
Alignment Scores:  
Pred. No.: 1,79e-177 Length: 1083  
Score: 195.00 Matches: 262  
Percent Similarity: 98.87% Conservative: 0  
Best Local Similarity: 98.87% Mismatches: 2  
Query Match: 71.96% Indels: 3  
DB: 5 Gaps: 0  
US-09-806-277a-6 (1-271) x BX427124 (1-1083)  
QY 1 MetArgGlyAenLeuAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeu 20  
DB 92 ATGAGGGGGAATCTGCGCTGGTGGGCGCTTCTAATCAGCTGCGCTTCTGCACTGCTG 151  
QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCySerValGlnIleLeuValPro 40  
DB 152 CCATTTGGACATCTCTCAGCGCGCTGGCCATGACGCTGCTCTGTGCAGATCTCTGCTCC 211  
QY 41 GlyLeuValGlyAspAlaGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 60  
DB 212 GGCCTCAAGGGGAGATGCGGAG 271  
QY 61 ValGlyProThrGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 80  
DB 272 GTCCGCCCCACCGGAG 331  
QY 81 ArgHisGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 100  
DB 332 CGTCAATGGAGAAATTTGGTCCATTTGGCTTAAAGGTGAGAAAGAGATTTCCGATGACATA 391  
QY 101 GlyProProGlyProAsnGlyGluProGlyLeuProGlyValGlyValGlyValGlyVal 120  
DB 392 GGCCTCAAGGGGAGATGCGGAG 451  
QY 121 AlaIleGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 140  
DB 452 GCCATCGGAGAGATGAG 511  
QY 141 AsnAlaValAlaGlyValAlaGlyValGlyValGlyValGlyValGlyValGlyValGly 160  
DB 512 AATGCTGTGCGCGGTGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 571  
QY 161 LysArgGlyValAlaAspAlaGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 180  
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QY 181 LysAspGlyValAlaAsnGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 200  
DB 632 AAGGAGAGAGAGATGCGGAG 690  
QY 201 ValPheIleGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyValGly 220  
DB 691 GTCTTCAATGAG 750  
QY 221 ProMetArgThrPheAsnLysTrpArgSerGlyGluProAsnAlaValGlyValGlyVal 240

Db 751 CCCATGCGGACCTTCAACAGTGGCGSMG-GGTGGAGCCCAACATGCTTACGACGAGA 809  
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 Db 810 GGACTGGGTGAGTGGTGGCTGGCGGCGCTGGAACGAGCTGGCTGCCACACACCAT 869  
 Qy 260 tlyrphamecys 264  
 Db 870 GTACTTCATGTGT 882  
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 Bf206254  
 LOCUS 672 bp mRNA linear EST 06-NOV-2000  
 DEFINITION 601869264F1 NIH\_MGC\_19 Homo sapiens CDNA clone IMAGE:4098278 5',  
 mRNA sequence.  
 Bf206254  
 Bf206254.1 GI:11099840  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 672)  
 NIH-MGC http://mgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov  
 Plate: LICM964 row: 0 column: 15  
 High quality sequence stop: 670.  
 Location/Qualifiers  
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 /tissue\_type="neuroblastoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_19"  
 /note="Organ: brain; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
 EcoRI; CDNA made by oligo-dt priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGACGAG(G). Library constructed by Ling Hong  
 in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC library."  
 ORIGIN  
 Alignment Scores: Length: 672  
 Pred. No.: 7,72e-173 Matches: 190  
 Score: 190.00 Conservatave: 0  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 70.11% Gaps: 0  
 DB: 2  
 US-09-806-277A-6 (1-271) x Bf206254 (1-672)  
 Qy 1 Mctatggllyasnleualaleuvalgllyalleuuleserleualaphleuenserleu 20  
 Db 75 ATGAGGGGGAATCTGGCTGGTGGGCTTTAAACAGCTGGCTTCTGTCATCTGTG 134  
 Qy 21 Prosergylvhprrglpronalagllyasapalacyserservalglnlleuvalpro 40  
 Db 135 CCATCTGGACATCTTCAGCCGGCTGGCGATGACGCTGTGTGACATCTCTGCTCCT 194

Qy 41 G1yleuylvglyaspalagllygllyserlyasplyvglyalaprogllyarprogllyarg 60  
 Db 195 GGCTTCMAAGGGAGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 254  
 Qy 61 Valgllyprothgllygllyserlyasplyvglyalaprogllyarprogllyarg 80  
 Db 255 GTGGGCCCCCGAG 314  
 Qy 81 ArgHsglylyvlylsglyprolleglyserlyvglygllyserlyasplyvglyalapro 100  
 Db 315 CGTCATGAAATAATGTCCTCCATGCTCTAAAGGTGAGAGAGAGAGAGAGAGAGATC 374  
 Qy 101 Glyproprogllyproasnlygllyprogllyleuprocyvglylcyssergllyleuarglys 120  
 Db 375 GAGCCCTGTCCTTATGAGAACCGAGCTCCCATGAGTGCAGCCAGCTGGCAGAG 434  
 Qy 121 AlailegllyluecaspasnlyvalsergllyleuThsergllyleuylspherlelyls 140  
 Db 435 GCATCGGGAGATGACACACAGCTCTCAGCTGACCGAGAGAGAGAGAGAGAGAGAG 494  
 Qy 141 Asnalvalalagllyvalarglylthrglyserlyllytyleuvallyvglyglly 160  
 Db 495 AATGCTGTGCGCGTGTGCGAGAGAGAGAGAGAGAGAGATCTACTGCTGTGAAGAGAG 554  
 Qy 161 lyaargtlyralaspalagllyleuSerCyvglygllyarglygllythreusermetpro 180  
 Db 555 AAGCGCTACGGAG 614  
 Qy 181 lyaaspgllyalalasnlyleuMetala 190  
 Db 615 AAGCAGAGAGCTGCCATGAGCTGATGCC 644

RESULT 8  
 BE383325  
 LOCUS 640 bp mRNA linear EST 21-JUL-2000  
 DEFINITION 601298236F1 NIH\_MGC\_19 Homo sapiens CDNA clone IMAGE:3628448 5',  
 mRNA sequence.  
 BE383325  
 BE383325.1 GI:9328690  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 640)  
 NIH-MGC http://mgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov  
 Plate: LICM313 row: 9 column: 09  
 High quality sequence stop: 638.  
 Location/Qualifiers  
 1..640  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3628448"  
 /tissue\_type="neuroblastoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_19"  
 /note="Organ: brain; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
 EcoRI; CDNA made by oligo-dt priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGACGAG(G). Library constructed by Ling Hong  
 in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit

FEATURES  
 source  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3628448"  
 /tissue\_type="neuroblastoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_19"  
 /note="Organ: brain; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
 EcoRI; CDNA made by oligo-dt priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGACGAG(G). Library constructed by Ling Hong  
 in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit



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Db      595 AAGGACGAGCTGCCAATGGCCTG 618
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RESULT 10
LOCUS   BE262656
DEFINITION BE262656 644 bp mRNA linear EST 26-OCT-2000
          601151465F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3507377 5',
          mRNA sequence.
ACCESSION BE262656
VERSION   BE262656
KEYWORDS BE262656.1 GI:9135855
SOURCE    EST.
ORGANISM  Homo sapiens (human)
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 644)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgabbs-remail.nih.gov
          Tissue Procurement: ATCC
          cDNA Library Preparation: Ling Hong/Rubin Laboratory
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
          Plate: L1CM187 row: b column: 18
          High quality sequence start: 643.
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            1..644
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              /mol_type="mRNA"
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              /tissue_type="neuroblastoma"
              /lab_host="DH10B (phage-resistant)"
              /clone_lib="NIH_MGC_19"
              /note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
              EcoRI; cDNA made by oligo-dt priming. Directionally
              cloned into EcoRI/XhoI sites using the following 5'
              adaptor: GGCAAGAG(G). Library constructed by Ling Hong
              in the laboratory of Gerald M. Rubin (University of
              California, Berkeley) using ZAP-cDNA synthesis kit
              (Stratagene) and Superscript II RT (Life Technologies).
              Note: this is a NIH_MGC library."

ORIGIN
Alignment Scores:
Pred. No.: 3.94e-165 Length: 644
Score: 182.00 Matches: 182
Percent Similarity: 100.00% Conservatave: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 67.16% Indels: 0
Gaps: 0

US-09-806-277a-6 (1-271) x BE262656 (1-644)
Oy      1 MetAArgGlyAanLeuAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeuLeu 20
Db      97 ATGAGGGGGAGATCTGGCCCTGTGGGCTTCTAATACACCTGGGCTTCTGTCACTGTG 156
Oy      21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40
Db      157 CCATCTGGACATCTCCACCGCGCTGGCGATACCGCTCTCTGTGCGAGATCTGTCCCT 216
Oy      41 GlyLeuValGlyAspAlaGlyValGlyValGlyValGlyValGlyValGlyValGlyValGly 60
Db      217 GGCCCTCAAGGGGAGATGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 276
Oy      61 ValGlyProThrGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyValGly 80

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Db      277 GTGGGCCCAACGGGAGAAAAAGAGACATGGGGGACAAAGAGACAAAGGACAGTGTGGGT 336
Oy      81 ArgHisGlyValSerIleGlyProIleGlySerIleValGlyValGlyValGlyValGlyValGly 100
Db      337 CGTCATGAGAAAAATTGTGCTCCATGGCTCTAAAGGTGAAGAAAGAAATTCCGGTGAACATA 396
Oy      101 GlyProProGlyProAsnGlyGluProGlyLeuProCysGlyGlySerGlnLeuAArgIle 120
Db      397 GGACCCCTGTGCTTCTAATGAGAACACAGGCTCTCCATGTGAGTGCAGCCAGCTGCCGAG 456
Oy      121 AlaIleGlyValMetAspAsnGlnValSerGlnLeuThrSerGlnLeuValSerIleLeuVal 140
Db      457 GCCATGGGGAGATGAGACACAGAGTCTCTCAGCTGACAGCAGCAGAGCTCAAGTTCATCAAG 516
Oy      141 AsnAlaValAlaGlyValAlaArgIleThrGluSerIleIleThrLeuLeuValValGlyGlu 160
Db      517 AATGCTGTGCTCCCGTGTGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 576
Oy      161 LysArgThrAlaAspAlaGlnLeuSerCysGlnGlyValGlyValThrLeuSerMetPro 180
Db      577 AAGCGCTACGCGAGACCGCAGCTGTCTCTGCGAGGCGCGGAGGACGCTGACATGCCCC 636
Oy      181 LysAsp 182
Db      637 AAGGAC 642

RESULT 11
LOCUS   BE382433
DEFINITION BE382433 683 bp mRNA linear EST 21-JUL-2000
          601297261F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3627375 5',
          mRNA sequence.
ACCESSION BE382433
VERSION   BE382433
KEYWORDS BE382433.1 GI:9327798
SOURCE    EST.
ORGANISM  Homo sapiens (human)
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 683)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgabbs-remail.nih.gov
          Tissue Procurement: ATCC
          cDNA Library Preparation: Ling Hong/Rubin Laboratory
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
          Plate: L1CM110 row: j column: 16
          High quality sequence stop: 595.
          Location/Qualifiers
            1..683
              /organism="Homo sapiens"
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              /db_xref="taxon:9606"
              /clone="IMAGE:3627375"
              /tissue_type="neuroblastoma"
              /lab_host="DH10B (phage-resistant)"
              /clone_lib="NIH_MGC_19"
              /note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
              EcoRI; cDNA made by oligo-dt priming. Directionally
              cloned into EcoRI/XhoI sites using the following 5'
              adaptor: GGCAAGAG(G). Library constructed by Ling Hong
              in the laboratory of Gerald M. Rubin (University of
              California, Berkeley) using ZAP-cDNA synthesis kit
              (Stratagene) and Superscript II RT (Life Technologies).
              Note: this is a NIH_MGC library."

ORIGIN
Alignment Scores:
Pred. No.: 3.84e-164 Length: 683

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Score: 181.00 Matches: 181  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 66.79% Indels: 0  
DB: 2 Gaps: 0

US-09-806-277a-6 (1-271) x BE313199 (1-683)

OY 1 MetArgGlyAenLeuAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeu 20  
DB 55 ATGAGGGGGAATCTGGCCCTGGTGGCTTCAATCAGCTGGCTTCTCTGCACTGGCTG 114  
OY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
DB 115 CCATCTGGACATCTCTCAGCCGGCTGGCCAGTACGCTCTGCTGTCACATCTCTCTCCCT 174  
OY 41 GlyLeuLysGlyAspAlaGlyGlyValLysGlyAspLysGlyAlaProGlyValArgProGlyArg 60  
DB 175 GGCCCTCAAGGGGATCGGGAG 234  
OY 61 ValGlyProThrGlyGlyLysGlyAspMetGlyAspLysGlyGlnLysGlySerValGly 80  
DB 225 GTCCGCCCCCAGCGGAG 294  
OY 81 ArgHisGlyLysIleGlyProIleGlySerLysGlyGlyLysGlyAspSerGlyAspIle 100  
DB 295 CGTCAATGAGAAATATGCTCCATTCCTTAAAGGTGAGAGAGAGAGAGAGAGAGAGAGAG 354  
OY 101 GlyProProGlyProAsnGlyGlyLysProGlyLeuProCysGlyCysSerGlnLeuArgLys 120  
DB 355 GGACCCCTGCTGCTCAATGAG 414  
OY 121 AlaIleGlyLysMetAspAsnGlnValSerGlnLeuThrSerGlnLeuLysPheIleLys 140  
DB 415 GCCATCGGGGAGATGAGACACAGAGCTCTCTCAGTACAGAGAGAGAGAGAGAGAGAGAG 474  
OY 141 AsnAlaValAlaGlyValArgLysThrGlySerLysIleTyrLeuLeuValLysGln 160  
DB 475 AATGCTGTGCGCGGATGCGAG 534  
OY 161 LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyArgGlyGlyThrLeuSerMetPro 180  
DB 535 AAGGCTACGCGGAG 594  
OY 181 Lys 181  
DB 595 AAG 597

RESULT 12  
BE313199 715 bp mRNA linear EST 26-OCT-2000  
LOCUS 601149012P1 NIH\_MGC\_19 Homo sapiens cDNA clone IMAGE:3501747 5',  
DEFINITION mRNA sequence.  
BE313199  
ACCESSION BE313199.1 GI:9132817  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 715)  
NIH-MGC http://mgi.mcl.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed By: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at: image.lnl.gov  
Plate: LNCM172 row: h column: 04

High quality sequence stop: 643.  
FEATURES  
Location/Qualifiers  
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/organism="Homo sapiens"  
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/clone="IMAGE:3501747"  
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/lab\_host="DH10B (phage-resistant)"  
/clone\_id="NIH\_MGC\_19"  
/note="Organ: brain; Vector: POT87; Site 1: XhoI; Site 2:  
EcoRI; CDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACTAG(G). Library constructed by Ling Hong  
in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-CDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

## ORIGIN

## Alignment Scores:

Prod. No.: 3,71e-163 Length: 715  
Score: 180.00 Matches: 180  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 66.42% Indels: 0  
DB: 2 Gaps: 0

US-09-806-277a-6 (1-271) x BE313199 (1-715)

OY 1 MetArgGlyAenLeuAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeu 20  
DB 55 ATGAGGGGGAATCTGGCCCTGGTGGCTTCAATCAGCTGGCTTCTCTGCACTGGCTG 114  
OY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
DB 115 CCATCTGGACATCTCTCAGCCGGCTGGCCAGTACGCTCTGTCAGATCTCTCTCCCT 174  
OY 41 GlyLeuLysGlyAspAlaGlyGlyValLysGlyAspLysGlyAlaProGlyValArgProGlyArg 60  
DB 175 GGCCCTCAAGGGGATCGGGAG 234  
OY 61 ValGlyProThrGlyGlyLysGlyAspMetGlyAspLysGlyGlnLysGlySerValGly 80  
DB 235 GTCCGCCCCCAGCGGAG 294  
OY 81 ArgHisGlyLysIleGlyProIleGlySerLysGlyGlyLysGlyAspSerGlyAspIle 100  
DB 295 CGTCAATGAGAAATATGCTCCATTCCTTAAAGGTGAGAGAGAGAGAGAGAGAGAGAGAG 354  
OY 101 GlyProProGlyProAsnGlyGlyLysProGlyLeuProCysGlyCysSerGlnLeuArgLys 120  
DB 355 GGACCCCTGCTGCTCAATGAG 414  
OY 121 AlaIleGlyLysMetAspAsnGlnValSerGlnLeuThrSerGlnLeuLysPheIleLys 140  
DB 415 GCCATCGGGGAGATGAGACACAGAGCTCTCTCAGTACAGAGAGAGAGAGAGAGAGAGAG 474  
OY 141 AsnAlaValAlaGlyValArgLysThrGlySerLysIleTyrLeuLeuValLysGln 160  
DB 475 AATGCTGTGCGCGGATGCGAG 534  
OY 161 LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyArgGlyGlyThrLeuSerMetPro 180  
DB 535 AAGGCTACGCGGAG 594

RESULT 13  
BF312666 613 bp mRNA linear EST 21-NOV-2000  
LOCUS BF312666  
DEFINITION 601898164P1 NIH\_MGC\_19 Homo sapiens cDNA clone IMAGE:4127486 5',  
ACCESSION BF312666  
VERSION BF312666.1 GI:11260511

KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 613)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov  
Plate: LNCMI018 row: p column: 15  
High quality sequence stop: 612.

FEATURES  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="IMAGE:4127486"  
/tissue\_type="neuroblastoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_19"  
/note="Organ: brain; Vector: pOT7; Site\_1: XhoI; Site\_2:  
EcoRI; CDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCAAGAG(G) library constructed by Ling Hong  
in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

ALIGNMENT SCORES:  
Pred. No.: 2,966-162 Length: 613  
Score: 179.00 Matches: 179  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 66.05% Indels: 0  
Gaps: 0

US-09-806-277A-6 (1-271) x BF312666 (1-613)

ORIGIN  
1 MetArgGlyAanLeuAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeu 20  
75 ATGAGGGGAGATCTGGCCCTGCTGCTTAATCAAGCTGGCCCTCTCTCACTGCTG 134  
21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
135 CCATCTGGACATCTCTCAAGCCGCTGGCGATGACGCTCTCTGTCAGATCTCTGCTCCT 194  
41 GlyLeuIleValGlyAspAlaGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 60  
195 GGCCTCAAAAGGAGATGCGGAG 254  
61 ValGlyProThrGlyGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 80  
255 GTCCGCCCCACGGGAG 314  
81 ArgHisGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 100  
315 CGTCAATGAGAAATATGCTCCATTTGGCTCTAAAGGTGAGAAAGGATTCGCGTGACATA 374  
101 GlyProProGlyProAsnGlyGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 120  
375 GAAACCCCTGCTCTTAATGAG 434  
121 AlaIleGlyIleMetAspAsnGlnValSerGlnLeuThrSerGlnLeuValGlyPheIleVal 140

DB 435 GCCATCGGGAGATGAGCAACAGATCTCTCACTACCAAGAGCTCAAGTTCATCAAG 494  
ORIGIN  
141 AsnAlaValAlaGlyValAlaGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 160  
495 AATGCTGTGCGCCGCTGTGGCGAG 554  
161 LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyValGlyValGlyValGlyValGlyValGlyVal 179  
555 AAGCGTACGAGGAG 611

RESULT 14  
BR312923  
LOCUS BR312923 654 bp mRNA linear EST 26-OCT-2000  
DEFINITION 60116744F1 NIH\_MGC\_19 Homo sapiens cDNA clone IMAGE:3161914 5',  
mRNA sequence.  
ACCESSION BR312923  
VERSION BR312923.1 GI:9132223  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 654)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov  
Plate: LNCMI20 row: h column: 11  
High quality sequence stop: 590.

FEATURES  
source  
1. 654  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3161914"  
/tissue\_type="neuroblastoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_19"  
/note="Organ: Brain; Vector: pOT7; Site\_1: XhoI; Site\_2:  
EcoRI; CDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCAAGAG(G) library constructed by Ling Hong  
in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

ALIGNMENT SCORES:  
Pred. No.: 2,296-158 Length: 654  
Score: 175.00 Matches: 175  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 64.58% Indels: 0  
Gaps: 0

US-09-806-277A-6 (1-271) x BR312923 (1-654)

ORIGIN  
1 MetArgGlyAanLeuAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeu 20  
55 ATGAGGGGAGATCTGGCCCTGCTGCTTAATCAAGCTGGCCCTCTCTCACTGCTG 114  
21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
115 CCATCTGGACATCTCTCAAGCCGCTGGCGATGACGCTCTCTGTCAGATCTCTGCTCCT 174



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Qy 41 G1yLeuYsg1yAapAlaG1yG1uYsg1yAapLysg1yAlaPProG1yAArg 60
Db 175 GGCCTCAAAAGGAGATGCGGAGAGAAAGGAGCAAAAGCGCCCGGACGGCTTGAAAGA 234
Qy 61 ValG1yProThrg1yG1uYsg1yAapMerG1yAapLysg1yG1uYsg1ySerValG1y 80
Db 235 GTCCGCCACGAGGAGAAAGAGACATGGGAGCAAAAGCAAGAAAGGCAGTGTGGGT 294
Qy 81 ArgH1sg1yLyS1leg1yPro1leg1ySer1ySg1yG1uYsg1yAapSerG1yAap1le 100
Db 295 CGTCATGAAAAAATTGCTCCATTCGCTTAAGGTGAGAAAGAGATTCCGGTACATA 354
Qy 101 G1yProPog1yProAeng1yG1uPProG1yLeuProCySg1yCySserG1uLeuAArg1yS 120
Db 355 GGACCCCTGCTCTTAATGAGAACAGCCCTCATGTGATGACCGACGCTGGCAAG 414
Qy 121 Ala1leg1yG1uMeAapAeng1yValSerG1uLeuThrsrG1uLeuYsPhe1leYs 140
Db 415 GCCATCGGGAGATGACACCAAGGTCTCTCACTGACAGGAGCTCAAGTTCAACAG 474
Qy 141 AsnAlaValAlaG1yValArgG1uThrg1uSer1yS1leY1yLeuLeuValYsg1uG1u 160
Db 475 AATGCTGCGCGGCTGCGGAGACGAGAGCAAGATCTACCTGCTGTGAAGAGAGAG 534
Qy 161 LysArg1yAlaAapAlaG1uLeuSerCySg1nG1yArgG1yG1y 175
Db 535 AAGCGCTACGGGAGACGCGGCTGCTGCGGAGCGCGGCGGCGG 579

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## RESULT 15

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LOCUS BE260904 1012 bp mRNA linear EST 26-OCT-2000
DEFINITION 601153812P1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3509811 5',
RNA sequence.
ACCESSION BE260904
VERSION BE260904.1 GI:9132588
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1012)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: rgs@bbs-rmail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
Plate: L16M193 row: h column: 04
High quality sequence stop: 615.
Location/Qualifiers
1..1012

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## FEATURES

## SOURCE

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="3509811"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_19"
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

```

ORIGIN

```

Alignment Scores:
Pred. No.: 3,45e-158 Length: 1012
Score: 175.00 Matches: 175
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 64.58% Indels: 0
DB: 2 Gaps: 0

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US-09-806-277a-6 (1-271) x BE260904 (1-1012)

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Qy 1 MetArgG1yAenLeuAlaLeuValG1yValLeu1leSerLeuAlaPheLeuSerLeu 20
Db 56 ATGAGGGGGAATCTGGCCCTGTGAGGCTTAACTACGCTTGCCCTCTCTCTG 115
Qy 21 ProSerG1yH1sProG1nProAlaG1yAapAapAlaCySserValG1n1leLeuValPro 40
Db 116 CCATCTGGACATCTCTCAAGCCGCTGGCGATACCGCTGCTGTGACAGATCTGTCCT 175
Qy 41 G1yLeuYsg1yAapAlaG1yG1uYsg1yAapLysg1yAlaPProG1yAArg 60
Db 176 GGCCTCAAAAGGAGATGCGGAGAGAGAGAGCAAAAGCGCCCGGACGGCTTGAAAGA 235
Qy 61 ValG1yProThrg1yG1uYsg1yAapMerG1yAapLysg1yG1uYsg1ySerValG1y 80
Db 236 GTCCGCCACGAGGAGAAAGAGACATGGGAGCAAAAGGAGCAAGAGGCAAGGTGGGT 295
Qy 81 ArgH1sg1yLyS1leg1yPro1leg1ySer1ySg1yG1uYsg1yAapSerG1yAap1le 100
Db 296 CGTCATGAAAAAATTGCTCCATTCGCTTAAGGTGAGAAAGAGATTCCGGTACATA 355
Qy 101 G1yProPog1yProAeng1yG1uPProG1yLeuProCySg1yCySserG1uLeuAArg1yS 120
Db 356 GGACCCCTGCTCTTAATGAGAACAGGCTCCCATGTGATGACCGACGCTGGCAAG 415
Qy 121 Ala1leg1yG1uMeAapAeng1yValSerG1uLeuThrsrG1uLeuYsPhe1leYs 140
Db 416 GCCATCGGGAGATGACACCAAGGTCTCTCACTGACAGGAGCTCAAGTTCAACAG 475
Qy 141 AsnAlaValAlaG1yValArgG1uThrg1uSer1yS1leY1yLeuLeuValYsg1uG1u 160
Db 476 AATGCTGCGCGGCTGCGGAGACGAGAGCAAGATCTACCTGCTGTGAAGAGAGAG 535
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Job time : 3871 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

# OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 17, 2004, 10:04:40 ; Search time 5448 Seconds  
(without alignment)  
2352.333 Million cell updates/sec

Title: US-09-806-277A-6

Sequence: 1 MRGNLALVGLISLAFSL.....NDVACHTTMTMCEFDXNM 271

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Searched: 4526729 seqs, 23644849745 residues

Word size: 1

Total number of hits satisfying chosen parameters: 9045947

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

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7: gb.ph:\*  
8: gb.pl:\*  
9: gb.pr:\*  
10: gb.ro:\*  
11: gb.scs:\*  
12: gb.sy:\*  
13: gb.un:\*  
14: gb.vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	271	100.0	813	6	BD103332 Novel col
2	271	100.0	1238	6	AR252616 Sequence
3	271	100.0	1238	6	AX403469 Sequence
4	271	100.0	1238	6	AX454582 Sequence

5	271	100.0	1238	6	AX491060
6	271	100.0	1238	9	AY358439
7	271	100.0	1248	9	BC000078
8	271	100.0	1341	6	BD103302
9	228	84.1	735	6	BD103333
10	228	84.1	1139	6	BD103303
11	205	75.6	741	6	BD103340
12	205	75.6	1269	6	BD103330
13	204	75.3	663	6	BD103336
14	204	75.3	1067	6	BD103305
15	204	75.3	1417	6	BC009951
16	181	66.8	663	6	BD103337
17	181	66.8	669	6	BD103339
18	181	66.8	741	6	BD103341
19	181	66.8	1067	6	BD103306
20	181	66.8	1197	6	BD103329
21	180	66.8	1269	6	BD103331
22	180	66.4	591	6	BD103335
23	180	66.4	995	6	BD103304
24	159	58.7	477	6	BD103334
25	142	52.4	708	6	CQ716215
26	130	48.0	139357	9	AC010907
27	49	18.1	246539	2	AC125638
28	47	17.3	813	6	BD103338
29	47	17.3	1522	6	BD103307
30	34	12.5	175475	2	AC123631
31	25	9.2	648	11	BV075463
32	25	9.2	175475	2	AC123631
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34	17	6.3	231062	2	AC109110
35	16	5.9	619	6	BD103308
36	15	5.5	5.9	6	CR338949
37	15	5.2	206332	10	AC136986
38	12	4.4	212049	5	EX005484
39	12	4.4	229319	2	CR354585
40	11	4.1	89	6	AX920471
41	11	4.1	89	6	BD056004
42	11	4.1	2721	3	SC4572
43	11	4.1	6006	3	SUSC0P
44	10	3.7	93	6	AR074458
45	10	3.7	93	6	AR081138

## ALIGNMENTS

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LOCUS	BD103332				
DEFINITION	Novel collectin.				
ACCESSION	BD103332.1				
VERSION	WO 0181401-A/31.				
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Wakamiya, N., Keshi, H., Otani, K., Sakamoto, T. and Kishi, Y.				
TITLE	Novel collectin				
JOURNAL	Patent: WO 0181401-A 31 01-NOV-2001; FUSO PHARMACEUTICAL INDUSTRIES LTD, NOBUTAKA WAKAMIYA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI SAKAMOTO, YUICHIRO KISHI				
COMMENT	OS Homo sapiens (human) PN WO 0181401-A/31 PD 01-NOV-2001 PF 23-APR-2001 WO 2001JP003468 PR 21-APR-2000 JP 00P 120358 PI NOBUTAKA WAKAMIYA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI SAKAMOTO, PI YUICHIRO KISHI PC C07K14/47, C12N15/12, C12P21/02, A01K67/027, C07K16/18, G01N33/53 FH Novel collectin Location/Qualifiers				

[illegible]

Db	781	TACTTCATGTGTGAGTTTGACAAGAGACATG	813
RESULT 2			
LOCUS	AR252616	1238 bp	DNA
DEFINITION	Sequence 356 from patent US 6478825.	linear	PAT 20-DEC-2002
ACCESSION	AR252616		
VERSION	AR252616.1	GI:27300524	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1238)		
TITLE	Witterbottom,J.W., Shimp,L., Boyce,T.M. and Kaes,D.		
JOURNAL	Implant, method of making same and use of the implant for the		
FEATURES	treatment of bone defects		
source	Patent: US 6478825-A 356 12-NOV-2002;		
	Location/Qualifiers		
	1..1238		
ORIGIN	/organism="unknown"		
	/mol_type="genomic DNA"		
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Pred. No.:	1.45e-262	Length:	1238
Score:	271.00	Matches:	271
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-806-277A-6 (1-271) x AR252616 (1-1238)

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QY 21 ProSerGIyHISProGInProAlaGIyASpAspAlaCYSerValGInIIsLeuValPro 40

Db 127 CCATCTGGACATCTCTCAGCCGGCTGGCGATGACGCTGCTGTGCAGATCTCGTCCCT 186

QY 41 GILyLeuLySgIyASpAlaGIyGILyLysGIyAspLyAspLySgIyAlaProGILyATrProGILyAArg 60

Db 187 GAGCTCAAGGGGAGAGCGGGAGAGAGAGAGCAAGAGGCGCCCGAGCGGCTGGAAAG 246

QY 61 ValGIyProThnGIyGILyLysGIyASpMetGIyAspLySgIyGILyLysGIySeraGIy 80

Db 247 GTGGCCCCCAGGGAGAGAAAAGAGACATGGGGGACAAAGACAGAAAGCATGTGTGGT 306

QY 81 ARGHSgIyLySIIegLYProIIIsGlySerLySgIyLysGIyASpSergIyAspIIIs 100

Db 307 CGTATGGAAAAATTGGTCCCATGGCTCTTAAGGTGAGAAAGAGATTCCGGTGACATA 366

QY 101 GILyProProGILyProAsnGILyGILyProGILyLeuProCYsGILyCySergIInLeuATGILy 120

Db 367 GGAACCCCTGCTCTTAATGAGAACCAAGGCTTCCATGTGATGACAGCACTGGCCAAAG 426

QY 121 AlaIIIsGIyLysMetASpAsnGILyValSergIInLeuTrSergIInLeuLyAspHeIIIs 140

Db 427 GCCATCGGGGAGATGAGCAACAGGCTCTCCAGCTGACACAGGCACTCAAGTTTCATCAAG 486

QY 141 AsnAlaValAlaGIyValArgILyLysGILyLysSerLySIIeTYrLeuLeuValLySgILyGILy 160

Db 487 AATGTGTGTGGCGGGGTGTGGGAGCGAGAGCAAGATCTACTCTGTGTGAAGGAGAG 546

QY 161 LysATrGILyAlaAspAlaGILyLeuSergCYsGILyAArgGIyGILyThrLeuSermetPro 180

Db 547 AAGGCGTACGGGAGCGCCAGCTGTCTGTCCAGGGCCCGGGGGCACGCTGAGCATGCC 606

QY 181 LysAspGILyAlaAlaAsnGILyLeuMetAlaAlaTYrLeuAlaGILyAlaGILyLeuAlaArg 200

Db 607 AAGAGCGAGGCTGCAATGGCTTATGGCGCATCTCTGTGGCCAAAGCGGCTGTGGCCCT 666

Qy 201 ValPheIIleGIYIIeaenAapLeuGIuIyegIuGIYalAaPheValTYrSerAaspHisSer 220  
Db 667 GTCTTCATGGGACATCAAGACCTGGAGAGAGGGCGCTTCGTGACTGCTGACCACTCC 726  
Qy 221 PrometArghThrPheAenAlyeTTPArSergIyGIuPProAenAenAlyeTYrAaspGIuGIu 240  
Db 727 CCATCGGGAGACTTCAACAGATGGGGCGAGCGGTGAGCCCAACATGCTTACAGAGAGAG 786  
Qy 241 AapCyValAGIuMetValAlaSerGIYGIYTPAenAapValAlaCyHisThrThMet 260  
Db 787 GACTCGCGGAGATGGTGGCTCGGGCGGTGGAACGAGTGGCTGCACACCACTCATG 846  
Qy 261 TyrPheMetCySgluPheAapLySgluAenMet 271  
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RESULT 3  
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LOCUS Sequence 356 from Patent WO0073454.  
DEFINITION AX403469  
ACCESSION AX403469.1 GI:21436970  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS 1  
Ferrara N., Gerber H., Gerritsen M., Goddard A., Godowski P.,  
Grimaldi C.J., Gurney A.L., Kijavlin I., Napier M.A., Pan J.,  
Paoni N.F., Roy M., Stewart T.A., Tunnas D., Watanabe C.K.,  
Williams P., Wood W.I. and Zhang Z.  
TITL Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0073454-A 356 07-DEC-2000;  
Genentech Inc. (US)  
FEATURES  
SOURCE Location/Qualifiers  
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/mol\_type="unassigned DNA"  
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Alignment Scores:  
Pred. No.: 1.45e-262 Length: 1238  
Score: 271.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
DB: 6

US-09-806-277A-6 (1-271) x AX403469 (1-1238)

Qy 1 MetArGlyAaenAlyeValAGIYalIleuIIeSerIeuaAlaPheIeSerIeueu 20  
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Qy 21 ProSeGIYHAPProGIAProIaGIYAPaAPaIaCySeSeValGIuIIeIeuaValPro 40  
Db 127 CCATTTGGAACATCTCAAGCGGCTGGCAATGACGCTGCTGTGCAATCTCTCTCCT 186  
Qy 41 GIYleuLySglYAPaIaGIYGIYIySglYAPLySglYAlaPProGIYArPProGIYArG 60  
Db 187 GGCCCTCAAGGAGATGGCGAGAGAGAGAGCAAGGCGCCCGGACGCGCTCGAAGA 246  
Qy 61 ValGIYProThrGIYGIuIyegIyAPMeTGIYAPMeTGIYGIYIySglYSerValGIY 80  
Db 247 GTGGGCGGCGGAG 306  
Qy 81 ArGHlAGIYLyIleGIYProIIeGIYSeIySglYGIYIySglYAPSeSglYAPSeIy 100  
Db 307 CGTCAATGGAGAAATTTGGTCCATTTGGCTTTAAAGAGAGAGAGAGAGAGAGAGAG 366

Qy 101 GIYProBrogIYProAenGIYGIuPProGIYIleuProCySglYCySeSergIeuaIyS 120  
Db 367 GGACCCCTGGTCTTAAAG 426  
Qy 121 AlalIeGIYIuMetAaPaeNGIYalIeSergIeueThrSergIeueIySphIeIyS 140  
Db 427 GCCATCGGGAGATGGAGACACCAAGTCTCTAGCTGACAGAGAGAGAGAGAGAGAG 486  
Qy 141 AenAlaValAlaGIYalIyAGIYIuThrGIuSerIySIIeTYrIleuIeuaValIyGIuGIu 160  
Db 487 AATCTGTGGCGGTGTGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546  
Qy 161 LyAaRGTyrAlaAaPAlaGIuIeueSergIeIuIyArGIYGIYIuThrIeueSMeTPro 180  
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Qy 201 ValPheIIleGIYIIeaenAapLeuGIuIyegIuGIYalAaPheValTYrSerAaspHisSer 220  
Db 667 GTCTTCATGGGACATCAAGACCTGGAGAGAGGGCGCTTCGTGTACTGACCACTCC 726  
Qy 221 PrometArghThrPheAenAlyeTTPArSergIyGIuPProAenAenAlyeTYrAaspGIuGIu 240  
Db 727 CCATCGGGAGACTTCAACAGATGGGGCGAGCGGTGAGCCCAACATGCTTACAGAGAGAG 786  
Qy 241 AapCyValAGIuMetValAlaSerGIYGIYTPAenAapValAlaCyHisThrThMet 260  
Db 787 GACTCGCGGAGATGGTGGCTCGGGCGGTGGAACGAGTGGCTGCACACCACTCATG 846  
Qy 261 TyrPheMetCySgluPheAapLySgluAenMet 271  
Db 847 TACTTCATGTGTGAGTTGACAGAGAACATG 879

RESULT 4  
AX454582 1238 bp DNA linear PAT 06-JUL-2002  
LOCUS Sequence 167 from Patent WO0208284.  
DEFINITION AX454582  
ACCESSION AX454582  
VERSION AX454582.1 GI:21713915  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS 1  
Baker K.P., Ferrara N., Gerber H., Gerritsen M.E., Goddard A.,  
Godowski P.J., Gurney A.L., Hillan K.J., Marsters S.A., Pan J.,  
Paoni N.F., Stephan J.P., Watanabe C.K., Williams P.M., Wood W.I.  
and Ye W.  
TITL Compositions and methods for the diagnosis and treatment of  
disorders involving angiogenesis  
JOURNAL Patent: WO 0208284-A 167 31-JUN-2002;  
Genentech, Inc. (US); Baker, Kevin P. (US); Ferrara, Napoleone  
(US); Gerber, Hanspeter (US); Gerritsen, Mary E. (US); Goddard,  
Audrey (US); Godowski, Paul J. (US); Gurney, Austin L. (US);  
Hillan, Kenneth J. (US); Marsters, Scott A. (US); Pan, James (US)  
; Paoni, Nicholas F. (US); Stephan, Jean-Philippe F. (US);  
Watanabe, Colin K. (US); Williams, P. Mickey (US); Wood, William  
I. (US)  
FEATURES  
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Score: 271.00 Matches: 271

Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 100.00%  
 Gaps: 0  
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 Mismatches: 0

US-09-806-277A-6 (1-271) x AK454582 (1-1238)

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 QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
 Db 127 CCATCTGGACATCTCTCAAGCCGCTGGCGATGACGCTGCTGCTGCTGCTGCTGCTGCT 186  
 QY 41 GlyLeuysGlyAspAlaGlyValGlyValGlyAspAspAlaCysSerValGlnIleLeuValPro 60  
 Db 187 GGCCCTCAAGAGGGGATGCGGAG 246  
 QY 61 ValGlyProThrGlyGlyValGlyValGlyAspMetGlyAspLeuGlyValGlyValGlyValGly 80  
 Db 247 GTCGGCCCAAG 306  
 QY 81 ArgHisGlyValIleGlyProIleGlySerLeuGlyValGlyValGlyAspSerGlyAspIle 100  
 Db 307 CGTCAATGAGAAATTTGCTCCATTTGCTCTTAAGGTTGAGAGAGAGAGAGAGAGAGAGAG 366  
 QY 101 GlyProProGlyProAsnGlyValProGlyLeuProCysGlyCysSerGlnLeuValGly 120  
 Db 367 GGACCCCTGCTGCTTAATGAG 426  
 QY 121 AlaIleGlyValMetAspAsnGlnValSerGlnLeuThrSerGlyValGlyValGlyValGly 140  
 Db 427 GCCATCGGGAG 486  
 QY 141 AsnAlaValAlaGlyValAlaGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 160  
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 QY 161 LysArgGlyValAlaAspAlaGlnLeuSerCysGlnGlyValGlyValGlyValGlyValGly 180  
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 QY 241 AspCysValGluMetValAlaSerGlyValTrpAsnAspValAlaCysHisSerThrMet 260  
 Db 787 GACTGCTGAG 846  
 QY 261 TyrPheMetCysGluPheAspLysGluAsnMet 271  
 Db 847 TACTTCAATGCTGAGTTGAG 879

RESULT 5  
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 DEFINITION Sequence 167 from Patent WO0200690.  
 ACCESSION AX491060  
 VERSION AX491060.1 GI:22323867  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## REFERENCE

1 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,  
 Godowski, P.J., Gunney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,  
 Pao, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.  
 and Ye, W.

## TITLE

Compositions and methods for the diagnosis and treatment of  
 disorders involving angiogenesis  
 Patent: WO 0200690-A 167 03-JAN-2002;

Genentech, Inc. (US)

## FEATURES

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## ORIGIN

## Alignment Scores:

Pred. No.: 1,45e-262 Length: 1238  
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 Best Local Similarity: 100.00% Mismatches: 0  
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US-09-806-277A-6 (1-271) x AK491060 (1-1238)

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 QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
 Db 127 CCATCTGGACATCTCTCAAGCCGCTGGCGATGACGCTGCTGCTGCTGCTGCTGCTGCTGCT 186  
 QY 41 GlyLeuysGlyAspAlaGlyValGlyValGlyAspMetGlyAspLeuGlyValGlyValGlyValGly 60  
 Db 187 GGCCCTCAAGAGGGGATGCGGAG 246  
 QY 81 ArgHisGlyValIleGlyProIleGlySerLeuGlyValGlyValGlyAspSerGlyAspIle 100  
 Db 307 CGTCAATGAGAAATTTGCTCCATTTGCTCTTAAGGTTGAGAGAGAGAGAGAGAGAGAGAG 366  
 QY 101 GlyProProGlyProAsnGlyValProGlyLeuProCysGlyCysSerGlnLeuValGly 120  
 Db 367 GGACCCCTGCTGCTTAATGAG 426  
 QY 121 AlaIleGlyValMetAspAsnGlnValSerGlnLeuThrSerGlyValGlyValGlyValGly 140  
 Db 427 GCCATCGGGAG 486  
 QY 141 AsnAlaValAlaGlyValAlaGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 160  
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 QY 161 LysArgGlyValAlaAspAlaGlnLeuSerCysGlnGlyValGlyValGlyValGlyValGly 180  
 Db 547 AAGGCTAAGCGGAG 606  
 QY 181 LysAspGlyValAlaAsnGlyValMetAlaIleValLeuIleGlnAlaGlyValLeuAlaArg 200  
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 QY 201 ValPheIleGlyIleAsnAspLeuGlyValGlyValAlaPheValIleYrSerAspHisSer 220  
 Db 667 GTCTTCAATCGGCATCAAGACCTGAG 726  
 QY 221 ProMetArgThrPheAsnLysTrpArgSerGlyValProAsnAsnAlaIleYrAspGlu 240

Db	727	CCCATGCGGACCTTCAACAGATGGGCGACGGGTGAGCCCAACATGCTTACGACGAGAG	786
Qy	211	AApCyvValIGlUmeValAlaSerGlyGlyTTPaanaApValAlaCyvHisThrThrMet	260
Db	787	GACTCGTGGAGATGGTGGCTCGGCGGCTGGAACGACGTGGCTGCACACACCATG	846
Qy	261	TyrPheMetCyvGluPheAspGlyGluAspMet	271
Db	847	TACTTCATGTGTGAGTTTGACAGAGAACATG	879
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LOCUS			linear
DEFINITION			PR1 03-OCT-2003
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
JOURNAL			
FEATURES			
gene			
CDS			
ORIGIN			
Alignment Scores:			
Pred. No.:			
Score:			
Percent Similarity:			
Best Local Similarity:			
Query Match:			
US-09-806-277A-6 (1-271) x AY358439 (1-1238)			

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stuplton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schaefer, T.E., Brownstein, M.J., Ueding, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loggellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Boeak, S.A., McEwen, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Wokley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hui, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Bouffard, G.G., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Dickinson, M.C., Rodriguez, A.C., Gilmwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalhus, D.E., Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932  
2 (bases 1 to 1248)

JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
JOURNAL

REMARK  
COMMENT

Strauberg, R.  
Direct Submission  
Submitted (03-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
On Aug 20, 2003 this sequence version replaced gi:12652660.  
Contact: MGC help desk  
Email: [cgapdb-remail.nih.gov](mailto:cgapdb-remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILMIL)  
DNA Sequencing by: Institute for Systems Biology  
<http://www.systemsbio.org>  
Contact: [amadan@systemsbio.org](mailto:amadan@systemsbio.org)  
Amp Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILMIL at: <http://image.llnl.gov>  
Series: IRL Plate: 7 Row: 9 Column: 20  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13128971.

FEATURES  
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Location/Qualifiers  
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/issue\_type="Brain, neuroblastoma"  
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/note="vector: pOTB7"  
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CDS

ORIGIN

Alignment Scores:  
Pred. No.: 1,466-262 Length: 1248

Score: 271.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-806-277A-6 (1-271) x BC000078 (1-1248)

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QY 41 GlyLeuLeuGlyAspAlaGlyValGlyValGlyValGlyValGlyValGlyVal 60  
Db 194 GGCCTCAAGAGGAGATCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 253

QY 61 ValGlyProThrGlyGlyValGlyValGlyValGlyValGlyValGlyValGly 80  
Db 254 GTGCGCCCAACGAG 313

QY 81 ArgHisGlyValLeuIleGlyProIleGlySerLeuGlyValGlyValGlyVal 100  
Db 314 CGTATGAGAAATTTGGTCCCTTCTTAAGTGTAGAGAGAGAGAGAGAGAGAG 373

QY 101 GlyProProGlyProAsnGlyGlyProGlyLeuProCysGlyCysSerGlnLeuArg 120  
Db 374 GAGCCCTGCTGCTATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 433

QY 121 AlaIleGlyValMetAspAsnGlnValSerGlnLeuThrSerGlnLeuValPhe 140  
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QY 141 AsnAlaValAlaGlyValArgGlyThrGlySerLeuIleTyrLeuLeuValGly 160  
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QY 161 LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyValGlyValGlyValGly 180  
Db 554 AAGCGTCAACGAGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 613

QY 181 LysAspGlnAlaAlaAsnGlyLeuMetAlaAlaTyrLeuAlaGlnAlaGly 200  
Db 614 AAGGACGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 673

QY 201 ValPheIleGlyIleAsnAspLeuGlyValGlyValAlaPheValTyrSerAsp 220  
Db 674 GTCTTCAATGGCATCAACGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 733

QY 221 ProMetArgThrPheAsnValTyrPargSerGlyGlyProAsnAsnAlaTyr 240  
Db 734 CCCATGCGGACCTTCAACAGTGGCGAGCGGAGGAGGAGGAGGAGGAGGAG 793

QY 241 AspCysValGlnMetValAlaSerGlyGlyTyrAsnAspValAlaCysHis 260  
Db 794 GACTGCGTGAAGATGTGGCTGCGGCGGCTGGAAGAGAGAGAGAGAGAGAG 853

QY 261 TyrPheMetCysGlnPheAspValGlyValMet 271  
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RESULT 8  
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LOCUS Novel collectin.  
DEFINITION Novel collectin.  
ACCESSION BD103302  
VERSION BD103302.1 GI:22648876  
KEYWORDS WD 0181401-A/1.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens



Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 1341)  
 Makamiya,N., Keshi,H., Otani,K., Sakamoto,T. and Kishi,Y.  
 Novel collectin  
 Patent: WO 0181401-A 1 01-NOV-2001;  
 FUSO PHARMACEUTICAL INDUSTRIES LTD, NOBUTAKA WAKAMIYA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI SAKAMOTO, YUICHIRO KISHI

## COMMENT

OS Homo sapiens (human)  
 PN WO 0181401-A/1  
 PD 01-NOV-2001  
 PF 23-APR-2001 WO 2001JP003468  
 PR 21-APR-2000 JP 00P 120358  
 PI NOBUTAKA WAKAMIYA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI SAKAMOTO,  
 YUICHIRO KISHI  
 PI YUICHIRO KISHI  
 PC C07K14/47, C12N15/12, C12P21/02, A01K67/027, C07K16/18, G01N33/53  
 CC Novel collectin  
 FH Key  
 FT CDS  
 Location/Qualifiers  
 (265)..(1077).

## FEATURES

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## ORIGIN

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 Score: 271.00 Matches: 271  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0  
 US-09-806-277A-6 (1-271) x BD103302 (1-1341)

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 DB 265 ATGAGGGGGAATCTGGCCCTGCTGAGCCCTTCAATCAGCCCTGCTGCTGCTGCTG 324  
 QY 21 ProSerGlyHleAProGlnProAlaGlyAAspAlaCySerValGlnleuValPro 40  
 DB 335 CCATCTGACATCTTCAGCCGCGCTGCGAGCGCTGCTGCTGCTGCTGCTGCTGCT 384  
 QY 41 GlyLeuLySGlyAAspAlaGlyGlyAAspLySGlyAAspLySGlyAAspLySGly 60  
 DB 365 GGCCTCAAGGGGAGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 444  
 QY 61 ValGlyProThrGlyGlyLySGlyAAspMetGlyAAspLySGlyGlnLySGlySerValGly 80  
 DB 445 GTGGGCCCCACGGGAG 504  
 QY 81 ArgHleGlyLySerIleGlyProIleGlySerLySGlyGlyLySGlyAAspSerGlyAAsp 100  
 DB 505 GCTCATGGAGAAATGGTCCATGGCTCTTAAGGAGAGAGAGAGAGAGAGAGAGAG 564  
 QY 101 GlyProProGlyProAAspGlyGlyProGlyLeuProGlyGlyGlyGlyGlyGlyGly 120  
 DB 565 GGAACCCCTGCTGCTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 624  
 QY 121 AlaIleGlyGlyMetAAspAAspGlnValSerGlnLeuThrSerGlnLeuLySGlySer 140  
 DB 625 GGCATCGGGAGATGAGCAACAGAGCTCTCTCAGCTGACAGAGAGAGAGAGAGAG 684  
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 DB 745 AAGCCTAGCGGGAG 804

QY 181 LyAAspGlyTyrAlaAAspAlaGlnLeuSerCySGlyGlnGlyGlyGlyGlyGlyGlyGly 200  
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 DB 865 GTCTTCATGGGATCAAG 924  
 QY 221 ProMetArgThrPheAAspLySerIlePheSerGlyGlyGlyProAAspAlaTyrAAspGly 240  
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RESULT 9  
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 DEFINITION Novel collectin.  
 ACCESSION BD103333  
 VERSION BD103333.1 GI:22648907  
 KEYWORDS WO 0181401-A/32.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 735)  
 Makamiya,N., Keshi,H., Otani,K., Sakamoto,T. and Kishi,Y.  
 Novel collectin  
 Patent: WO 0181401-A 32 01-NOV-2001;  
 FUSO PHARMACEUTICAL INDUSTRIES LTD, NOBUTAKA WAKAMIYA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI SAKAMOTO, YUICHIRO KISHI

## COMMENT

OS Homo sapiens (human)  
 PN WO 0181401-A/32  
 PD 01-NOV-2001  
 PF 23-APR-2001 WO 2001JP003468  
 PR 21-APR-2000 JP 00P 120358  
 PI NOBUTAKA WAKAMIYA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI SAKAMOTO,  
 YUICHIRO KISHI  
 PI YUICHIRO KISHI  
 PC C07K14/47, C12N15/12, C12P21/02, A01K67/027, C07K16/18, G01N33/53  
 CC Novel collectin  
 FH Key  
 FT source  
 Location/Qualifiers  
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 Pred. No.: 1,636-219 Length: 735  
 Score: 228.00 Matches: 228  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 84.13% Indels: 0  
 DB: 6 Gaps: 0  
 US-09-806-277A-6 (1-271) x BD103333 (1-735)

QY 44 GlyAAspAlaGlyGlyLySGlyAAspLySGlyAAspLySGlyAAspLySGlyAAsp 63  
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 QY 64 ThrGlyGlyLySGlyAAspMetGlyAAspLySGlyGlnLySGlySerValGlyArgHleGly 83

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Db      112 ACGGAGAAAAAGAGACATGGGGACAAAGAGACAAAGGAGCTGTGGTCTCATGGA 171
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Qy      104 G1yProAAsp1yG1uProG1yLeuProCySer1yG1uCySer1yLeuA1yG1yA1leg1y 123
Db      232 GGTCTTATGAGAAACAGGCGCTCCATGTAGTGCAGCCAGCTGAGCCAGGCGCATCGGG 291
Qy      124 GluMetAspAAsp1yValSer1yLeuThSer1yLeuThSer1yPhe1yLeuAAsp1yVal 143
Db      292 GAGATGACACCAAGTCTCTCACTGACCAAGCTCAAGTTCATCAAGAAATGCTGTC 351
Qy      144 AlA1yValAArg1uThrG1uSer1ySer1yLeu1yLeuA1ySer1yVal1yAArg1yTyr 163
Db      352 GCCGCTGTGGCGAGAGAGAGAAATCTAAGTGTGTGAGAGAGAGAGAGAGAGAGAGAG 411
Qy      164 AlAAsp1yAAsp1ySer1yG1yAArg1yG1yThrLeuSerMetPro1yAAsp1yGlu 183
Db      412 GCGGAGCGCCAGCTGTCTGTCAGAGCGCGCGGAGCGAGCTGAGACATGAGCCAGAGAG 471
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Db      472 GCTGCCAATGGCTGATGGCGCATACCTGGCGCAAGCGCGCTGGCCGCTGTCTTATC 531
Qy      204 G1y1yLeuAAsp1yLeuG1yG1yG1yA1yAAsp1yTyrSer1yAAsp1ySer1yMetAArg 223
Db      532 GGCATCAACAGCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 591
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Qy      264 CyG1uPheAAsp1yG1uAAsp1yMet 271
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LOCUS   BD103303                      1139 bp    DNA       linear   PAT 27-AUG-2002
DEFINITION Novel collectin.
ACCESSION BD103303
VERSION   BD103303.1 GI:22648877
KEYWORDS WO 0181401-A/2.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
          1 (bases 1 to 1139)
REFERENCE
AUTHORS  Wakamiya, N., Keshi, H., Otani, K., Sakamoto, T. and Kishi, Y.
TITLE    Novel collectin
JOURNAL  Patient: WO 0181401-A 2 01-NOV-2001;
          FUSO PHARMACEUTICAL INDUSTRIES LTD, NOBUTAKA WAKAMIYA, HIROYUKI
          KESHI, KATSUKI OTANI, TAKASHI SAKAMOTO, YUICHIRO KISHI
COMMENT  OS Homo sapiens (human)
          PN WO 0181401-A/2
          PD 01-NOV-2001
          PF 23-APR-2001 WO 2001JP003468
          PR 21-APR-2000 JP 00P 120358
          PI NOBUTAKA WAKAMIYA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI PI
          SAKAMOTO,
          YUICHIRO KISHI
          PC C07K14/47, C12N15/12, C12P21/02, A01K67/027, C07K16/18, G01N33/53
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          FT CDS
          Location/Qualifiers
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FEATURES
SOURCE

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Best Local Similarity: 100.00%  Mismatches:   0
Query Match:    84.13%         Indels:       0
DB:              6             Gaps:         0

US-09-806-277a-6 (1-271) x BD103303 (1-1139)

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Db      252 ACGGAGAAAAAGAGACATGGGGACAAAGAGACAAAGAGAGAGAGAGAGAGAGAGAG 311
Qy      84  Lys11leg1Pro1leg1Ser1ySer1yG1u1ySer1yAAsp1leg1yPro1Pro 103
Db      312 AAAATTGGTCCATTGGCTCTAAAGGTGAGAAAGAGATTCCGGTGAATAGACACCCCT 371
Qy      104 G1yProAAsp1yG1uProG1yLeuProCySer1yG1uCySer1yLeuA1yG1yA1leg1y 123
Db      372 GGTCTTATGAGAAACAGGCGCTCCATGTAGTGCAGCCAGCTGAGAGAGAGAGAGAGAG 431
Qy      124 GluMetAAsp1yValSer1yLeuThSer1yLeuThSer1yPhe1yLeuAAsp1yVal 143
Db      432 GAGATGACACCAAGTCTCTCACTGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 491
Qy      144 AlA1yValAArg1uThrG1uSer1ySer1yLeu1yLeuA1ySer1yVal1yAArg1yTyr 163
Db      492 GCCGCTGTGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 551
Qy      164 AlAAsp1yAAsp1ySer1yG1yAArg1yG1yThrLeuSerMetPro1yAAsp1yGlu 183
Db      552 GCGGAGCGCCAGCTGTCTGTCAGAGCGCGCGGAGCGAGCTGAGACATGAGCCAGAGAGAG 611
Qy      184 AlA1yAAsp1yLeuMetAlA1yTyrLeuA1yAAsp1yLeuA1yAArg1yAArg1yPhe1y 203
Db      612 GCTGCCAATGGCTGATGGCGCATACCTGGCGCAAGCGCGCTGCGCTGTCTTATC 671
Qy      204 G1y1yLeuAAsp1yLeuG1yG1yG1yA1yAAsp1yTyrSer1yAAsp1ySer1yMetAArg 223
Db      672 GGCATCAACAGCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 731
Qy      224 ThrPheAAsp1yTyrAAsp1ySer1yG1yG1yProAAsp1yA1yTyrAAsp1yG1yAAsp1yVal 243
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Qy      244 GluMetValA1yAAsp1yG1yTyrAAsp1yValA1yAAsp1yTyrAAsp1yPhe1y 263
Db      792 GAGATGTGGCTGCGCGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 851
Qy      264 CyG1uPheAAsp1yG1uAAsp1yMet 271
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RESULT 11
LOCUS   BD103340                      741 bp    DNA       linear   PAT 27-AUG-2002
DEFINITION Novel collectin.
ACCESSION BD103340
VERSION   BD103340.1 GI:22648914
KEYWORDS WO 0181401-A/39.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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REFERENCE 1 (bases 1 to 741)  
AUTHORS Makamiya,N., Keshi,H., Otani,K., Sakamoto,T. and Kishi,Y.  
TITLE Novel collection  
JOURNAL Patent: WO 0181401-A 39 01-NOV-2001;  
FUSO PHARMACEUTICAL INDUSTRIES LTD,NOBUTAKA MAKAMITA,HIROYUKI  
KESHI, KATSUKI OTANI,TAKASHI SAKAMOTO,YUICHIRO KISHI  
COMMENT OS Homo sapiens (human)  
PN WO 0181401-A/39  
PD 01-NOV-2001  
PF 23-APR-2001 WO 2001JP003468  
PR 21-APR-2000 JP 00P 120358  
PI NOBUTAKA MAKAMITA,HIROYUKI KESHI,KATSUKI OTANI,TAKASHI PI  
SAKAMOTO,  
PI YUICHIRO KISHI  
PC C07K14/47,C12N15/12,C12P21/02,A01K67/027,C07K16/18,G01N33/53  
CC Novel collection  
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FT source 1..741  
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ORIGIN

Alignment Scores:  
Pred. No.: 2,266-196 Length: 741  
Score: 205.00 Matches: 205  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 75.65% Indels: 0  
Gaps: 0  
DB: 6

US-09-806-277A-6 (1-271) x BD103340 (1-741)

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DB 187 CCCATTGGCTCTAAAGGTGAGAAAGAAATTCGGGTGACATAGGACCCCTGGTCTTAT 246  
QY 107 GlyLysProGlyLysLeuProCysSerGlnLeuArgLysAlaIleGlyGluMetAsp 126  
DB 247 GGAAGAACAGGCGCTCCATGTGAGTGCAGCCAGCTGCCCAAGGCCATGGGGAGATGAC 306  
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DEFINITION Novel collection.  
ACCESSION BD103330  
VERSION BD103330.1 GI:22648904  
KEYWORDS WO 0181401-A/29.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1269)  
AUTHORS Makamiya,N., Keshi,H., Otani,K., Sakamoto,T. and Kishi,Y.  
TITLE Novel collection  
JOURNAL Patent: WO 0181401-A 29 01-NOV-2001;  
FUSO PHARMACEUTICAL INDUSTRIES LTD,NOBUTAKA MAKAMITA,HIROYUKI  
KESHI, KATSUKI OTANI,TAKASHI SAKAMOTO,YUICHIRO KISHI  
COMMENT OS Homo sapiens (human)  
PN WO 0181401-A/29  
PD 01-NOV-2001  
PF 23-APR-2001 WO 2001JP003468  
PR 21-APR-2000 JP 00P 120358  
PI NOBUTAKA MAKAMITA,HIROYUKI KESHI,KATSUKI OTANI,TAKASHI PI  
SAKAMOTO,  
PI YUICHIRO KISHI  
PC C07K14/47,C12N15/12,C12P21/02,A01K67/027,C07K16/18,G01N33/53  
CC Novel collection  
FH Key Location/Qualifiers  
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DB 451 CCCATTGGCTCTAAAGGTGAGAAAGAAATTCGGGTGACATAGGACCCCTGGTCTTAT 510  
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ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 663)  
AUTHORS Wakamiya,N., Keshi,H., Otani,K., Sakamoto,T. and Kishi,Y.  
TITLE Novel collectin  
JOURNAL Patent: WO 0181401-A 35 01-NOV-2001;  
FUSO PHARMACEUTICAL INDUSTRIES LTD,NOBUTAKA WAKAMIYA,HIROYUKI  
KESHI, KATSUKI OTANI,TAKASHI SAKAMOTO,YUICHIRO KISHI  
COMMENT OS Homo sapiens (human)  
PN WO 0181401-A/35  
PD 01-NOV-2001  
PF 23-APR-2001 WO 2001JP003468  
PR 21-APR-2000 JP 00P 120358  
PI NOBUTAKA WAKAMIYA,HIROYUKI KESHI,KATSUKI OTANI,TAKASHI PI  
SAKAMOTO,  
PI YUICHIRO KISHI  
PC C07K14/47,C12N15/12,C12P21/02,A01K67/027,C07K16/18,G01N33/53  
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DEFINITION BD103305.1 GI:22648879  
ACCESSION WO 0181401-A/4.  
VERSION WO 0181401-A/4.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1067)  
AUTHORS Wakamiya,N., Keshi,H., Otani,K., Sakamoto,T. and Kishi,Y.  
TITLE Novel collectin  
JOURNAL Patent: WO 0181401-A 4 01-NOV-2001;  
FUSO PHARMACEUTICAL INDUSTRIES LTD,NOBUTAKA WAKAMIYA,HIROYUKI  
KESHI, KATSUKI OTANI,TAKASHI SAKAMOTO,YUICHIRO KISHI  
COMMENT OS Homo sapiens (human)  
PN WO 0181401-A/4  
PD 01-NOV-2001  
PF 23-APR-2001 WO 2001JP003468  
PR 21-APR-2000 JP 00P 120358  
PI NOBUTAKA WAKAMIYA,HIROYUKI KESHI,KATSUKI OTANI,TAKASHI PI  
SAKAMOTO,  
PI YUICHIRO KISHI  
PC C07K14/47,C12N15/12,C12P21/02,A01K67/027,C07K16/18,G01N33/53  
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location/Qualifiers



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## ORIGIN

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DB	607	CAGGTCTCTCAGTCGACGACGAGCTCAATTCAAGAAATGCTGCGCGGTGCGC	666
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Search completed: December 17, 2004, 13:15:16  
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RESULT 2
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; Sequence 356, Application US/09989723
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guiney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tunes, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C62
; CURRENT APPLICATION NUMBER: US/09/989,723
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
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[illegible]

PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 98.2%; Score 1230; DB 9; Length 1238;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GCGACGGGACGAGACGCGCGCTTCCGCTTACGCGCTGCTCAGAGATTGCTGCTGCTGCG 83  
DB 1 GCGACGGGACGAGACGCGCGCTTCCGCTTACGCGCTGCTCAGAGATTGCTGCTGCTGCG 60  
QY 84 CTCAGATGAGGGGAGATCTGGGCGCTGAGGGGCTTCAATACGCTGAGCGCTTCTGCA 143  
DB 61 CTCAGATGAGGGGAGATCTGGGCGCTGAGGGGCTTCAATACGCTGAGCGCTTCTGCA 120  
QY 144 CTGCTGCCATCTGACATCTCAGCGCGCTGCGATGACGCGCTGCTGCTGCAATCTTC 203  
DB 121 CTGCTGCCATCTGACATCTCAGCGCGCTGCGATGACGCGCTGCTGCTGCAATCTTC 180  
QY 204 GTCCCTGGCTCTCAAAAGGGATGCGGAGAGAAAGGAGCAAAAGCGCGCGCGAGCGCT 263  
DB 181 GTCCCTGGCTCTCAAAAGGGATGCGGAGAGAAAGGAGCAAAAGCGCGCGAGCGCT 240  
QY 264 GGAAGAGTCGGGCGGACGAGGAGAAAGGAGCATGGGGGCAAAAGGACAGAAAGCGAGT 323  
DB 241 GGAAGAGTCGGGCGGACGAGGAGAAAGGAGCATGGGGGCAAAAGGAGCAAAAGCGAGT 300  
QY 324 GTGGTCTCATGAAAAATTGGTCCCATTTGGCTCTAAAGTGAGAAAGAGATTCCGGT 383  
DB 301 GTGGTCTCATGAAAAATTGGTCCCATTTGGCTCTAAAGTGAGAAAGAGATTCCGGT 360  
QY 384 GACATAGACCCCTGTGCTCTTATGAGAAACAGGCTTCCATGTGAGTGACAGCGCTG 443  
DB 361 GACATAGACCCCTGTGCTCTTATGAGAAACAGGCTTCCATGTGAGTGACAGCGCTG 420  
QY 444 CGCAAGGCGATCGGGGAGATGAGCAACAGGCTTCCAGCTGACAGGAGCTCAAGTTC 503  
DB 421 CGCAAGGCGATCGGGGAGATGAGCAACAGGCTTCCAGCTGACAGGAGCTCAAGTTC 480  
QY 504 ATCAAGATGTGTGCGCGGTGTGCGGAGACGAGAGCAAGATTACTGCTGTGTAAG 563  
DB 481 ATCAAGATGTGTGCGCGGTGTGCGGAGACGAGAGCAAGATTACTGCTGTGTAAG 540  
QY 564 GAGGAGAAAGCGCTACGCGAGCGCCAGCTGTCTTCCAGGCGCGCGGGGACGCTGAGC 623  
DB 541 GAGGAGAAAGCGCTACGCGAGCGCCAGCTGTCTTCCAGGCGCGCGGGGACGCTGAGC 600  
QY 624 ATGCCCAAGGAGGAGGCTGCGCAATGAGCTGAGGCGGATTCCTGGCCCAAGCGGCGCTG 683  
DB 601 ATGCCCAAGGAGGAGGCTGCGCAATGAGCTGAGGCGGATTCCTGGCCCAAGCGGCGCTG 660  
QY 684 GCCCGTGTCTTCATCGGATCAACGACTGAGAGAGAGGCGCTTCTGTACTCTGAC 743  
DB 661 GCCCGTGTCTTCATCGGATCAACGACTGAGAGAGAGGCGCTTCTGTACTCTGAC 720

QY 744 CACTCCCCCATGCGGACCTTCAACAGTGGCGGCGGTGAGCCCAACAAATGCTTAGAC 803  
DB 721 CACTCCCCCATGCGGACCTTCAACAGTGGCGGCGGTGAGCCCAACAAATGCTTAGAC 780  
QY 804 GAGGAGAGCTGCGTGGAGATGTTGGCTCGGCGGCTGGAACGAGCTGCGCACACC 863  
DB 781 GAGGAGAGCTGCGTGGAGATGTTGGCTCGGCGGCTGGAACGAGCTGCGCACACC 840  
QY 864 ACCATGTACTTCATGTGAGTTTGAACAAGAAACATGTAGCTTAGGCTGCGGCTGC 923  
DB 841 ACCATGTACTTCATGTGAGTTTGAACAAGAAACATGTAGCTTAGGCTGCGGCTGC 900  
QY 924 CCATTGGGGGGCCCAACATGTCCTGCGAGGCTTGGCAGAGACAGGCCCAACATGCTGC 983  
DB 901 CCATTGGGGGGCCCAACATGTCCTGCGAGGCTTGGCAGAGACAGGCCCAACATGCTGC 960  
QY 984 CAGCCAGGAGCTGCTCCTCTGTGAAGGTTGAGAGCTCACTGATGAGAGGCTGTTGCT 1043  
DB 961 CAGCCAGGAGCTGCTCCTCTGTGAAGGTTGAGAGCTCACTGATGAGAGGCTGTTGCT 1020  
QY 1044 AAACGTAGAAAATGCGCTTATGCTTAAGAGAAAATGAAAGTTCCTGGGGTCTGCTC 1103  
DB 1021 AAACGTAGAAAATGCGCTTATGCTTAAGAGAAAATGAAAGTTCCTGGGGTCTGCTC 1080  
QY 1104 TGAAGAAACAGATTTCTATTAATCTGTATGAGCCCAATGCTCAATTAATTAATTA 1163  
DB 1081 TGAAGAAACAGATTTCTATTAATCTGTATGAGCCCAATGCTCAATTAATTAATTA 1140  
QY 1164 CAGAAATGCTCTTCCATTAAGCTTGTGCTTGTGCAAGCTATCAATTAATCTTTAG 1223  
DB 1141 CAGAAATGCTCTTCCATTAAGCTTGTGCTTGTGCAAGCTATCAATTAATCTTTAG 1200  
QY 1224 TAGTCAGTAAAGTCCAAAAA 1253  
DB 1201 TAGTCAGTAAAGTCCAAAAA 1230

RESULT 3  
US-09-989-279-356  
Sequence 356, Application US/09989279  
Patent No. US20020072496A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavh, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1G56  
CURRENT APPLICATION NUMBER: US/09/989, 279  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787

[illegible]

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; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      98.2% Score 1230; DB 9; Length 1238;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      24 GCGAGGCGGAGAGCCCGCTTCCCTAGCCGCTGCTCAGAGTTGTTGCTTCCGCG 83
DB      1 GCGAGGCGGAGAGCCCGCTTCCCTAGCCGCTGCTCAGAGTTGTTGCTTCCGCG 60
QY      84 CTCAGATGAGGGGAGATCTGGCGCTGGGCGTTCTTAATAGGCTGGCCCTTCTGCA 143
DB      61 CTCAGATGAGGGGAGATCTGGCGCTGGGCGTTCTTAATAGGCTGGCCCTTCTGCA 120
QY      144 CTGCTGCCATCTGACATCTTCAGCGCGCTGCGATGACGCTGCTGCTGTCAGATCTTC 203
DB      121 CTGCTGCCATCTGACATCTTCAGCGCGCTGCGATGACGCTGCTGCTGTCAGATCTTC 180
QY      204 GTCCCTGGCTCAAAAGGGGATCGGGAGAGAAAGGAGACAAAGCGCCCGCGAGCGCT 263
DB      181 GTCCCTGGCTCAAAAGGGGATCGGGAGAGAAAGGAGACAAAGCGCCCGCGAGCGCT 240
QY      264 GGAAGAGTCGGGCGCCAGCGGAGAGAAAGGAGACATGGGGGACAAAGGACAGAAAGCGAGT 323
DB      241 GGAAGAGTCGGGCGCCAGCGGAGAGAAAGGAGACATGGGGGACAAAGGAGCGAGT 300
QY      324 GTGGGTCTCATGAGAAATTTGGTCCATTGGCTCTAAAGGTGAGAAAGAGATTCGGGT 383
DB      301 GTGGGTCTCATGAGAAATTTGGTCCATTGGCTCTAAAGGTGAGAAAGAGATTCGGGT 360
QY      384 GACATAGAGACCCCTGGTCTTAATGAGAGAACAGGCTTCCATGTGAGTGCAGCGAGCTG 443
DB      361 GACATAGAGACCCCTGGTCTTAATGAGAGAACAGGCTTCCATGTGAGTGCAGCGAGCTG 420
QY      444 CGCAAGGCGCATGGGGAGATGAGCAACAGGCTCTCAAGCTGACAGAGAGCTCAAGTTC 503
DB      421 CGCAAGGCGCATGGGGAGATGAGCAACAGGCTCTCAAGCTGACAGAGAGCTCAAGTTC 480
QY      504 ATCAAGAAATGCTGTGCGCGGTGTGCGCGAGACGAGAGAGATTAACCTGTGTGAAG 563
DB      481 ATCAAGAAATGCTGTGCGCGGTGTGCGCGAGACGAGAGAGATTAACCTGTGTGAAG 540
QY      564 GAGAGAAAGCGCTACGCGGAGCGCCAGCTGTCTTCCAGAGGCGCGGGGGGACGCTGAGC 623
DB      541 GAGAGAAAGCGCTACGCGGAGCGCCAGCTGTCTTCCAGAGGCGCGGGGGGACGCTGAGC 600
QY      624 ATGCCCAAGAGAGAGGCTGCGCAATGGCGTGAATGGCGGATACCTGGCGGACGCGGCTG 683
DB      601 ATGCCCAAGAGAGAGGCTGCGCAATGGCGTGAATGGCGGATACCTGGCGGACGCGGCTG 660
QY      684 GCCCGTGTCTTCATCGGATCAACGACCTGAGAGAGAGGCGCTTGTGTAATCTGAC 743
DB      661 GCCCGTGTCTTCATCGGATCAACGACCTGAGAGAGAGGCGCTTGTGTAATCTGAC 720
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QY      744 CACTCCCCCATGGGAGACCTTCAACAGAGGCGGACGCGGTGAGCCCAACATGCTAGAC 803
DB      721 CACTCCCCCATGGGAGACCTTCAACAGAGGCGGACGCGGTGAGCCCAACATGCTAGAC 780
QY      804 GAGAGAGACCTGCGAGATGATGAGCTCGGCGCGCTGGAACGAGCTGCGCTGCACACC 863
DB      781 GAGAGAGACCTGCGAGATGATGAGCTCGGCGCGCTGGAACGAGCTGCGCTGCACACC 840
QY      864 ACCATGTACTTCATGTGTGATGATTTGACAGAGAAACATGTAGCTCAGGCTGGGGCTGC 923
DB      841 ACCATGTACTTCATGTGTGATGATTTGACAGAGAAACATGTAGCTCAGGCTGGGGCTGC 900
QY      924 CCATTTGGGGGCGCCCAATGTCCTGCGAGGGTTGGCAGGGAACAGAGCCCAACATGTGTC 983
DB      901 CCATTTGGGGGCGCCCAATGTCCTGCGAGGGTTGGCAGGGAACAGAGCCCAACATGTGTC 960
QY      984 CAGCAGGAGAGCTGTCCCTCTGTGAAAGGATGAGAGCTCACTGATGAGAGGCTGTGTCT 1043
DB      961 CAGCAGGAGAGCTGTCCCTCTGTGAAAGGATGAGAGCTCACTGATGAGAGGCTGTGTCT 1020
QY      1044 AAACGTAGAAATAGGCTATGCTTAAGAGAAATGAAGTGTCTCGGGTCTGTCTC 1103
DB      1021 AAACGTAGAAATAGGCTATGCTTAAGAGAAATGAAGTGTCTCGGGTCTGTCTC 1080
QY      1104 TGAAGAGCAAGATTTCACTTACCTGTATTTAGGCCCAATGCTATTAATTAATACC 1163
DB      1081 TGAAGAGCAAGATTTCACTTACCTGTATTTAGGCCCAATGCTATTAATTAATACC 1140
QY      1164 CAGAAATGCTCTTCCATTAAGCTTGTGCTTGTCCAAAGCTATCAATTAATCTTTAAG 1223
DB      1141 CAGAAATGCTCTTCCATTAAGCTTGTGCTTGTCCAAAGCTATCAATTAATCTTTAAG 1200
QY      1224 TAGTGCACTAGTTAAGTCAAAAAA 1253
DB      1201 TAGTGCACTAGTTAAGTCAAAAAA 1230

RESULT 4
US-09-989-727-356
; Sequence 356, Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bocstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltzen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guiney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zenlin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C65
; CURRENT APPLICATION NUMBER: US/09/989,727
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
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1	PRIOR FILING DATE: 1997-06-16
2	PRIOR APPLICATION NUMBER: 60/062250
3	PRIOR FILING DATE: 1997-10-17
4	PRIOR APPLICATION NUMBER: 60/065186
5	PRIOR FILING DATE: 1997-11-12
6	PRIOR APPLICATION NUMBER: 60/065311
7	PRIOR FILING DATE: 1997-11-13
8	PRIOR APPLICATION NUMBER: 60/066770
9	PRIOR FILING DATE: 1997-11-24
10	PRIOR APPLICATION NUMBER: 60/075945
11	PRIOR FILING DATE: 1998-02-25
12	PRIOR APPLICATION NUMBER: 60/078910
13	PRIOR FILING DATE: 1998-03-20
14	PRIOR APPLICATION NUMBER: 60/083322
15	PRIOR FILING DATE: 1998-04-28
16	PRIOR APPLICATION NUMBER: 60/084600
17	PRIOR FILING DATE: 1998-05-07
18	PRIOR APPLICATION NUMBER: 60/087106
19	PRIOR FILING DATE: 1998-05-28
20	PRIOR APPLICATION NUMBER: 60/087607
21	PRIOR FILING DATE: 1998-06-02
22	PRIOR APPLICATION NUMBER: 60/087609
23	PRIOR FILING DATE: 1998-06-02
24	PRIOR APPLICATION NUMBER: 60/087759
25	PRIOR FILING DATE: 1998-06-02
26	PRIOR APPLICATION NUMBER: 60/087827
27	PRIOR FILING DATE: 1998-06-03
28	PRIOR APPLICATION NUMBER: 60/088021
29	PRIOR FILING DATE: 1998-06-04
30	PRIOR APPLICATION NUMBER: 60/088025
31	PRIOR FILING DATE: 1998-06-04
32	PRIOR APPLICATION NUMBER: 60/088026
33	PRIOR FILING DATE: 1998-06-04
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39	PRIOR FILING DATE: 1998-06-04
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43	PRIOR FILING DATE: 1998-06-04
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51	PRIOR FILING DATE: 1998-06-05
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53	PRIOR FILING DATE: 1998-06-09
54	PRIOR APPLICATION NUMBER: 60/088734
55	PRIOR FILING DATE: 1998-06-10
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58	PRIOR APPLICATION NUMBER: 60/088742
59	PRIOR FILING DATE: 1998-06-10
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61	PRIOR FILING DATE: 1998-06-10
62	PRIOR APPLICATION NUMBER: 60/088824
63	PRIOR FILING DATE: 1998-06-10
64	PRIOR APPLICATION NUMBER: 60/088826
65	PRIOR FILING DATE: 1998-06-10
66	PRIOR APPLICATION NUMBER: 60/088858
67	PRIOR FILING DATE: 1998-06-11
68	PRIOR APPLICATION NUMBER: 60/088861
69	PRIOR FILING DATE: 1998-06-11
70	PRIOR APPLICATION NUMBER: 60/088876
71	PRIOR FILING DATE: 1998-06-11
72	PRIOR APPLICATION NUMBER: 60/089105
73	PRIOR FILING DATE: 1998-06-12

[illegible]

PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
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PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 98.2%; Score 1230; DB 9; Length 1238;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GCGAGGCGAGAGACCCCGCTTCCCTAGCCGCTGCTCAGAGTTGTGTCTGCTGCG 83  
DB 1 GCGAGGCGAGAGACCCCGCTTCCCTAGCCGCTGCTCAGAGTTGTGTCTGCTGCG 60  
QY 84 CTCAGAGAGAGGAGAACTGCGCCCTGCGGCGCTTCAATAGCCTGCGCTTCTGCA 143  
DB 61 CTCAGAGAGAGGAGAACTGCGCCCTGCGGCGCTTCAATAGCCTGCGCTTCTGCA 120  
QY 144 CTGCTGCATCTGACATCTCAGCGCGCTGCGAGTGAAGCCTGCTGCTGCAATCTC 203  
DB 121 CTGCTGCATCTGACATCTCAGCGCGCTGCGAGTGAAGCCTGCTGCTGCAATCTC 180  
QY 204 GTCCCTGCGCTCAAAAGGGAGTCCGGAGAGAAAGAGAACAGCCGCCCGGAGCGCT 263  
DB 181 GTCCCTGCGCTCAAAAGGGAGTCCGGAGAGAAAGAGAACAGCCGCCCGGAGCGCT 240  
QY 264 GGAAGAGTCCGGCCCAACGGAGAGAAAGAGACATGGGGAGAAAGAGACAGAAAGCGCT 323  
DB 241 GGAAGAGTCCGGCCCAACGGAGAGAAAGAGACATGGGGAGAAAGAGACAGAAAGCGCT 300  
QY 324 GTGGGTGCTCATGAGAAATTTGCTCCATTTGCTCTAAAGTGAAGAGATTCGGT 383  
DB 301 GTGGGTGCTCATGAGAAATTTGCTCCATTTGCTCTAAAGTGAAGAGATTCGGT 360  
QY 384 GACATAGAGACCCCTGCTCTAATGAGAACAGGCTTCCATGTGAGTGACAGCGCTG 443  
DB 361 GACATAGAGACCCCTGCTCTAATGAGAACAGGCTTCCATGTGAGTGACAGCGCTG 420  
QY 444 CGCAAGGCTATGGGAGATGAGCAACAGGCTCTCACTGACAGCAAGAGCTCAAGTTC 503  
DB 421 CGCAAGGCTATGGGAGATGAGCAACAGGCTCTCACTGACAGCAAGAGCTCAAGTTC 480  
QY 504 ATCAAGATGCTGTGCGCGGTGCGCGAGAGAGAGCAAGATCTACCTGCTGTGAAG 563  
DB 481 ATCAAGATGCTGTGCGCGGTGCGCGAGAGAGAGCAAGATCTACCTGCTGTGAAG 540  
QY 564 GAGGAGAGCGCTACGCGAGACGCCAGCTGTCTTCCAGAGGCTCGCGGGGACGCTGAGC 623  
DB 541 GAGGAGAGCGCTACGCGAGACGCCAGCTGTCTTCCAGAGGCTCGCGGGGACGCTGAGC 600  
QY 624 ATGCCCAAGAGAGAGCTCCCAATGGCTGAGTGGCCGCACTACTGGCCGCAACCGGCTG 683  
DB 601 ATGCCCAAGAGAGAGCTCCCAATGGCTGAGTGGCCGCACTACTGGCCGCAACCGGCTG 660  
QY 684 GCCCGGTCTTCTATCGGATCAACGAGCTGAGAGAGAGGCGCTTCTGTACTGTGAC 743  
DB 661 GCCCGGTCTTCTATCGGATCAACGAGCTGAGAGAGAGGCGCTTCTGTACTGTGAC 720

QY 744 CACTCCCCCATGAGGAGACCTTCAACAGAGGCGAGCGGTGAGCCCAAAATGCTTACGAC 803  
DB 721 CACTCCCCCATGAGGAGACCTTCAACAGAGGCGAGCGGTGAGCCCAAAATGCTTACGAC 780  
QY 804 GAGGAGAGCTGCGTGAAGTGTGCTCGGCGGCTGGAACGAGTGGCTGCGCACAC 863  
DB 781 GAGGAGAGCTGCGTGAAGTGTGCTCGGCGGCTGGAACGAGTGGCTGCGCACAC 840  
QY 864 ACCATGTAATTCATGTGTGAGTTGACAGAGAACTGTGAGCTTCAAGGCTGGGCTGC 923  
DB 841 ACCATGTAATTCATGTGTGAGTTGACAGAGAACTGTGAGCTTCAAGGCTGGGCTGC 900  
QY 924 CCATTGGGGGCGCCCAACATGTCCTGACAGGCTTGGCAGGAGACAGGCCCAACATGAGTGC 983  
DB 901 CCATTGGGGGCGCCCAACATGTCCTGACAGGCTTGGCAGGAGACAGGCCCAACATGAGTGC 960  
QY 984 CAGCAGGAGAGCTGCTCCTCTGTGAGAGGCTGAGAGCTCAGTGAAGAGGCTGTGTCT 1043  
DB 961 CAGCAGGAGAGCTGCTCCTCTGTGAGAGGCTGAGAGCTCAGTGAAGAGGCTGTGTCT 1020  
QY 1044 AAACAGAGAAATGAGCTTATGCTTAAAGAGAAATGAAAGTTCCTGGGCTGTGTCT 1103  
DB 1021 AAACAGAGAAATGAGCTTATGCTTAAAGAGAAATGAAAGTTCCTGGGCTGTGTCT 1080  
QY 1104 TGAAGAGCAGAGTTCACTTACCTGTATGTGAGCCCAATGTCAATTAATTAATTAAC 1163  
DB 1081 TGAAGAGCAGAGTTCACTTACCTGTATGTGAGCCCAATGTCAATTAATTAATTAAC 1140  
QY 1164 CAGAAATGCTTCTCATTAAGCTTGTGCTTGTCAAGCTATTAATTAATTAATTAAG 1223  
DB 1141 CAGAAATGCTTCTCATTAAGCTTGTGCTTGTGTCAAGCTATTAATTAATTAATTAAG 1200  
QY 1224 TAGTGCACTTAAGTCAAAAAA 1253  
DB 1201 TAGTGCACTTAAGTCAAAAAA 1230

RESULT 5  
US-09-989-731-356  
Sequence 356, Application US/09989731  
Patent No. US20020103125A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: KJavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tamas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C70  
CURRENT APPLICATION NUMBER: US/09/989,731  
CURRENT FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/049787

[illegible]



PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
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PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 98.2%; Score 1230; DB 9; Length 1238;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GCGAGGCGGAGAGCGCCCGCTTCCGCTAGCGCGCTGCTCAGAGTTGGTCTCTGCTCGC 83  
DB 1 GCGAGGCGGAGAGCGCCCGCTTCCGCTAGCGCGCTGCTCAGAGTTGGTCTCTGCTCGC 60  
QY 84 CTCAGATGAGGAGGAGATGCGCGCTGCGGCGTTCTAATAGCGCTGCGCTTCCGCTGCA 143  
DB 61 CTCAGATGAGGAGGAGATGCGCGCTGCGGCGTTCTAATAGCGCTGCGCTTCCGCTGCA 120  
QY 144 CTGCTGCGATCTGAGCATCTCAGCGCGCTGCGGAGAGCGCTGCTCTGTGCGATCTCTC 203  
DB 121 CTGCTGCGATCTGAGCATCTCAGCGCGCTGCGGAGAGCGCTGCTCTGTGCGATCTCTC 180  
QY 204 GTCCCTGCGCTTCAAGGAGGAGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 263  
DB 181 GTCCCTGCGCTTCAAGGAGGAGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
QY 264 GGAAGAGTCGCGCGCGGAG 323  
DB 241 GGAAGAGTCGCGCGCGGAG 300  
QY 324 GTGGGTCGTCATGAG 383  
DB 301 GTGGGTCGTCATGAG 360  
QY 384 GACATAG 443  
DB 361 GACATAG 420  
QY 444 GCGAGAGCGGAG 503  
DB 421 GCGAGAGCGGAG 480  
QY 504 ATCAAGAGATGCTGTGCGCGGTCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 563  
DB 481 ATCAAGAGATGCTGTGCGCGGTCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540  
QY 564 GAG 623  
DB 541 GAG 600  
QY 624 ATGCCAG 683  
DB 601 ATGCCAG 660  
QY 684 GCCCGTGTCTTCTATCGGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 743  
DB 661 GCCCGTGTCTTCTATCGGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720

QY 744 CACTCCCCCATGCGGAG 803  
DB 721 CACTCCCCCATGCGGAG 780  
QY 804 GAG 863  
DB 781 GAG 840  
QY 864 ACCATGATCTTCTATGAG 923  
DB 841 ACCATGATCTTCTATGAG 900  
QY 924 CCATTTGG 983  
DB 901 CCATTTGG 960  
QY 984 CAGCCAGGAG 1043  
DB 961 CAGCCAGGAG 1020  
QY 1044 AAATGAG 1103  
DB 1021 AAATGAG 1080  
QY 1104 TGAAG 1163  
DB 1081 TGAAG 1140  
QY 1164 CAGAGATGCTCTTCTATGAG 1223  
DB 1141 CAGAGATGCTCTTCTATGAG 1200  
QY 1224 TAGTCAG 1253  
DB 1201 TAGTCAG 1230

RESULT 6  
US-09-989-732-356  
Sequence 356, Application US/09989732  
Patent No. US20020123463A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Geider, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C57  
CURRENT APPLICATION NUMBER: US/09/989,732  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787

[illegible]



[illegible]



PRIOR APPLICATION NUMBER:	60/089440
PRIOR FILING DATE:	1998-06-16
PRIOR APPLICATION NUMBER:	60/089512
PRIOR FILING DATE:	1998-06-16
PRIOR APPLICATION NUMBER:	60/089514
PRIOR FILING DATE:	1998-06-16
PRIOR APPLICATION NUMBER:	60/089522
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089538
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089598
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089599
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089600
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089653
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089801
PRIOR FILING DATE:	1998-06-18
PRIOR APPLICATION NUMBER:	60/089907
PRIOR FILING DATE:	1998-06-18
PRIOR APPLICATION NUMBER:	60/089908
PRIOR FILING DATE:	1998-06-18
PRIOR APPLICATION NUMBER:	60/089947
PRIOR FILING DATE:	1998-06-19
PRIOR APPLICATION NUMBER:	60/089948
PRIOR FILING DATE:	1998-06-19
PRIOR APPLICATION NUMBER:	60/089952
PRIOR FILING DATE:	1998-06-19
PRIOR APPLICATION NUMBER:	60/090246
PRIOR FILING DATE:	1998-06-19
PRIOR APPLICATION NUMBER:	60/090252
PRIOR FILING DATE:	1998-06-22
PRIOR APPLICATION NUMBER:	60/090254
PRIOR FILING DATE:	1998-06-22
PRIOR APPLICATION NUMBER:	60/090349
PRIOR FILING DATE:	1998-06-23
PRIOR APPLICATION NUMBER:	60/090355
PRIOR FILING DATE:	1998-06-23
PRIOR APPLICATION NUMBER:	60/090429
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090431
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090435
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090444
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090445
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090472
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090535
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090540
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090542
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090557
PRIOR FILING DATE:	1998-06-24
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PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090678
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090690
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090694
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090695
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090696
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090682
PRIOR FILING DATE:	1998-06-25

PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 98.2%; Score 1230; DB 9; Length 1238;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

24 GCGAGGCGAGAGCGCCCGCTTGGCTTACGCGCTGCTCAGAGTTGTGTCTGCTGCG 83  
1 GCGAGGCGAGAGCGCCCGCTTGGCTTACGCGCTGCTCAGAGTTGTGTCTGCTGCG 60  
84 CTCAGAGAGAGGAGAACTGTGCGCTTGGCTTACGCGCTGCTCAGAGTTGTGTCTGCTGCG 143  
61 CTCAGAGAGAGGAGAACTGTGCGCTTGGCTTACGCGCTGCTCAGAGTTGTGTCTGCTGCG 120  
144 CTGCTGCTGCTGAGCATCTCTCAGCGCGCTGCGAGTGAAGCTGCTGCTGCTGCTGCTGCT 203  
121 CTGCTGCTGCTGAGCATCTCTCAGCGCGCTGCGAGTGAAGCTGCTGCTGCTGCTGCTGCT 180  
204 GTCCCTGCTGCTGAG 263  
181 GTCCCTGCTGCTGAG 240  
264 GGAAGAGTGGGCGCCCAAG 323  
241 GGAAGAGTGGGCGCCCAAG 300  
324 GTGGGTGCTGATGAG 383  
301 GTGGGTGCTGATGAG 360  
384 GACATAG 443  
361 GACATAG 420  
444 GCGAAGGCGATGGGAG 503  
421 GCGAAGGCGATGGGAG 480  
504 ATCAAG 563  
481 ATCAAG 540  
564 GAG 623  
541 GAG 600  
624 ATGCGCAAG 683  
601 ATGCGCAAG 660  
684 GCGCGGTGCTTATGAG 743  
661 GCGCGGTGCTTATGAG 720

744 CACTCCCCCATGCGGAGCTTGAACAAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 803  
721 CACTCCCCCATGCGGAGCTTGAACAAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780  
804 GAG 863  
781 GAG 840  
864 ACCATGATCTTATGAG 923  
841 ACCATGATCTTATGAG 900  
924 CCATTGGGGGCGCCCAAG 983  
901 CCATTGGGGGCGCCCAAG 960  
984 CAGCCAGGAG 1043  
961 CAGCCAGGAG 1020  
1044 AAACCTGAG 1103  
1021 AAACCTGAG 1080  
1104 TGAAG 1163  
1081 TGAAG 1140  
1164 CAGAGTGTCTCTTCCATTAAG 1223  
1141 CAGAGTGTCTCTTCCATTAAG 1200  
1224 TAGTGCAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1253  
1201 TAGTGCAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1230

RESULT 9  
US-09-991-163-356  
Sequence 356, Application US/09991163  
Patent No. US2002013253A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltzen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, Paul J.  
APPLICANT: Gurney, Auebin L.  
APPLICANT: Klavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C17  
CURRENT APPLICATION NUMBER: US/09/991,163  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787

[illegible]



;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/090863  
;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/091360  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091478  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091544  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091626  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 98.2%; Score 1230; DB 9; Length 1238;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GCGAGGGGAGGACCCCGCTTGGCTAGCGGCTCTCAGAGTGTGTCTCTGCTCGG 83  
DB 1 GCGAGGGGAGGACCCCGCTTGGCTAGCGGCTCTCAGAGTGTGTCTCTGCTCGG 60  
QY 84 CTCAGAGTGGGGGAAATCTGCGCTGTGGGCGTTCTTAATCAGGCTGGCTTCTCTCA 143  
DB 61 CTCAGAGTGGGGGAAATCTGCGCTGTGGGCGTTCTTAATCAGGCTGGCTTCTCTCA 120  
QY 144 CTGCTGCATCTGACATCTCTCAGCGGCTGGCGATGAGCGCTGTCTGTGCAATCTTC 203  
DB 121 CTGCTGCATCTGACATCTCTCAGCGGCTGGCGATGAGCGCTGTCTGTGCAATCTTC 180  
QY 204 GTCCCTGGCTCTCAAGGGATGCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 263  
DB 191 GTCCCTGGCTCTCAAGGGATGCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
QY 264 GGAAGAGTGGGGGAG 323  
DB 241 GGAAGAGTGGGGGAG 300  
QY 324 GTGGGTCTCATGAAAAATTGGTCCATTGGCTCTAAAGTGAGAAAAAGAGATTCCGAT 383  
DB 301 GTGGGTCTCATGAAAAATTGGTCCATTGGCTCTAAAGTGAGAAAAAGAGATTCCGAT 360  
QY 384 GACATAGAGACCCCTGTGCTCTTAATGAGAACAGGCTTCCATGTGAGTGCAGGAGCTG 443  
DB 361 GACATAGAGACCCCTGTGCTCTTAATGAGAACAGGCTTCCATGTGAGTGCAGGAGCTG 420  
QY 444 GCGAAGGCGCATGGGAGATGAGAACAGGCTCTCAGCTGACAGAGAGAGAGAGAGAG 503  
DB 421 GCGAAGGCGCATGGGAGATGAGAACAGGCTCTCAGCTGACAGAGAGAGAGAGAGAG 480  
QY 504 ATCAAGAAATGTGTGCGCGGTGTGGCGAGACGAGAGAGAGATTAATCTGTGTGAAG 563  
DB 481 ATCAAGAAATGTGTGCGCGGTGTGGCGAGACGAGAGAGATTAATCTGTGTGAAG 540  
QY 564 GAGGAGAAAGCGCTTACGCGGAGCGCCAGCTGTCTTCCAGGAGCGCGGGGGGACGCTGAGC 623  
DB 541 GAGGAGAAAGCGCTTACGCGGAGCGCCAGCTGTCTTCCAGGAGCGCGGGGGGACGCTGAGC 600  
QY 624 ATGCCCAAG 683  
DB 601 ATGCCCAAG 660  
QY 684 GCCCGTGTCTTATGCGGATCAACAGACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 743  
DB 661 GCCCGTGTCTTATGCGGATCAACAGACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720

QY 744 CACTCCCCCATGCGGACCTTGAACAGAGTGGGCGAGCGGTGAGCCCAACAATGCTTACAGC 803  
DB 721 CACTCCCCCATGCGGACCTTGAACAGAGTGGGCGAGCGGTGAGCCCAACAATGCTTACAGC 780  
QY 804 GAGGAGAGCTGCGTGAAGATGATGCGCTCGGGCGGCTGGAAGAGAGAGAGAGAGAGAG 863  
DB 781 GAGGAGAGCTGCGTGAAGATGATGCGCTCGGGCGGCTGGAAGAGAGAGAGAGAGAGAG 840  
QY 864 ACCATGTAATTCATGTGTGAGTGTGACAGAGAGAAATGTGAGAGCTTCAAGCTGGGGCTGC 923  
DB 841 ACCATGTAATTCATGTGTGAGTGTGACAGAGAGAAATGTGAGAGCTTCAAGCTGGGGCTGC 900  
QY 924 CCATTGGGGGGCCCAAGATGCTCCGACAGGCTTGGAGAGGAGAGAGAGAGAGAGAGAGAG 983  
DB 901 CCATTGGGGGGCCCAAGATGCTCCGACAGGCTTGGAGAGGAGAGAGAGAGAGAGAGAGAG 960  
QY 984 CAGCCAGGAGAGCTGTCCCTCTGTGAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1043  
DB 961 CAGCCAGGAGAGCTGTCCCTCTGTGAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020  
QY 1044 AAAGTGAAGAAATGAGCTTATCTTAAGAGAGAAATGAAAGTGTCTCGGGGTGCTGTCTC 1103  
DB 1021 AAAGTGAAGAAATGAGCTTATCTTAAGAGAGAAATGAAAGTGTCTCGGGGTGCTGTCTC 1080  
QY 1104 TGAAG 1163  
DB 1081 TGAAG 1140  
QY 1164 CAGAAATGCTCTTCATTAAG 1223  
DB 1141 CAGAAATGCTCTTCATTAAG 1200  
QY 1224 TAGTGAGAGTGAAGTCAAAAAA 1253  
DB 1201 TAGTGAGAGTGAAGTCAAAAAA 1230

RESULT 10  
US-09-993-604-356  
Sequence 356, Application US/09993604  
Patent No. US20020137075A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltzen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C25  
CURRENT APPLICATION NUMBER: US/09/993.604  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787

[illegible]

;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/090863  
;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/091360  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091478  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091544  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091626  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 98.2%; Score 1230; DB 9; Length 1238;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GGAAGGCGAGACCCCGCTTCGCTAGCGGTGCTCAGAGTGTGTCTCTGCTGCG 83  
DB 1 GGAAGGCGAGACCCCGCTTCGCTAGCGGTGCTCAGAGTGTGTCTCTGCTGCG 60  
QY 84 CTCAGAGTGAAGGAGATCTGAGCCTGTGAGGCGTTCTTAATCAGCCTGCTTCTGCTCA 143  
DB 61 CTCAGAGTGAAGGAGATCTGAGCCTGTGAGGCGTTCTTAATCAGCCTGCTTCTGCTCA 120  
QY 144 CTGCTGCATCTGACATCTCAGCGCTGCGAGTGAAGCGCTGCTGTGTGCAATCTCTC 203  
DB 121 CTGCTGCATCTGACATCTCAGCGCTGCGAGTGAAGCGCTGCTGTGTGCAATCTCTC 180  
QY 204 GTCCCTGCGCTTAAAGGGATGCGGAGAGAAAGGAGAGAGGCGCGCGCGAGAGGCGCT 263  
DB 181 GTCCCTGCGCTTAAAGGGATGCGGAGAGAGAGAGAGAGGCGCGCGCGAGAGGCGCT 240  
QY 264 GGAAGAGTGCAGCGCGAG 323  
DB 241 GGAAGAGTGCAGCGCGAG 300  
QY 324 GTGGGTGCTGATGAGAAAAATGGTCCCATTTGGCTCTTAAAGGTGAGAAAGAGATTCCGGT 383  
DB 301 GTGGGTGCTGATGAGAAAAATGGTCCCATTTGGCTCTTAAAGGTGAGAAAGAGATTCCGGT 360  
QY 384 GACATAGAGACCCCTGCTGCTTAAATGAGAAACAGGCTTCCATTTGAGTGCAGCGAGCTG 443  
DB 361 GACATAGAGACCCCTGCTGCTTAAATGAGAAACAGGCTTCCATTTGAGTGCAGCGAGCTG 420  
QY 444 CGCAAGGCGCATGCGGAGAGATGAGAACAGGCTCTCTCAGCTGACAGAGAGTCAAGTTTC 503  
DB 421 CGCAAGGCGCATGCGGAGAGATGAGAACAGGCTCTCTCAGCTGACAGAGAGTCAAGTTTC 480  
QY 504 ATCAAGAAATGCTGTGCGCGGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 563  
DB 481 ATCAAGAAATGCTGTGCGCGGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540  
QY 564 GAGGAGAAAGCGCTTACGCGGAGCGCCAGCTGTCTTGCAGAGGCGCGGAGAGAGAGAG 623  
DB 541 GAGGAGAAAGCGCTTACGCGGAGCGCCAGCTGTCTTGCAGAGGCGCGGAGAGAGAGAG 600  
QY 624 ATGCCCAAG 683  
DB 601 ATGCCCAAG 660  
QY 684 GCCCGGTGCTTCTGATGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 743  
DB 661 GCCCGGTGCTTCTGATGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720

QY 744 CACTCCCCCATGCGGAGACTTCAACAGAGTGGGAGAGCGGTGAGGCCCAACATGCTTACGAC 803  
DB 721 CACTCCCCCATGCGGAGACTTCAACAGAGTGGGAGAGCGGTGAGGCCCAACATGCTTACGAC 780  
QY 804 GAGAGAGACTGCTGAGAGATGAGCTTCCGAGCGGCTTGAAAGAGAGTGGCTTCCAGAC 863  
DB 781 GAGAGAGACTGCTGAGAGATGAGCTTCCGAGCGGCTTGAAAGAGAGTGGCTTCCAGAC 840  
QY 864 ACCATGTAATCTTCAATGTGAGTGTGAGCAAGAGAAATGATGAGCTTCAAGCTGGGAGCTGC 923  
DB 841 ACCATGTAATCTTCAATGTGAGTGTGAGCAAGAGAAATGATGAGCTTCAAGCTGGGAGCTGC 900  
QY 924 CCATTGGGGGGGGCCCAATGCTCCGAGGTTGGAGGAGAGAGAGCCAGACCATGCTGC 983  
DB 901 CCATTGGGGGGGGCCCAATGCTCCGAGGTTGGAGGAGAGAGAGCCAGACCATGCTGC 960  
QY 984 CAGCAGAGAGACTGCTGCTGAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1043  
DB 961 CAGCAGAGAGACTGCTGCTGAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020  
QY 1044 AAATGAGAAATGAGCTTATCTTAAAGAGAAATGAAAGTGTCTTGGGAGTGTCTC 1103  
DB 1021 AAATGAGAAATGAGCTTATCTTAAAGAGAAATGAAAGTGTCTTGGGAGTGTCTC 1080  
QY 1104 TGAAGAGAGAGAGTTCATTAACCTGATTTGAGCCCAATGATTAATTAATTAAC 1163  
DB 1081 TGAAGAGAGAGAGTTCATTAACCTGATTTGAGCCCAATGATTAATTAATTAAC 1140  
QY 1164 CAGAAATGCTTCTTCAATTAAGCTTGTGCTTGTGCAAGTATTAATTAATTAAG 1223  
DB 1141 CAGAAATGCTTCTTCAATTAAGCTTGTGCTTGTGCAAGTATTAATTAATTAAG 1200  
QY 1224 TAGTGAGTAAATGCTTCAATTAAGCTTGTGCTTGTGCAAGTATTAATTAAG 1253  
DB 1201 TAGTGAGTAAATGCTTCAATTAAGCTTGTGCTTGTGCAAGTATTAATTAAG 1230

RESULT 11  
US-09-990-456-356  
Sequence 356, Application US/09990456  
Patent No. US20020137890A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Bockstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Baton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Geider, Hanspeter  
APPLICANT: Gerlt, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zhenli  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C22  
CURRENT APPLICATION NUMBER: US/09/990.456  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787

[illegible]



[illegible]

1 PRIOR FILING DATE: 1998-06-26  
2 PRIOR APPLICATION NUMBER: 60/090863  
3  
4 PRIOR FILING DATE: 1998-06-26  
5 PRIOR APPLICATION NUMBER: 60/091360  
6  
7 PRIOR FILING DATE: 1998-07-01  
8 PRIOR APPLICATION NUMBER: 60/091478  
9  
10 PRIOR FILING DATE: 1998-07-02  
11 PRIOR APPLICATION NUMBER: 60/091544  
12  
13 PRIOR FILING DATE: 1998-07-01  
14 PRIOR APPLICATION NUMBER: 60/091519  
15  
16 PRIOR FILING DATE: 1998-07-02  
17 PRIOR APPLICATION NUMBER: 60/091626  
18  
19 PRIOR FILING DATE: 1998-07-02  
20 PRIOR APPLICATION NUMBER: 60/091633  
21  
22 PRIOR FILING DATE: 1998-07-02  
23 PRIOR APPLICATION NUMBER: 60/091978  
24  
25 PRIOR FILING DATE: 1998-07-07  
26 PRIOR APPLICATION NUMBER: 60/091982  
27  
28 PRIOR FILING DATE: 1998-07-07  
29 PRIOR APPLICATION NUMBER: 60/092182  
30  
31 PRIOR FILING DATE: 1998-07-09

Query Match	98.2%	Score 1230;	DB 9;	Length 1238;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1230; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

QY	24	CGACAGGGCAGAGACGCCCGTTGGCTTACGCGGTCTACAGAGTTGGTCTCGTCGG	83
Dp	1	GGACAGGCGAGACGCCCGCTTGGCTTACGCGGTCTACAGAGTTGGTCTCGTCGG	60
QY	84	CTCAGGATGAGGGGGAATCTGGCGCCCTGGTGGCGTTCTTAATCAGCCTGGCTTCTGTCA	143
Dp	61	CTCAGGATGAGGGGGAATCTGGCGCCCTGGTGGCGGTCTTAATCAGCCTGGCTTCTGTCA	120
QY	144	CTGCTGGCATCTGGAATCTTCACGCGCGCTGGCCGATGACCGCTGCTGTGTGAGATCTTC	203
Dp	121	CTGCTGGCATCTGGAATCTTCACGCGCGCTGGCCGATGACCGCTGCTGTGTGAGATCTTC	180
QY	204	GTCCTGGCCTCAAAAGGGGATGCGGGAGAAAGGAGACAAAGCGCCCTCGAGCGGCT	263
Dp	181	GTCCTGGCCTCAAAAGGGGATGCGGGAGAAAGGAGACAAAGCGCCCTCGAGCGGCT	240
QY	264	GGAAGATGTCGGCCCCACGGGAGAAAAAAGACATGGGGGACAAAGACAGAAAGCACT	323
Dp	241	GGAAGATGTCGGCCCCACGGGAGAAAAAAGACATGGGGGACAAAGAGACAGAAAGCACT	300
QY	324	GTGGGTGCTCATGGAATAATTGGTCCCATTTGGCTCTAAAGGTGAGAAAGAAATTCGGGT	383
Dp	301	GTGGGTGCTCATGGAATAATTGGTCCCATTTGGCTCTAAAGGTGAGAAAGAAATTCGGGT	360
QY	384	GACATAGGACCCCCCTGTGCTCTAATGAGAACCAAGCCTTCCATGTGATGACGCCACTG	443
Dp	361	GACATAGGACCCCCCTGTGCTCTAATGAGAACCAAGCCTTCCATGTGATGACGCCACTG	420
QY	444	CGCAAGGCGCATCGGGGAGATGGACAAACAGGCTCTCAGCTGACACAGGGAGCTCAAGTTTC	503
Dp	421	CGCAAGGCGCATCGGGGAGATGGACAAACAGGCTCTCTCAGCTGACACAGGGAGCTCAAGTTTC	480
QY	504	ATCAAGAAATGCTGTGCGCGGTGTGCGAGACGAGAGCAGAAATCTACTGTGTGTGAAG	563
Dp	481	ATCAAGAAATGCTGTGCGCGGTGTGCGAGACGAGAGCAGAAATCTACTGTGTGTGAAG	540
QY	564	GAGAGGAAGCGCTACGCGGACGCCAGCTGTCTCCACAGGGCGCGGGGGACACGCTGAGC	623
Dp	541	GAGAGGAAGCGCTACGCGGACGCCAGCTGTCTCCACAGGGCGCGGGGGACACGCTGAGC	600
QY	624	ATGCCCAAGACGAGGCTTGCCCAATGGCTGATGGCCGACATACCTGAGCGCAACCGGACTTG	683
Dp	601	ATGCCCAAGACGAGGCTTGCCCAATGGCTGATGGCCGACATACCTGAGCGCAACCGGACTTG	660
QY	684	GCCCGTGTCTTCATGCGCATCAACGACTGAGAGAAAGAGGGCGCTTGTGTATCTCTGAC	743
Dp	661	GCCCGTGTCTTCATGCGCATCAACGACTGAGAGAAAGAGGGCGCTTGTGTATCTCTGAC	720

[illegible]

RESULT 13  
 US-09-992-598-356  
 / Sequence 356, Application US/09992598  
 / Patent No. US20020160384A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Ashkenazi, Avi J.  
 / APPLICANT: Baker, Kevin P.  
 / APPLICANT: Botstein, David  
 / APPLICANT: Deenoyers, Luc  
 / APPLICANT: Eaton, Dan L.  
 / APPLICANT: Ferrara, Napoleone  
 / APPLICANT: Fong, Sherman  
 / APPLICANT: Gerber, Hanspeter  
 / APPLICANT: Gerritsen, Mary B.  
 / APPLICANT: Goddard, Audrey  
 / APPLICANT: Godowski, Paul J.  
 / APPLICANT: Grimaldi, J. Christopher  
 / APPLICANT: Gurney, Austin L.  
 / APPLICANT: Kijavini, Ivar J.  
 / APPLICANT: Napier, Mary A.  
 / APPLICANT: Pan, James  
 / APPLICANT: Paoni, Nicholas F.  
 / APPLICANT: Roy, Margaret Ann  
 / APPLICANT: Stewart, Timothy A.  
 / APPLICANT: Tumas, Daniel  
 / APPLICANT: Watanabe, Colin K.  
 / APPLICANT: Williams, P. Mickey  
 / APPLICANT: Wood, William I.  
 / APPLICANT: Zhang, Zemin  
 / TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 / FILE REFERENCE: P2730PIC20  
 / CURRENT FILING DATE: 2001-11-14  
 / PRIOR APPLICATION NUMBER: 60/049787

[illegible]



;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/090863  
;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/091360  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091478  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091544  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091626  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 98.2%; Score 1230; DB 9; Length 1238;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GGAGGGGAGGAGGCGGCTTCCGCTAGCGGCTGCTCAGAGTGTGTCTCTGCTGG 83  
DB 1 GGGAGGGGAGGAGGCGGCTTCCGCTAGCGGCTGCTCAGAGTGTGTCTCTGCTGG 60  
QY 84 CTGAGAGTGGGGGAGATGTGGCCCTGTGGGCGTTCTAATCAGCCTTCCCTGCA 143  
DB 61 CTCAGAGTGGGGGAGATGTGGCCCTGTGGGCGTTCTAATCAGCCTTCCCTGCA 120  
QY 144 CTGCTGCATCTGACATCTTCAAGCGGCTGCGATGACGCTGCTCTGTGCAATCTCT 203  
DB 121 CTGCTGCATCTGACATCTTCAAGCGGCTGCGATGACGCTGCTCTGTGCAATCTCT 180  
QY 204 GTCCCTGGCTCAAGGGGATGCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 263  
DB 181 GTCCCTGGCTCAAGGGGATGCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
QY 264 GGAAGAGTGGGCGCCCAAGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 323  
DB 241 GGAAGAGTGGGCGCCCAAGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
QY 334 GTGGGTCTGTCATGAG 383  
DB 301 GTGGGTCTGTCATGAG 360  
QY 384 GACATAG 443  
DB 361 GACATAG 420  
QY 444 GCGAAGGCGCATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 503  
DB 421 GCGAAGGCGCATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480  
QY 504 ATCAAGAGTGTGTGCGCGGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 563  
DB 481 ATCAAGAGTGTGTGCGCGGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540  
QY 564 GAG 623  
DB 541 GAG 600  
QY 624 ATGCCCAAG 683  
DB 601 ATGCCCAAG 660  
QY 684 GCCCGTGTCTTCTGATGAG 743  
DB 661 GCCCGTGTCTTCTGATGAG 720

QY 744 CACTCCCCCATGCGGAGACCTTCAAGAGTGGCGAGCGGTGAGGCCCAAGATGCTTACGAGC 803  
DB 721 CACTCCCCCATGCGGAGACCTTCAAGAGTGGCGAGCGGTGAGGCCCAAGATGCTTACGAGC 780  
QY 804 GAGAGAGAGTGGGTGAGATGTTGGCTCGGCGGCTGGAAGAGAGTGGCTTCCAGAGC 863  
DB 781 GAGAGAGAGTGGGTGAGATGTTGGCTCGGCGGCTGGAAGAGAGTGGCTTCCAGAGC 840  
QY 864 ACCATGTAATCTTATGTGAGATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 923  
DB 841 ACCATGTAATCTTATGTGAGATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900  
QY 924 CCATTGGGGGGCCCAATAGTCCCTGAGGGTTGGAGGGAGAGAGAGAGAGAGAGAGAGAG 983  
DB 901 CCATTGGGGGGCCCAATAGTCCCTGAGGGTTGGAGGGAGAGAGAGAGAGAGAGAGAGAG 960  
QY 984 CAGCCAGGAGAGTGTCCCTGTGTGAGAGGGTGGAGGCTCACTGATGAGAGGGCTGTGTCT 1043  
DB 961 CAGCCAGGAGAGTGTCCCTGTGTGAGAGGGTGGAGGCTCACTGATGAGAGGGCTGTGTCT 1020  
QY 1044 AAAGTGAAG 1103  
DB 1021 AAAGTGAAG 1080  
QY 1104 TGAAGAGAGAGAGTTCATTAACCTGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1163  
DB 1081 TGAAGAGAGAGAGTTCATTAACCTGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140  
QY 1164 CAGAAATGCTCTTCCATTAAG 1223  
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QY 1224 TAGTGAGTGTAAAGTCAAAAAA 1253  
DB 1201 TAGTGAGTGTAAAGTCAAAAAA 1230

RESULT 14  
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; Sequence 356, Application US/09989293A  
; Patent No. US20020177164A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, David  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Getzler, Hanspeter  
; APPLICANT: Gerlt, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: KJavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C66  
; CURRENT APPLICATION NUMBER: US/09/989, 293A  
; CURRENT FILING DATE: 2001-11-20  
; PRIOR APPLICATION NUMBER: 60/049787

[illegible]

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; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      98.2%; Score 1230; DB 9; Length 1238;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      24 GCGACGGGAGAGACCCCGCTTCCCTAGCGCGCTGCTCAGAGTTGGTGTCTCTGCTCGC 83
DB      1 GCGACGGGAGAGACCCCGCTTCCCTAGCGCGCTGCTCAGAGTTGGTGTCTCTGCTCGC 60
QY      84 CTCAGAGTGGGGGAATCTGGCCCTGGTGGGCTTTCTAATAGGCTGGCCCTCTCTGCA 143
DB      61 CTCAGAGTGGGGGAATCTGGCCCTGGTGGGCTTTCTAATAGGCTGGCCCTCTCTGCA 120
QY      144 CTGCTGCATCTGACATCTCTCAGCCGCGCTGCGATGACGCTGCTGTGTGAGATCTCTC 203
DB      121 CTGCTGCATCTGACATCTCTCAGCCGCGCTGCGATGACGCTGCTGTGTGAGATCTCTC 180
QY      204 GTCCCTGGCTCAAAAGGGGATCGGGAGAGAAAGGAGACAAAGGCGCCCGGACGGCT 263
DB      181 GTCCCTGGCTCAAAAGGGGATCGGGAGAGAAAGGAGACAAAGGCGCCCGGACGGCT 240
QY      264 GGAAGATCGGGCCCAAGGGGAGAAAGGAGACATGGGGGCAAAAGGACAGAAAGGCACT 323
DB      241 GGAAGATCGGGCCCAAGGGGAGAAAGGAGACATGGGGGCAAAAGGACAGAAAGGCACT 300
QY      324 GTGGTGTCTGATGAAAAAATGGTCCATTTGGCTCTAAAGTGAGAAAAAGATTCGGGT 383
DB      301 GTGGTGTCTGATGAAAAAATGGTCCATTTGGCTCTAAAGTGAGAAAAAGATTCGGGT 360
QY      384 GACATAGACCCCTGTGTCTTAATGAGAACAGGCGCTTCCATGTGAGTGCAGCACTG 443
DB      361 GACATAGACCCCTGTGTCTTAATGAGAACAGGCGCTTCCATGTGAGTGCAGCACTG 420
QY      444 CGCAAGGCGCATGGGGAGATGAGCAACAGGCTCTCAAGCTACAGAGAGCTCAAGTTC 503
DB      421 CGCAAGGCGCATGGGGAGATGAGCAACAGGCTCTCAAGCTACAGAGAGCTCAAGTTC 480
QY      504 ATCAAGAAATGCTGTGCGCGGTGTGCGGAGACGAGAGAGAAATCTACTGCTGTGAAG 563
DB      481 ATCAAGAAATGCTGTGCGCGGTGTGCGGAGACGAGAGAGAAATCTACTGCTGTGAAG 540
QY      564 GAGAGAAAGCGCTACGCGGACGCCAGCTGTCTTGCAGAGGCGCGGGGGACGCTGAGC 623
DB      541 GAGAGAAAGCGCTACGCGGACGCCAGCTGTCTTGCAGAGGCGCGGGGGACGCTGAGC 600
QY      624 ATGCCCAAGGAGAGGCTGCCAATGGCTCGAGAGCGCGCATCTAGTCCGCAACCGGCTG 683
DB      601 ATGCCCAAGGAGAGGCTGCCAATGGCTCGAGAGCGCGCATCTAGTCCGCAACCGGCTG 660
QY      684 GCCCGTGTCTTATCGGCACTCAACGACTGAGAGAGAGGCGGCTTCTGTACTCTGAC 743
DB      661 GCCCGTGTCTTATCGGCACTCAACGACTGAGAGAGAGGCGGCTTCTGTACTCTGAC 720
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QY      744 CACTCCCCCATGGGAGACCTTCAACAAGTGGGCAAGCGGTGAGCCCAACATAGCTTACGAC 803
DB      721 CACTCCCCCATGGGAGACCTTCAACAAGTGGGCAAGCGGTGAGCCCAACATAGCTTACGAC 780
QY      804 GAGAGAGACTGCTGAGAGATGGTGGCTCGGCGGCTGGAACGAGCTGGCTGCACACC 863
DB      781 GAGAGAGACTGCTGAGAGATGGTGGCTCGGCGGCTGGAACGAGCTGGCTGCACACC 840
QY      864 ACCATGTACTTCAATGTGTGAGTTTGAACAAGAAACATGTGAGCTTCAAGCTGGGCTGC 923
DB      841 ACCATGTACTTCAATGTGTGAGTTTGAACAAGAAACATGTGAGCTTCAAGCTGGGCTGC 900
QY      924 CCATTTGGGGGGCCCAACATGTCCTGCAAGGTTGGCAGGGAACAAGCCCAACATGTGTC 983
DB      901 CCATTTGGGGGGCCCAACATGTCCTGCAAGGTTGGCAGGGAACAAGCCCAACATGTGTC 960
QY      984 CAGCAGGAGACTGTCCCTCTGTGAAGGGTGAAGGCTCACTGATGAGAGGCTGTGTCT 1043
DB      961 CAGCAGGAGACTGTCCCTCTGTGAAGGGTGAAGGCTCACTGATGAGAGGCTGTGTCT 1020
QY      1044 AAACAGAGAAATGGCTTATGAGAGAAATGAAAGTGTCTCTGGGTCTGTCTC 1103
DB      1021 AAACAGAGAAATGGCTTATGAGAGAAATGAAAGTGTCTCTGGGTCTGTCTC 1080
QY      1104 TGAAGAACAGAGTTTCAATTAAGTATGATGAGCCCAATGCAATTAATTAATTAAC 1163
DB      1081 TGAAGAACAGAGTTTCAATTAAGTATGATGAGCCCAATGCAATTAATTAATTAAC 1140
QY      1164 CAGAAATGCTCTTCCATTAAGCTTGTGCTTGTCAAGCTATCAATTAATCTTTAAG 1223
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DB      1201 TAGTGACGTAGTTAAGTCAAAAAA 1230

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; Sequence 356, Application US/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltzen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zhenli
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C61
; CURRENT APPLICATION NUMBER: US/09/989, 735
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049387
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[illegible]

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; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      98.2%; Score 1230; DB 9; Length 1238;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      24 GCGAGGGGAGAGACCCCGCTTCCGCTAGCGCGTGTCTCAGAGTGTGTCTCTGCTCGG 83
DB      1  GCGAGGGGAGAGACCCCGCTTCCGCTAGCGCGTGTCTCAGAGTGTGTCTCTGCTCGG 60
QY      84 CTCAGAGTGAAGGGGAAATCTGGCCCGTGGGGCGTTCTAATCAGCGCTTGCCCTTCGCA 143
DB      61 CTCAGAGTGAAGGGGAAATCTGGCCCGTGGGGCGTTCTAATCAGCGCTTGCCCTTCGCA 120
QY      144 CTGCTGCCATCTGACATCTCAGCGCGCTGGCGATGACGCGCTGTCTGTGCAATCTCTC 203
DB      121 CTGCTGCCATCTGACATCTCAGCGCGCTGGCGATGACGCGCTGTCTGTGCAATCTCTC 180
QY      204 GTTCCTGGGCTCAAAAGGGGATGCGGGAGAGAAAGGAGCAAAAGGGCGCCCGGAGGCGCT 263
DB      181 GTTCCTGGGCTCAAAAGGGGATGCGGGAGAGAAAGGAGCAAAAGGGCGCCCGGAGGCGCT 240
QY      264 GGAAGAGTGGGCGCCCAAGGAGAAAGGAGCATGGGGGAGCAAAAGGAGCAAGGAGCACT 323
DB      241 GGAAGAGTGGGCGCCCAAGGAGAAAGGAGCATGGGGGAGCAAAAGGAGCAAGGAGCACT 300
QY      324 GTGGGTCTCATGAGAAATTTGTTCCCATTTGGCTCTAAAGTGAAGAAAGAGATTCGGGT 383
DB      301 GTGGGTCTCATGAGAAATTTGTTCCCATTTGGCTCTAAAGTGAAGAAAGAGATTCGGGT 360
QY      384 GACATAGGACCCCTGTGCTTAATGAGAACAGGCGCTCCCATGTGAGTGCAGCGACTG 443
DB      361 GACATAGGACCCCTGTGCTTAATGAGAACAGGCGCTCCCATGTGAGTGCAGCGACTG 420
QY      444 CGCAAGGCCATGGGGAGATGAGCAACAGGTCTCTCACTGAGCAAGCGAGCTCAAGTTTC 503
DB      421 CGCAAGGCCATGGGGAGATGAGCAACAGGTCTCTCACTGAGCAAGCGAGCTCAAGTTTC 480
QY      504 ATCAAGAAATGTGTGCGCGGTGTGCGAGAGCGAGAGCAAGATCTAAGTGTGAG 563
DB      481 ATCAAGAAATGTGTGCGCGGTGTGCGAGAGCGAGAGCAAGATCTAAGTGTGAG 540
QY      564 GAGGAGAGCGCTACGCGGACCGCCAGCTGTCTTCAGAGGCGCGGGGGGCAAGCTGAGC 623
DB      541 GAGGAGAGCGCTACGCGGACCGCCAGCTGTCTTCAGAGGCGCGGGGGGCAAGCTGAGC 600
QY      624 ATGCCCAAGAGAGAGGCTGCAATGAGCGAGAGCGGAGTACCTGCGGCAAGCGGCGCTG 683
DB      601 ATGCCCAAGAGAGAGGCTGCAATGAGCGAGAGCGGAGTACCTGCGGCAAGCGGCGCTG 660
QY      684 GCCCGTGTCTTCAATGAGCAAGCACTGAGAGAGAGAGGCGGCTTGTGTACTGTGAC 743
DB      661 GCCCGTGTCTTCAATGAGCAAGCACTGAGAGAGAGAGGCGGCTTGTGTACTGTGAC 720
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QY      744 CACTCCCATGCGGACCTTCAACAAGTGGCGCAGCGGTGAGCCCAACAATGCTTACGAC 803
DB      721 CACTCCCATGCGGACCTTCAACAAGTGGCGCAGCGGTGAGCCCAACAATGCTTACGAC 780
QY      804 GAGAGAGCTGCGTGAAGATGTGGCTCGGGCGGCTTGAACGACGTGGCTTGCACACC 863
DB      781 GAGAGAGCTGCGTGAAGATGTGGCTCGGGCGGCTTGAACGACGTGGCTTGCACACC 840
QY      864 ACCATGATCTTCAATGTGAATTTGAACAAGAGAAATGTGAAGCTCAGAGGCTGGGGCTGC 923
DB      841 ACCATGATCTTCAATGTGAATTTGAACAAGAGAAATGTGAAGCTCAGAGGCTGGGGCTGC 900
QY      924 CCATTGGGGGCGCCCAATGTCCCTGACAGGGTTGGCAGGGACAGAGCCAGACATGTGTGC 983
DB      901 CCATTGGGGGCGCCCAATGTCCCTGACAGGGTTGGCAGGGACAGAGCCAGACATGTGTGC 960
QY      984 CAGCGAGGAGCTGTCCCTCTGTGAAGGGTGAAGGCTCAGTGAAGAGGCTGTGTCT 1043
DB      961 CAGCGAGGAGCTGTCCCTCTGTGAAGGGTGAAGGCTCAGTGAAGAGGCTGTGTCT 1020
QY      1044 AAACCTGAGAAATGGCTATGCTTAAGAGAAATGAAGGTTCCTGGGGTGTGTCTC 1103
DB      1021 AAACCTGAGAAATGGCTATGCTTAAGAGAAATGAAGGTTCCTGGGGTGTGTCTC 1080
QY      1104 TGAAGAGCAGAGTTTCACTTCTGTATGTATGAGCCCAATGTCAATATATATTACC 1163
DB      1081 TGAAGAGCAGAGTTTCACTTCTGTATGTATGAGCCCAATGTCAATATATATTACC 1140
QY      1164 CAGAAATGCTTCTCATTAAGCTTGTGCTTGTCAAGCTATACATTAATCTTTAAG 1223
DB      1141 CAGAAATGCTTCTCATTAAGCTTGTGCTTGTGTCAAGCTATACATTAATCTTTAAG 1200
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 DB 63 CAGAGTGTGTCTCTGCTGCTCAGAGTGAAGGGGAAATCTGGCCCTGTGGCGCTTC 122  
 QY 121 TAATAGGCTGGCTCTCTGCTGCTCAGAGTGAAGGGGAAATCTGGCCCTGTGGCGCTTC 180  
 DB 123 TAATAGGCTGGCTCTCTGCTGCTCAGAGTGAAGGGGAAATCTGGCCCTGTGGCGCTTC 182  
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 DB 183 AGGCTGTCTGTGAGATCTCTGCTGCTCAGAGTGAAGGGGAAATCTGGCCCTGTGGCGCTTC 242  
 QY 241 ACAAAAGGCGCCCGGAGCGCTGGAAGAAGTGGCGCCCAAGAGAGAAAGAGAGATGG 300  
 DB 243 ACAAAAGGCGCCCGGAGCGCTGGAAGAAGTGGCGCCCAAGAGAGAAAGAGAGATGG 302  
 QY 301 GGGACAAAGAGACAGAAAGGAGTGGGTGGTCAATGAGAAATTTGGTCCATTGGCTCTA 360  
 DB 303 GGGACAAAGAGACAGAAAGGAGTGGGTGGTCAATGAGAAATTTGGTCCATTGGCTCTA 362  
 QY 361 AAGTGAAGAAAGAGATTCGGGTGAATAGAGACCCCTGTGCTTAATGAGAGACAGGCC 420  
 DB 363 AAGTGAAGAAAGAGATTCGGGTGAATAGAGACCCCTGTGCTTAATGAGAGACAGGCC 422  
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 QY 541 GCAAGATTTACCTGTGTGTGAAGAGAGAAAGCGCTACGCGAGACGCGGAGTGTCTGCC 600  
 DB 543 GCAAGATTTACCTGTGTGTGAAGAGAGAAAGCGCTACGCGAGACGCGGAGTGTCTGCC 602  
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 DB 603 AGGGCGCGGGGGGAGCGCTGAGAGATGCGCAAGAGAGAGTGGCTGATGGCGG 662  
 QY 661 CATACCTGGCGCAAGCGCGCTGGCGCTGTCTTCAATGCGATCAACGACTGTGAGAGAG 720  
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 QY 1081 AAGTGTCTCTGGGCTGTGTCTGAGAGAGAGAGTTCATTACCTGTATTTGAGCCCC 1140  
 DB 1083 AAGTGTCTCTGGGCTGTGTCTGAGAGAGAGAGTTCATTACCTGTATTTGAGCCCC 1142

QY 1141 AATGCTAATATGTAATATTATCCAGAAATGCTCTTCCATAAAGCTTGTGTCTCA 1200  
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 DB 1203 AGCTATCAATATAATCTTTAATAGAGAGTGTGTTAAGTCCAAATA 1249  
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 DEFINITION  
 full-length cDNA clone CS0DC024YP19 of Neuroblastoma Cot  
 25-normalized of Homo sapiens (human).  
 ACCESSION  
 CR604552  
 VERSION  
 CR604552.1 GI:50485359  
 KEYWORDS  
 HTC; CNSLT cDNA.  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE  
 AUTHORS  
 Li, W. B., Gruber, C., Jessee, J., and Polayes, D.  
 TITLE  
 Full-length cDNA libraries and normalization  
 JOURNAL  
 Unpublished  
 CONTACT  
 Contact : Feng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
 Faraday Avenue  
 Redwood City, CA 94063  
 REFERENCE  
 Genoscope.  
 2 (bases 1 to 1252)  
 TITLE  
 Direct Submission  
 JOURNAL  
 Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
 BP 191 91060 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)  
 COMMENT  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen.  
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 DB 195 AGCCTGCTCTGTGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 254  
 QY 241 ACAAAAGCGCCCGGAGCGGCTGGAAGAAGTGGCGCCCAAGAGAGAAAGAGAGATGG 300  
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Db 675 CATACCTGGCGGCAAGCCGCGCTGCGCTGTCTTCAATGGGATCAACGACCTGGAGAAAG 734
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QY 1141 AATGTCATTATTAATTATTAACCAAGATTTGCTTCCATTAAGAGTGTGCTTTGTCCA 1200
Db 1155 AATGTCATTATTAATTATTAACCAAGATTTGCTTCCATTAAGAGTGTGCTTTGTCCA 1214
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Db 1215 AGCTATACAAATAATCTTTAAGTAGTGAAGTAA 1252

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RESULT 3
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LOCUS Full-length cDNA clone CS0DC018YD07 of Neuroblastoma Cot
DEFINITION 25-normalized of Homo sapiens (human).
ACCESSION CRS99770
VERSION CRS99770.1 GI:50480577
KEYWORDS HTC; cnsLUT_cDNA.

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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1150)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1150)
REFERENCE Genoscope.
AUTHORS Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 Evry cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
into the Not I and BcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
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Query Match 84.7%; Score 1061; DB 3; Length 1150;
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Matches 1143; Conservative 0; Mismatches 0; Indels 72; Gaps 1;

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QY 1 GGGGGGAGTGTCTTCGCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
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QY 61 CAGAGATTGAGTGTCTTCGCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
Db 68 CAGAGATTGAGTGTCTTCGCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 127
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Db 128 TAATCAGCTTGAGTGTCTTCGCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 187
QY 181 ACGCTGTCTGTGCAATCTCTGCTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Db 188 ACGCTGTCTGTGCAATCTCTGCTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 222
QY 241 ACAAAAGGCGCCCGGAGAGCGGCTGAAAGAGTGGCGCCACGAGAGAAAGAGAGAGATGG 300
Db 223 -----AAAGAGACATGG 235
QY 301 GGGACAAAGACAGAAAGGCAAGTGTGGTCTCATGAAAAAATTGGTCCCATTTGGCTCTA 360
Db 236 GGGACAAAGACAGAAAGGCAAGTGTGGTCTCATGAAAAAATTGGTCCCATTTGGCTCTA 295
QY 361 AAGGTGAGAAAGAGATTCGGGTGACATAGAACCCCTGTCCTTAATGAGAGAACCAAGGCC 420
Db 296 AAGGTGAGAAAGAGATTCGGGTGACATAGAACCCCTGTCCTTAATGAGAGAACCAAGGCC 355
QY 421 TCCCATGTAGTGCAGCCAGCTGCGCAAGGCCATCGGGGAGATGAGCAACCAAGTCTCTC 480
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QY 481 AGCTAACCAAGGAGCTCAAGTTCAATCAAGAAATGCTGTGCGGTGTGGCCGAGACGAGA 540
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QY	661	CATACCTGGCGCAACGCGGCTGTGGCCCGTGTTCATCGGAGCATCAACGACTGTGAGAAAG	720	
Db	596	CATACCTGGCGCAACGCGGCTGTGGCCCGTGTTCATCGGAGCATCAACGACTGTGAGAAAG	655	
QY	721	AGGGCGGCTTCTGTATCTGTACCACTCCCCATGCGGACTTTCAACAGTGGCGACGC	780	
Db	656	AGGGCGGCTTCTGTATCTGTACCACTCCCCATGCGGACTTTCAACAGTGGCGCACGC	715	
QY	781	GTGAGCCCAACAAATGCTTACACGAGAGAGAACTGGGTGAGATGGTGGCTCGGGCGGCT	840	
Db	716	GTGAGCCCAACAAATGCTTACACGAGAGAGAACTGGGTGAGATGGTGGCTCGGGCGGCT	775	
QY	841	GGAAAGAGCTGGCTGTGCCACACCAACCATGTACTATGTGTGATTTGACAAAGAGAA	900	
Db	776	GGAAAGAGCTGGCTGTGCCACACCAACCATGTACTATGTGTGATTTGACAAAGAGAA	835	
QY	901	TGTGAGCTTCAGGCTGGGGCTGCCATTGGGGGGCCCCACATGTCCCTGACAGGTGGCAG	960	
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QY	961	GGACAGAGCCCGACGACCATGAGTGCACAGGAGAGGAGCTGCCCTCTGTGAAGGGTGAAGCT	1020	
Db	896	GGACAGAGCCCGACGACCATGAGTGCACAGGAGAGGAGCTGCCCTCTGTGAAGGGTGAAGCT	955	
QY	1021	CACCTAGTAAAGGGCTGTGTCTTAACCTGAGAAAATGGCTTAATGCTTAAGAGAAATGA	1080	
Db	956	CACCTAGTAAAGGGCTGTGTGTCTTAACCTGAGAAAATGGCTTAATGCTTAAGAGAAATGA	1015	
QY	1081	AAGTGTCTCTGGGGGTGCTGCTCTGAGAAAGAGAGTTTCATTAACCTGTAATTTAGCCCC	1140	
Db	1016	AAGTGTCTCTGGGGGTGCTGCTCTGAGAAAGAGAGTTTCATTAACCTGTAATTTAGCCCC	1075	
QY	1141	AATGCTATTATGTATTAATTAACCGAAGATGCTCTTCCATAAAGCTTGTGCTTGTCCA	1200	
Db	1076	AATGCTATTATGTATTAATTAACCGAAGATGCTCTTCCATAAAGCTTGTGCTTGTGTCCA	1135	
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Db	1136	AGCTTATCAATTAATA 1150		
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LOCUS	BX427124			
DEFINITION	BX427124 Homo sapiens FETAL LIVER Homo sapiens cDNA clone			
ACCESSION	GS00DM08Y118 5-PRIME, mRNA sequence.			
VERSION	BX427124			
KEYWORDS	BX427124.2 GI:47002248			
SOURCE	EST.			
ORGANISM	Homo sapiens (human)			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
TITLE	Li, W.B., Gruber, C., Jesssee, J. and Polayes, D.			
JOURNAL	Full-length cDNA libraries and normalization			
COMMENT	Unpublished (2001)			
	On May 15, 2003 this sequence version replaced gi:30774621.			

Contact: Genoscope - Centre National de Séquençage  
BP 151 91008 EVRY cedex - France  
Email: [segref@genoscope.cns.fr](mailto:segref@genoscope.cns.fr), Web: [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primers  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library  
was not normalized. Library was constructed by Life Technologies, a

division of Invitrogen.  
This sequence belongs to sequence cluster 1719.f  
For more information about this cluster, see  
<http://www.genoscope.cns.fr/cdna?c=CS0AM008DF09QPI&c=1719.f>  
location/Qualifiers  
1..1083  
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enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMSPORT 6
vector. Library was not normalized."

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ORIGIN

Query Match	75.2%;	Score 942.2;	DB 5;	Length 1083;
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Matches 966;	Conservative 11;	Mismatches 14;	Indels 2;	Gaps 2

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Oy		61	CAGAGATTGTGTCTTGCTGCTGCGCTCAGAGATGAGGGGGAATCTGACCCTTGATGGAGCTTC	120
Dd		63	CAGAGATTGTGTCTTGCTGCTGCGCTCAGAGATGAGGGGGAATCTGACCCTTGATGGAGCTTC	122
Oy		121	TAAATCAGCTTGAGCTTCTCTGTCACTGCTGCCATCTGCATCTTCAGCCGGCTGGCGATG	180
Dd		123	TAAATCAGCTTGAGCTTCTCTGTCACTGCTGCCATCTGCATCTTCAGCCGGCTGGCGATG	182
Oy		181	ACGCGTGTCTGTGACAGTCTGCTCCCTGGCCCAAAGGGGATGCGGGAGAGAAGGAG	240
Dd		183	ACGCGTGTCTGTGACAGTCTGCTCCCTGGCCCAAAGGGGATGCGGGAGAGAAGGAG	242
Oy		241	ACAAAGCGCCCCCGGACGCGCTTGAGAGAGTCGCGCCCACGGAGAAAAGAGACATG	300
Dd		243	ACAAAGCGCCCCCGGACGCGCTTGAGAGAGTCGCGCCCACGGAGAAAAGAGACATG	302
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Dd		303	GGGCAAAAGGACAGAAAGGCAGTGTGGTGTCTCATGAAAAATTGCTCCAATTGGCTCTA	362
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Dd		363	AAGGTGAGAAAGGAGATTCGCGGTGACATPAGAACCCCGTGCTTAATGAGAACCAAGGCC	422
Oy		421	TCCCATGTGATGACGACGCTGCGCAAGGCGCATCGGGAGATGAGACAACAGAGTCTTC	480
Dd		423	TCCCATGTGATGACGACGCTGCGCAAGGCGCATCGGGAGATGAGACAACAGAGTCTTC	482
Oy		481	AGCTGACGAGAGCTCAAGTTCAACAAGATGCTGTGCGGTTGTGCGGAGACGAGAGA	540
Dd		483	AGCTGACGAGAGCTCAAGTTCAACAAGATGCTGTGCGGTTGTGCGGAGACGAGAGA	542
Oy		541	GCAAGACTTACCTGCTGTGTGAAGAGAGAAAGCGCTACGCGGAGGCCACAGTGTCTGCC	600
Dd		543	GCAAGACTTACCTGCTGTGTGAAGAGAGAAAGCGCTACGCGGAGGCCACAGTGTCTGCC	602
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Dd		603	AGGGCGCGGGGGGACACTGAGCATGCGCCAAAGACAGGCTGCGCAATGAGCTGTATGGCG	662
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Qy	781	GTGAGCCCCAACATGCCCTACGACGAGAGAGACTGGCTGGAGATGTGTGGCTCGGGCGGCT	840
Db	782	TGGAGCCCAACATGCTCTTACGACGAGAGAGACTGGCTGGAGATGTGTGGCTCGGGCGGCT	841
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Qy	901	TGTGAGCTCTACAGCTGTGGGCT-GGCCATGTGGGGGCCCCACATGTCCCTGACAGGTTGGCA	959
Db	902	TGTGAASCTCAGSGSTTGGGGTGGCCCATTTGGGGGGGCCACATGTGCTCTGACAGGTTGCSA	961
Qy	960	GGGACAGAGGCCCAACCATGTGTGCCAGGCCAGGG	992
Db	962	GGGAAAGAGCCGCAACCATGTGTGCCAGGCCAGGG	994

RESULT	5
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LOCUS	BX33394
DEFINITION	BX33394 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
ACCESSION	CDNA clone CSDDC024YP19-5-PRIME, mRNA sequence.
VERSION	BX33394
KEYWORDS	BX33394.2 GI:4626347
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Homo sapiens

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 1078)	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.	Full-length cDNA libraries and normalization	Unpublished (2001)	On May 1, 2003 this sequence version replaced gi:30306204.

**Contact:** Genoscope  
Genoscope - Centre National de Séquençage  
BP 191 91006 Evry cedex - France  
Email: [segrete@genoscope.cns.fr](mailto:segrete@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-Oligo (d1) primer. Five primer  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
1719.f

For more information about this cluster, see  
<http://www.genoscope.cns.fr/cdna?e=CS0DDC024CH10QPl&c=1719.f>.

FEATURES	SOURCE
Location/Qualifiers	1. 1078
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	/note="1st strand cDNA was primed with a NotI-oligo (drr) primer. Five prime end enriched, double-strand cDNA was digested with NotI and cloned into the NotI and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

Query Match	75.1%	Score 941.2	DB 5	Length 1078
Best Local Similarity	98.0%	Pred. No. 7.8e-227		
Matches 1013, Conservative	3	Mismatches 11	Indels 7	Gaps 6

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Db 15 GGGGGCACTGTCTCGCGGGCCAGGGA CGGGGAGAGACGCCGTTTCGCTTACCGGTGT 74  
0y 61 CAGAGTTGGTGTCTGCTGCGCTCAGGATAGAGGGGAAATTGGCCCTGTGGGCGTTTC 120

Db	75	CAGAGATTGGTGTCTCTGCTGCTGCTCARGAATGAGGGGGAAACTGTGACCTCGTGTGGCGCTTC	134
OY	121	TAAATCAGCTTGACCTTCTCTGTGATCATCTGTGCCATTTGGACATCTCCATAGCCCGGCTGGCAGT	180
Db	135	TAAATCAGCTTGACCTTCTCTGTGATCATCTGTGCCATTTGGACATCTCCATAGCCCGGCTGGCAGT	194
OY	181	ACGCTGCTGTGTGCAGATCCTCGTCCCTGGGCTCAAGAGGGAGATGCGGAGAGAGAGAG	240
Db	195	ACGCTGCTGTGTGCAGATCCTCGTCCCTGGGCTCAAGAGGGAGATGCGGAGAGAGAGAG	254
OY	241	ACAAAGCGCCCCCGGACGCGCTTGAAAGATCGGCCCCCAGGGAGAAAAGAGACATGG	300
Db	255	AMAAAGCGCCCCCGGACGCGCTTGAAAGATCGGCCCCCAGGGAGAAAAGAGACATGG	314
OY	301	GGGCAAAAGGACAAAAGCAGTGTGGTGCCTATGTGAAAAATTTGTGCCATTGGCTCTA	360
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OY	361	AAGGTGAGAAAGAGATTCCGGTGACATATAGAACCCCTGTGCTCTATATGAGAACAGAGCC	420
Db	375	AAGGTGAGAAAGAGATTCCGGTGACATATAGAACCCCTGTGCTCTATATGAGAACAGAGCC	434
OY	421	TCCCATGTAGTGCAGCCAGCTGCTGGCAAGSCCATCGGGAGATGACAAACAGGTCTTTC	480
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OY	481	AGCTGACCAAGGAACTCAAGTTATCAAGATGTGTGCGCGGTGTGGCGGAGACGAGAG	540
Db	495	AGCTGACCAAGGAACTCAAGTTATCAAGATGTGTGCGCGGTGTGGCGGAGACGAGAG	554
OY	541	GCAAGATCTACCTCTGGTGAAGAGAGAGAGCGCTACGCGG-ACGCCACATGCTCTGCG	599
Db	555	GCAAGATCTACCTCTGGTGAAGAGAGAGAGCGCTACGCGGAGGCCCTACGCGGAGGCCACATGCTCTGCG	614
OY	600	CAGGGCGCGGGGGCAAGCTGAGCATGCCCCAAGAGCGAGGCTGCCAATGSCCTGATGGCC	659
Db	615	CAGGGCGCGGGGGCAAGCTGAGCATGCCCCAAGAGCGAGGCTGCCAATGSCCTGATGGCC	674
OY	660	GCAATACCTGGGGGCAAGCGCGGCTGGCCCGTGTCTTCAATCGGCATCAACGACTGGAGAG	719
Db	675	GCAATACCTGGGGGCAAGCGCGGCTGGCCCGTGTCTTCAATCGGCATCAACGACTGGAGAG	733
OY	720	GAGGGCGCTTCTGTACTGTGACCACTCCCCCATGCGGACCTTCAACAACTGGCGCAGC	779
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OY	780	GGTAGGCCCAATATGCTTACGACGAGAGAGACTGCGTGAATGTTGGCTCGGCGCGC	839
Db	793	GGTAGGCCCAATATGCTTACGACGAGAGAGACTGCGTGAATGTTGGCTCGGCGCGC	852
OY	840	TGGAAACGACGAGCTGCGACACACCACTGATCTTCAATGTGTGATTGACAAAGAGAAC	899
Db	853	TGGAAACGACGAGCTGCGACACACCACTGATCTTCAATGTGTGATTGACAAAGAGAAC	912
OY	900	ATGTAGGCTTCAGGCTGGGCTGGCCCATTTGGGGGCCCCACATGTCTCCCTGACGGGTTTGC	959
Db	913	ATGTAGGCTTCAGGCTGGGCTGGCCCATTTGGGGGCCCCACATGTCTCCCTGACGGGTTTGC	972
OY	960	GGGACAGAGCCCAAGCAATGTGTGCGACGACGAGAGCTGTCCCTCTGTGAAGGTTGAGGC	1015
Db	973	GGGACAGAGCCCAAGCAATGTGTGCGACGAGAGCTGTCCCTCTGTGAAGGTTGAGGC	1028
OY	1020	TCACCTAGTAGAGG 1033	
Db	1029	TCACCTAGTAGAGG 1042	

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LOCUS			CDNA clone CS0DC024VP19 3-PRIME, mRNA sequence.	
DEFINITION				
ACCESSION	EX394893			

VERSION BX394893.2 GI:46921106  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 1095)  
 AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT On May 13, 2003 this sequence version replaced gi:30628356.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 Evry cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by life technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 1719.f  
 For more information about this cluster, see  
 http://www.genoscope.cns.fr/cdnas?CS0DC024CH1ONP1&c=1719.f.  
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 digested with Not I and cloned into the Not I and EcoR V  
 sites of the pCMVSPORT 6 vector. Library was normalized."  
 ORIGIN  
 Query Match 74.0%; Score 927.4; DB 5; Length 1095;  
 Best Local Similarity 97.5%; Pred. No. 2,4e-223;  
 Matches 1015; Conservative 10; Mismatches 7; Indels 9; Gaps 8;  
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 Db 1033 GACATCCCTCAGCGCTGCT-GCATGACG-CTGCTGTGTGCAATCTCTCTCCCTGCTCA 976  
 Oy 217 AAGGGGATGCGGAG 275  
 Db 975 AAGGGGATGCGGAG 916  
 Oy 276 CCCACGGGAG 335  
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 Oy 336 GAAAAAATTTGCTCCATTTGCTTAAGGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 395  
 Db 855 GAAAAAATTTGCTCCATTTGCTTAAGGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 797  
 Oy 396 CTTGCTCTTAATGAG 455  
 Db 796 CTTGCTCTTAATGAG 738  
 Oy 456 GGGGAGATGAG 515  
 Db 737 GGGGAGATGAG 678  
 Oy 516 GTCCGCGGTGTGCGGAG 575  
 Db 677 GTCCGCGGTGTGCGGAG 620  
 Oy 576 TAGCGGAG 635  
 Db 619 TAGCGGAG 560

Oy 636 GAGGCTCCCAATGAGCTGATGCGCGCATACCTGCGGAGAGAGAGAGAGAGAGAGAGAG 695  
 Db 559 GAGGCTCCCAAT-GCCGATGAGCTGCAATGCTGCGGAGAGAGAGAGAGAGAGAGAGAG 501  
 Oy 696 ATGGGATCAAG 755  
 Db 500 ATGGGATCAAG 441  
 Oy 756 CGGAGCTTCAACAG 815  
 Db 440 CGGAGCTTCAACAG 381  
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 Oy 1116 GTTTCATTAACCTGATTTAG 1175  
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 ACCESSION BUI47034  
 VERSION BUI47034.1 GI:22660566  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 894)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-rcmail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: LNCM532 row: 1 column: 13  
 High quality sequence stop: 621.  
 Location/Qualifiers  
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 /note="Organ: brain; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NH\_MGC Library."

## ORIGIN

Query Match 69.7%; Score 873.2; DB 5; Length 894;  
 Best Local Similarity 99.2%; Pred. No. 1.2e-209;  
 Matches 886; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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QY 19 GGCACGACGAGGAGAGGCGCCGTTGGCTTACGCGCTCAGAGAGTGGTCTCTGC 78
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DB 61 CTGCGCTCAGATGAGGAGGAGATCTGCGCTGCTGGGCGCTTCTAATCAGCCTGGCCTTCC 120
QY 139 TGTCACTGCTGCTCAGATCTGCACTCTCAGCGGCTGCGATGACGCTGCTCTGTGAGA 198
DB 121 TGTCACTGCTGCTCAGATCTGCACTCTCAGCGGCTGCGATGACGCTGCTCTGTGAGA 180
QY 129 TCTCTGCTGCTGCTCAGAGGAGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 258
DB 181 TCTCTGCTGCTGCTCAGAGGAGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
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DB 301 GCAAGTGTGGTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 360
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DB 721 CTGACCACTCTCCCATGCGGAGCTTCAAGAGTGGCGAGCGGTGAGAGAGAGAGAGAGAG 780
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DB 781 ACGAG 840  
 QY 859 ACACCACTATATAC-TTCATGTGTGAGTTTACAGAGAGAGAGAGAGAGAGAGAGAGAG 910  
 DB 841 ACACCACTAT 893

## RESULT 8

BX394624/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1071 bp mRNA linear EST 29-APR-2004  
 BX394624 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens  
 cDNA clone CS0DC018YD07.3-PRIME, mRNA sequence.  
 BX394624  
 BX394624.2 GI:46877297  
 EST.  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 1071)  
 Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
 Full-length cDNA libraries and normalization  
 Unpublished (2001)  
 On May 13, 2003 this sequence version replaced gi:30624327.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 Evry cedex - France  
 Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 1719.f  
 For more information about this cluster, see  
 http://www.genoscope.cns.fr/cdnas/cS0DC018YD04NP1&c=1719.f.  
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## FEATURES

source

## ORIGIN

Query Match 69.5%; Score 871; DB 5; Length 1071;  
 Best Local Similarity 88.8%; Pred. No. 4.4e-209;  
 Matches 1010; Conservative 14; Mismatches 37; Indels 77; Gaps 5;

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QY 138 CTGTCACTGCTGCTCAGATCTGCACTCTCAGCGGCTGCGATGAGAGAGAGAGAGAGAGAG 197
DB 1002 CTGTCACTGCTGCTCAGATCTGCACTCTCAGCGGCTGCGATGAGAGAGAGAGAGAGAG 943
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DB 942 ATCTGTGCTGCTGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 914
QY 258 CGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 317
DB 913 CGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 896
QY 318 GGCAGTGTGGTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 377
DB 895 GGCAGTGTGGTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 836
  
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OY		438	CAGCTGCCGACAGGCCATCGGGAGATGACAACAGGTTCTTCACTGAACAGCGAGCTC	497
Db		775	CCASATGCGCAAGGCCATCGGGAGATGACAACAGGTTCTTCACTGAACAGCGAGCTC	716
OY		498	AAGTTCATCAAAATGCTGCGCGGTGAGCGAGACGGAAGCAAAATCTAACCTGCTG	557
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DEFINITION	AGENCOURT_8804355 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:637965			
VERSION	BQ927000			
KEYWORDS	BQ927000.1 GI:22342031			
SOURCE	EST.			
ORGANISM	Homo sapiens (human)			
REFERENCE	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi;			
AUTHORS	1 (bases 1 to 962)			
TITLE	NIH-MGC http://mgc.nci.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC)			

JOURNAL  
 Unpublished (1999)  
 Contract: Robert Strausberg, Ph.D.  
 Email: csgabre-remail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLMC2562 row: j column: 14  
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 EcoRI; cDNA made by oligo-dt priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCAAGAG(G). Size-selected >50bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

ORIGIN  
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 Best Local Similarity 93.3%, Pred. No. 2.3e-193,  
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 1 GGCACGACGCGGACGACGCGCCGTCCTAGCGCGTCTCAGAGATTGTCGCG 60  
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 QY GCAGGTGGGTGCTCATGGAAAAATTGGTCCATTGGCTCTAAAGGTGAGAAAGAGATT 378  
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 Db 301 GCAGGTGGGTGCTCATGGAAAAATTGGTCCATTGGCTCTAAAGGTGAGAAAGAGATT 360  
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Qy 679 GCCTGGCCCCGTGTCTTCAATCGGCATCAAGACCTTGA--GAGAGAGGGCGCCTTGCTGT 735

Db 661 GCCTGGCCCCGTGTCTTTCATCGGCATCAACGACCTGTMNAGAGAGGGGCGCCTTGCTGT 720

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Db 721 ACTGAGACACATCCCCCATGCGGACCTTCAAGAATGGGCGACGGTGAAGCCCAACAATG 780

Qy 796 CCTACGACGAGGAGAGACTG-CGTGAGATGATGGCCCTCGGGGGGCGCTGGAAACGACGTTGGCC 854

Db 781 CCTACGACGAGGAGAGACTGCTCTTGGAAATGATGGCCCTCGGGGGGCGCTGGGACGACGTTGGCC 840

Qy 855 TGCCACACCAACCATATTACTTTC--ATGTGTGACTTTGACAGGAGAACATGTGAGCC--TC 910

Db 841 TGCCACACCAACCATATTACTTTCATGGGGGAACTTTTGACAGGAGAACATGTGAGCCCTTC 900

Qy 911 AGGCTGGGAGCTGCCCATTTGGGGGCCCCACATGTCTCCTGCAAGGCTTGGACGGAACAGAGCC 970

Db 901 AGCTGGGGCCGTCGCCCATTTGGGGGCCCCACATGTGAGCCCTTTGAAAGGTTTGGACGGAAGCC 960

Qy 971 CA 972

Db 961 AA 962

RESULT 10					
B0069775					
LOCUS	B0069775	962 bp	mRNA	linear	EST 02-APR-2007
DEFINITION	AGENCOCRT 7054486 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5922062				
	5', mRNA sequence.				

ACCESSION	BC069775
VERSION	BC069775.1
KEYWORDS	GI:19898821
SOURCE	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	1 (bases 1 to 962)
JOURNAL	NIH-MGC <a href="http://mgs.nci.nih.gov/">http://mgs.nci.nih.gov/</a> .
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
	Contact: Robert Strausberg, Ph.D.

Email: [csagabs-r@mail.nih.gov](mailto:csagabs-r@mail.nih.gov)  
Tissue Procurement: ATCC  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: LCM2088 row: f column: 15  
High quality sequence scop: 624.  
Location/Qualifiers  
1..962

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5922062"
/tissue_type="neuroblastoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NH MGC 47"
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCACAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in

```

the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC Library."

[illegible]



LOCUS	969 bp	mRNA	linear	EST 04-MAY-2004
DEFINITION	BX427123	Homo sapiens FETAL LIVER	Homo sapiens cDNA clone	
ACCESSION	CS00DM08Y118.3-PRIME.	mRNA sequence.		
VERSION	BX427123			
KEYWORDS	BX427123.2	GI:47001340		
SOURCE	EST.			
ORGANISM	Homo sapiens (human)			
REFERENCE	Bukayeva, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	Li, W.B., Gruber, C., Jesssee, J. and Polayes, D.			
TITLE	Full-length cDNA libraries and normalization			
JOURNAL	unpublished (2001)			
COMMENT	On May 15, 2003 this sequence version replaced gi:30772637.			
	Contact: Genoscope			
	Genoscope - Centre National de Sequencage			
	BP 191 91006 EVRY cedex - France			
	Email: sege@genoscope.cns.fr, Web : www.genoscope.cns.fr			
	1st strand cDNA was primed with a NotI-Oligo(dt) primer. Five primers			
	end enriched, double-strand cDNA was digested with Not I and cloned			
	into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library			
	was not normalized. Library was constructed by Life Technologies, a			
	division of Invitrogen.			
	This sequence belongs to sequence cluster 1719.f			
	For more information about this cluster, see			
	http://www.genoscope.cns.fr/cdna/?s=CS0ANM08DF09NP1&c=1719.f.			

FEATURES	Location/Qualifiers
source	1. .969

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DM00811.8"
/tissue_type="FETAL LIVER"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL LIVER"
/note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime
end, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

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ORIGIN	
Query Match	60.0%; Score 751.2; DB 5; length 969;
Best Local Similarity	96.5%; Pred. No. 8.8e-175;
Machs 772; Conservative	14; Mismatches 12; Indels 2; Gaps 2

[illegible]

Db	587	AGGACGCGTGAGAGATGGTGGCCCTCCGGCCGGCTGGAGACAGAGTGGCTGCGACACCAACA	528
QY	868	TGTACTTATGTGTGAGCTTTGACAAAGAGAAACATGTGAGCCTCAAGCCTGGGGCTGCCAT	927
Db	527	TGTACTTATGTGTGAGCTTTGACAAAGAGAAACATGTGAGCCTCAAGCCTGGGGCTGCCAT	468
QY	928	TGGGGGCCCCACATGTCCCTCGCAGGGTTGGCAGGGACAGAGCCCGACCATGTGTCCAGC	987
Db	467	TGGGGGCCCCACATGTCCCTCGCAGGGTTGGCAGGGACAGAGCCCGACCATGTGTCCAGC	408
QY	988	CAGGAGCTGTCCCTCTGTGTGAAGGGGTGAGGCTCACTAGTAGAGGGCTGTGTCTAAAC	1047
Db	407	CAGGAGCTGTCCCTCTGTGTGAAGGGGTGAGGCTCACTAGTAGAGGGCTGTGTCTAAAC	348
QY	1048	TGAGAAAATGGCCCTATGCTTAAGAGGAAAATGAAGAAGTTCTCTGGGGTGCCTCTCTAA	1107
Db	347	TGAGAAAATGGCCCTATGCTTAAGAGGAAAATGAAGAAGTTCTCTGGGGTGCCTCTCTAA	288
QY	1108	GAAGCAGAGTTTCATTAACCTGTATGTAGAGCCCAATGCTATTATGTAATTTAACCCAGA	1167
Db	287	GAAGCAGAGTTTCATTAACCTGTATGTAGAGCCCAATGCTATTATGTAATTTAACCCAGA	228
QY	1168	ATTGCTCTTCCATAAAGCTGTGTGCTTTGTCCAAAGCTATACATTAATAATCTTTAAGTAGT	1227
Db	227	ATTGCTCTTCCATAAAGCTGTGTGCTTTGTCCAAAGCTATACATTAATAATCTTTAAGTAGT	168
QY	1228	GCAGTAGTTAAGTCCAAAAA	1247
Db	167	GCAGTAGTTAAGTCCAAAAA	148

RESULT 12					
BX394625					
LOCUS					
DEFINITION	BX394625	1015 bp	mRNA	linear	EST 01-MAY-2004
ACCESSION	BX394625				
VERSION	CDNA clone CS0DD018YD07 5-PRIME,				
KEYWORDS	BX394625.2	GI:46920154			
SOURCE	EST.				
ORGANISM	Homo sapiens (human)				
	Homo sapiens				
	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1. (bases 1 to 1015)				
AUTHORS	L.I.W.B., Gruber,C., Jesses,J. and Polayres,D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished (2001)				
COMMENT	On May 13, 2003 this sequence version replaced gi:30628263.				

Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: [segrif@genoscope.cns.fr](mailto:segrif@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primed  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalised. Library was constructed by Life technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 1719.f  
 For more information about this cluster, see  
<http://www.genoscope.cns.fr/cdna?c=CS00C018CB04Q1&c=1719.f>.  
 Location/Qualifiers  
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/organism="Homo sapiens"
/mol_type="RNA"
/db_xref="taxon:9606"
/clone="CS0DC018YD07"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_1ib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/ncbi="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

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/clone="IMAGE:4127454"  
 /tissue\_type="neuroblastoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_19"  
 /note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 54.9%; Score 687.4; DB 2; Length 788;  
 Best Local Similarity 96.7%; Pred. No. 1.1e-162;  
 Matches 744; Conservative 0; Mismatches 21; Indels 4; Gaps 4;

QY 16 GCGGGCCAGGACGCGGACGAGAGCGCCGTTGCGCTTACGAGGAGTGGTCTCC 75  
 DB 1 GCGGGCCAGGACGCGGACGAGAGCGCCGTTGCGCTTACGAGGAGTGGTCTCC 60  
 QY 76 TGCCCTGCGCTGAGATGAGGGGGAATCTGCGCTGAGGCGCTTAAATCAGCCTGGCCT 135  
 DB 61 TGCCCTGCGCTGAGATGAGGGGGAATCTGCGCTGAGGCGCTTAAATCAGCCTGGCCT 120  
 QY 136 TCTGTCACTGCTGTCATCTGACATCTCTCAGCCGCTGCGATGACGCTGCTCTGTGC 195  
 DB 121 TCTGTCACTGCTGTCATCTGACATCTCTCAGCCGCTGCGATGACGCTGCTCTGTGC 180  
 QY 196 AGATCTGCTGCTGCTGCTGCTCAAAAGGAGATGCGGAGAGAAAGGAGACAAAGCGCCCGC 255  
 DB 181 AGATCTGCTGCTGCTGCTGCTCAAAAGGAGATGCGGAGAGAAAGGAGACAAAGCGCCCGC 240  
 QY 256 GACGCGCTGGAAGATGCGGCGCCACGCGGAGAAAGAGACATGCGGAGCAAAAGGACAGA 315  
 DB 241 GACGCGCTGGAAGATGCGGCGCCACGCGGAGAAAGAGACATGCGGAGCAAAAGGACAGA 300  
 QY 316 AAGCAGTGTGGGTGCTCATGAGAAATTTGCTCCATTGCTCTAAAGGTGAGAAAGAG 375  
 DB 301 AAGCAGTGTGGGTGCTCATGAGAAATTTGCTCCATTGCTCTAAAGGTGAGAAAGAG 360  
 QY 376 ATTCGGTGAATAGAGACCCCTGCTCTTAATGAGAAACAGGCTCTCCATGTAGTGA 435  
 DB 361 ATTCGGTGAATAGAGACCCCTGCTCTTAATGAGAAACAGGCTCTCCATGTAGTGA 420  
 QY 436 GCGAGCTGCGCAAGGCAATCGGAGAGATGAGCAACACAGGCTCTCAGCTGACAGCAGAGC 495  
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 QY 496 TCAAGTTCAATCAAGATGCTGTGCGCGGTGTGCGGAGACGAGAGCAAGATCTTACTGCG 555  
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 QY 615 ACGGTGAGAGATGCGCAAGG-ACGAGAGCTGCGCAATGCGGCTGATGCGCGATACCTGAGCGGA 673  
 DB 601 ACGGTGAGAGATGCGCAAGGATGAGAGCTGCGCAATGCGGCTGATGCGCGATACCTGAGCGGA 660  
 QY 674 AGCGGCGCTGCGCGCTGCTTCTGATC-GGCATCAACGAGCTGAGAA-GAAGGCGCGCTTTC 731  
 DB 661 AGCGGCGCTGCGCGCTGCTTCTGATC-GGCATCAACGAGCTGAGAA-GAAGGCGCGCTTTC 720  
 QY 732 GTGTACTGACACATCCCGCATGCGGAGCTTCAACAAGTGGCGGAGCG 780  
 DB 721 GTGTACTGACACATCCCGCATGCGGAGCTTCAACAAGTGGCGGAGCG 769

RESULT 15  
 BF206254

LOCUS BF206254 672 bp mRNA linear EST 06-NOV-2000  
 DEFINITION 601863264F1 NIH\_MGC\_19 Homo sapiens cDNA clone IMAGE:4098278 5',  
 mRNA sequence.  
 ACCESSION BF206254  
 VERSION BF206254.1 GI:11099840  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 672)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
 TITLES National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgsbgs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov  
 Plate: L1CM964 row: 0 column: 15  
 High quality sequence stop: 670.  
 Location/Qualifiers  
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 /clone="IMAGE:4098278"  
 /tissue\_type="neuroblastoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_19"  
 /note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 52.1%; Score 653.2; DB 2; Length 672;  
 Best Local Similarity 99.4%; Pred. No. 5e-154;  
 Matches 666; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 16 GCGGGCCAGGACGCGGACGAGAGCGCCGTTGCGCTTACGAGGAGTGGTCTCC 75  
 DB 1 GCGGGCCAGGACGCGGACGAGAGCGCCGTTGCGCTTACGAGGAGTGGTCTCC 60  
 QY 76 TGCCCTGCGCTGAGATGAGGGGGAATCTGCGCTGAGGCGCTTAAATCAGCCTGGCCT 135  
 DB 61 TGCCCTGCGCTGAGATGAGGGGGAATCTGCGCTGAGGCGCTTAAATCAGCCTGGCCT 120  
 QY 136 TCTGTCACTGCTGTCATCTGACATCTCTCAGCCGCTGCGATGACGCTGCTCTGTGC 195  
 DB 121 TCTGTCACTGCTGTCATCTGACATCTCTCAGCCGCTGCGATGACGCTGCTCTGTGC 180  
 QY 196 AGATCTGCTGCTGCTGCTGCTCAAAAGGAGATGCGGAGAGAAAGGAGACAAAGCGCCCGC 255  
 DB 181 AGATCTGCTGCTGCTGCTGCTCAAAAGGAGATGCGGAGAGAAAGGAGACAAAGCGCCCGC 240  
 QY 256 GACGCGCTGGAAGATGCGGCGCCACGCGGAGAAAGAGACATGCGGAGCAAAAGGACAGA 315  
 DB 241 GACGCGCTGGAAGATGCGGCGCCACGCGGAGAAAGAGACATGCGGAGCAAAAGGACAGA 300  
 QY 316 AAGCAGTGTGGGTGCTCATGAGAAATTTGCTCCATTGCTCTAAAGGTGAGAAAGAG 375  
 DB 301 AAGCAGTGTGGGTGCTCATGAGAAATTTGCTCCATTGCTCTAAAGGTGAGAAAGAG 360  
 QY 376 ATTCGGTGAATAGAGACCCCTGCTCTTAATGAGAAACAGGCTCTCCATGTAGTGA 435

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Db      361 ATTCCGATGACATAGAGACCCCTGGTCCTAATGAGAAACAGGCTCCCATGTGAGTCA 420
OY      436 GCCAGCTGCGCAAGGCCATCGGGAGATGACAAACAGGTCTTCAGCTGACCAAGCAGC 495
Db      421 GCCAGCTGCGCAAGGCCATCGGGAGATGACAAACAGGTCTTCAGCTGACCAAGCAGC 480
OY      496 TCAGTTGATGAGAAATGCTGTGCGCGGTGTGCGCGGAGACGAGAGCAAGATCTAAGTGC 555
Db      481 TCAGTTGATGAGAAATGCTGTGCGCGGTGTGCGCGGAGACGAGAGCAAGATCTAAGTGC 540
OY      556 TGGTGAAGAGAGAGAGCGCTACGCGGACGCGCAGCTGTCTGCCAGGCGCGGGGCA 615
Db      541 TGGTGAAGAGAGAGAGCGCTACGCGGACGCGCAGCTGTCTGCCAGGCGCGGGGCA 600
OY      616 CGCTGAGCATGCCCAAGACGAGGCTGCCAATGGCTGTGATGGCGCATACCTGGGGCAG 675
Db      601 CGCTGAGCATGCCCAAGAGCAGGCTGCCAATGGCTGTGATGGCGCATACCTGGGGCAG 659
OY      676 CCGGCTGGC 685
Db      660 CCGGCTGGC 669

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Search completed: December 16, 2004, 20:45:04  
 Job time : 6196 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

# OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 17, 2004, 10:00:00 ; Search time 590 Seconds  
(without alignments)  
2411.175 Million cell updates/sec

Title: US-09-806-277A-6  
Perfect score: 271  
Sequence: 1 MRGNALVGVLSLAFSL.....NDVACHTTMMCEPDKENM 271

Scoring table:  
OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Word size: 1

Total number of hits satisfying chosen parameters: 8266295

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Command line parameters:

MODEL=frame+ p2n\_model -DEV=xlp  
-Q=/sgn2.1/USPTO/spool\_p/US09806277/runcat.15122004.101700.29742/app\_query.fasta\_1.455  
-DB=N\_Geneseq\_23Sep04 -QFWT=fastap -SUFFIX=Oligo.rng -MINMATCH=0.1 -LOOPL=0  
-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=Oligo -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MTN=1 -ALIGN=15 -MODE=LOCAL  
-OUTFWT=eto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09806277@SGN\_1.1.885@runcat.15122004.101700.29742 -NCPU=6 -ICPU=3  
-NO MMAP -LARGESUBSTRY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOC  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : N\_Geneseq\_23Sep04:\*

1: geneeqn19806:\*\n2: geneeqn19908:\*\n3: geneeqn20008:\*\n4: geneeqn20018:\*\n5: geneeqn20028:\*\n6: geneeqn20038:\*\n7: geneeqn20048:\*\n8: geneeqn20058:\*\n9: geneeqn20068:\*\n10: geneeqn20078:\*\n11: geneeqn20088:\*\n12: geneeqn20098:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	271	100.0	813	6	ABA91201	ABA91201 Human col
2	271	100.0	1238	3	AAZ65084	AAZ65084 Membrane
3	271	100.0	1238	3	AAC58385	AAC58385 Human PRO
4	271	100.0	1238	5	AAFA4230	AAFA4230 Human PRO
5	271	100.0	1238	6	ABL88155	ABL88155 Human PRO
6	271	100.0	1238	6	ABL95644	ABL95644 Human ang

7	271	100.0	1238	8	ACA64399	ACA64399 Novel hum
8	271	100.0	1238	8	ABX80858	ABX80858 Human sec
9	271	100.0	1238	8	ACD44367	ACD44367 CDNA enc
10	271	100.0	1238	8	ABX79538	ABX79538 Human sec
11	271	100.0	1238	8	ACA93559	ACA93559 Novel hum
12	271	100.0	1238	8	ABX81241	ABX81241 Novel hum
13	271	100.0	1238	8	ACA93057	ACA93057 Novel hum
14	271	100.0	1238	8	ABX17141	ABX17141 Human PRO
15	271	100.0	1238	9	ACA67996	ACA67996 Novel hum
16	271	100.0	1238	9	ACA88445	ACA88445 Human sec
17	271	100.0	1238	9	ACD81952	ACD81952 CDNA enc
18	271	100.0	1238	9	ADA37867	ADA37867 Human CDN
19	271	100.0	1238	9	ADA21553	ADA21553 Human CDN
20	271	100.0	1238	9	ADA10340	ADA10340 Human CDN
21	271	100.0	1238	9	ADA17884	ADA17884 CDNA enc
22	271	100.0	1238	9	ADA27992	ADA27992 Human CDN
23	271	100.0	1238	9	ADA94572	ADA94572 Human CDN
24	271	100.0	1238	9	ADA38797	ADA38797 Human CDN
25	271	100.0	1238	9	ADA92918	ADA92918 Human CDN
26	271	100.0	1238	9	ACH65513	ACH65513 Human CDN
27	271	100.0	1238	9	ADA22479	ADA22479 Human CDN
28	271	100.0	1238	9	ACD39503	ACD39503 Human CDN
29	271	100.0	1238	9	ADA06645	ADA06645 Human sec
30	271	100.0	1238	9	ADA39338	ADA39338 Human CDN
31	271	100.0	1238	9	ADB96364	ADB96364 Human PRO
32	271	100.0	1238	10	ADC57836	ADC57836 Human PRO
33	271	100.0	1238	10	ADC55200	ADC55200 Human PRO
34	271	100.0	1238	10	ADC12067	ADC12067 Human CDN
35	271	100.0	1238	10	ADC65489	ADC65489 Human PRO
36	271	100.0	1238	10	ADC07544	ADC07544 Human CDN
37	271	100.0	1238	10	ADC11534	ADC11534 Human CDN
38	271	100.0	1238	10	ADC14656	ADC14656 Novel hum
39	271	100.0	1238	10	ADD08188	ADD08188 Novel hum
40	271	100.0	1238	10	ADC82013	ADC82013 Human PRO
41	271	100.0	1238	10	ADD07655	ADD07655 Novel hum
42	271	100.0	1238	10	ADC82546	ADC82546 Human PRO
43	271	100.0	1238	10	ADD10456	ADD10456 Human sec
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## ALIGNMENTS

RESULT 1	ABA91201	standard; DNA; 813 BP.
ID	ABA91201	standard; DNA; 813 BP.
AC	ABA91201;	
XX		
DT	19-FEB-2002 (first entry)	
DE	Human collectin polynucleotide SEQ ID NO 45.	
XX		
DE	Human; collectin; CL-L2-1; CL-L2-2; mouse; antibacterial; virucide;	
KW	protein therapy; infection; ds.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200181401-A1.	
XX		
PD	01-NOV-2001.	
XX		
PF	23-APR-2001; 2001WO-JP003468.	
XX		
PR	21-APR-2000; 2000JP-00120358.	
XX		
PA	(FUSO) FUSO PHARM IND LTD.	
XX		
PI	Wakamiya N, Keshi H, Ohtani K, Sakamoto T, Kishii Y;	
XX		
DR	WPI; 2002-055345/07.	
XX		
PT	New collectin family proteins, designated CL-L2-1 and CL-L2-2, expressed	

PT in kidney and for treatment and prevention of bacterial and viral  
PT infections.

PS Claim 2, Page 121; 134pp; Japanese.

XX The invention relates to human collectin family proteins (CL-L2-1 and CL-  
CC L2-2, sequences given in the specification, ABB56407-ABB56411 and  
CC ABB56414-ABB56416), their derivatives and fragments and a related  
CC collection (CL-L2) of mouse origin (ABB56412) and polynucleotides encoding  
CC all or part of the proteins. The proteins have antibacterial and virucide  
CC activity and are used for protein therapy and treatment, prevention and  
CC diagnosis of bacterial and viral infections. The present sequence is that  
CC of a collectin polynucleotide of the invention

XX Sequence 813 BP; 183 A; 225 C; 271 G; 134 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.:	6,54e-263	Length:	813
Score:	271.00	Matches:	271
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
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DB:	6	Gaps:	0

US-09-806-277A-6 (1-271) x ABA91201 (1-813)

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OY 1 MetArgGlyAenLeuAlaLeuValGlyValIleuIleSerLeuAlaPheLeuSerLeuLeu 20
DB 1 ATGAGGGGGGAATCTGGCCCTGGTGGCGCTTCTTAACACCGCTGGCCCTTCTCTCACTGCTG 60
OY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40
DB 61 CCATCTGCAATCTCTCAACCGCGGTCGATGACGCTCTCTCTGTCAGATCTCTGCTCCT 120
OY 41 GlyLeuIleGlyAspAlaGlyGlyIleGlyAspIleGlyValProGlyValArgProGlyValArg 60
DB 121 GGCCCTCAAAAGGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
OY 61 ValGlyProThrGlyGlyIleGlyValAspMetGlyAspIleGlyIleGlyValGlySerValGly 80
DB 181 GTGGGCCCCACGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
OY 81 ArgHisGlyIleValIleGlyProIleGlySerIleGlyIleGlyValGlyAspSerGlyValAspIle 100
DB 241 CGTCATGAGAAAATTGCTCCATTTGGCTCTTAAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 300
OY 101 GlyProProGlyProAsnGlyGlyProGlyLeuProCysGlyIleCysSerGlyLeuValArgIle 120
DB 301 GGAGCCCTGCTGCTCTTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
OY 121 AlaIleGlyIleMetAspAsnGlyValSerGlnLeuThrSerGlyIleLeuValPheIleLys 140
DB 361 GCCATTCGGGGAGATGAGACACCAAGTCTCTCAAGCTGACACAGAGCTCAAGTTATCAACAG 420
OY 141 AsnAlaValAlaGlyValArgGlyThrGlySerIleIleIleLeuValIleGlyGlyIle 160
DB 421 AATGCTGTCGCGGTCGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
OY 161 LysArgIleGlyIleAspAlaGlyIleLeuSerCysGlnIleValArgIleGlyIleThrLeuSerMetPro 180
DB 481 AAGGCTAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
OY 181 LysAspGlyIleAlaAsnGlyLeuMetAlaIleIleLeuAlaGlyIleValAlaArg 200
DB 541 AAGAGACAGAGCTGCTCAATGCTGCTGATGCGCCCAATCTGAGGAGAGAGAGAGAGAGAG 600
OY 201 ValPheIleGlyIleAsnAspLeuGlyIleGlyIleAlaPheValIleYSerAspHisSer 220
DB 601 GTCTTCATCGGACATCAACGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
OY 221 PrometArgThrPheAsnLysIleThrArgSerGlyIleProAsnAlaAlaIleYArgGlyGly 240
DB 661 CCATGCGGAGACTTCAACAGTGGCGAGCGGTGAGGCCCAATGCTCAAGAGAGAGAG 720
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OY 241 AspCysValGlyMetValAlaSerGlyIleThrAsnAspValAlaCysHisIleThrMet 260
DB 721 GACTGCGTGAAGATGATGGCTCGGGGCGCTGAGAACGATGGCGCTGCCACACCAACATG 780
OY 261 TyrPheMetCysGlyPheAspIleGlyIleValAsnMet 271
DB 781 TACTTCAATGTGTGAGTTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 813
RESULT 2
AAZ65084
ID AAZ65084 standard; cDNA; 1238 BP.
AC AAZ65084;
XX 05-APR-2000 (first entry)
DT 05-APR-2000 (first entry)
XX
XX Membrane-bound protein PRO1182 encoding cDNA.
XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
XX pharmaceutical; receptor immunoadhesin; gene mapping; ss.
XX Homo sapiens.
XX WC9963088-A2.
XX
XX 09-DEC-1999.
XX
XX 02-JUN-1999; 99WC-US012252.
XX
XX 02-JUN-1998; 98US-0087607P.
XX 02-JUN-1998; 98US-0087609P.
XX 02-JUN-1998; 98US-0087759P.
XX 03-JUN-1998; 98US-0087827P.
XX 04-JUN-1998; 98US-0088021P.
XX 04-JUN-1998; 98US-0088025P.
XX 04-JUN-1998; 98US-0088028P.
XX 04-JUN-1998; 98US-0088029P.
XX 04-JUN-1998; 98US-0088030P.
XX 04-JUN-1998; 98US-0088033P.
XX 04-JUN-1998; 98US-0088326P.
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XX 10-JUN-1998; 98US-0088738P.
XX 10-JUN-1998; 98US-0088740P.
XX 10-JUN-1998; 98US-0088741P.
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XX 11-JUN-1998; 98US-0088861P.
XX 11-JUN-1998; 98US-0088863P.
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XX 17-JUN-1998; 98US-0089653P.
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PR 30-JUL-1998; 98US-0093339P.  
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PR 04-AUG-1998; 98US-0095282P.  
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PR 04-AUG-1998; 98US-0095325P.  
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PR 10-AUG-1998; 98US-0095929P.  
PR 10-AUG-1998; 98US-0096012P.  
PR 11-AUG-1998; 98US-0096143P.  
PR 11-AUG-1998; 98US-0096146P.  
PR 12-AUG-1998; 98US-0096329P.  
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PR 17-AUG-1998; 98US-0096895P.  
PR 17-AUG-1998; 98US-0096897P.  
PR 18-AUG-1998; 98US-0096949P.

PR 18-AUG-1998; 98US-0096950P.  
PR 18-AUG-1998; 98US-0096959P.  
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PR 20-AUG-1998; 98US-0097218P.  
PR 24-AUG-1998; 98US-0097661P.  
PR 26-AUG-1998; 98US-0097951P.  
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PR 26-AUG-1998; 98US-0097955P.  
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PR 26-AUG-1998; 98US-0097974P.  
PR 26-AUG-1998; 98US-0097978P.  
PR 26-AUG-1998; 98US-0097979P.  
PR 26-AUG-1998; 98US-0097986P.  
PR 26-AUG-1998; 98US-0098014P.  
PR 31-AUG-1998; 98US-0098525P.  
PR 16-SEP-1998; 98US-0100634P.  
PR 12-JAN-1999; 99US-0115565P.  
  
XX (GETH ) GENENTECH INC.  
XX  
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK,  
PI Wood WJ, Yuan J;  
XX WPI; 2000-072883/06.  
XX P-PSDB; AAY66738.  
XX  
XX Membrane-bound proteins and related nucleotide sequences.  
XX  
XX Claim 2; Fig 251; 822pp; English.  
XX  
XX The invention provides membrane-bound PRO polypeptides and  
CC polynucleotides encoding them. The PRO sequences of the invention were  
CC identified based on extracellular domain homology screening. The PRO  
CC sequences have homology with proteins including LDL receptors, TIE  
CC ligands and various enzymes. The membrane-bound proteins and receptor  
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
CC immunodesigns, for instance, can be used as therapeutic agents to block  
CC receptor-ligand interactions. The membrane-bound proteins can also be  
CC employed for screening of potential peptide or small molecule inhibitors  
CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
CC are useful as hybridization probes, in chromosome and gene mapping and in  
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will  
CC also be useful for the preparation of PRO polypeptides, especially by  
CC recombinant techniques  
XX  
XX Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;  
SQ  
  
Alignment Scores:  
Pred. No.: 9,91e-263 Length: 1238  
Score: 271.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Matchn: 100.00% Indels: 0  
DB: Gaps: 0  
  
US-09-806-277A-6 (1-271) x AAZ65084 (1-1238)  
  
QY 1 MetArgGlyAenLeuAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeuIleu 20  
DB 67 ATGAGGGGGGAATCTGGCGCTGTGGCTTCTTAATCAAGCCCTGCTTCACTGTG 126  
QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
DB 127 CCATCTGGAACATCTCTCAAGCCGCTGCGCATACCCCTGCTGTGCAAGTCTGTCCCT 186  
QY 41 GlyLeuIysGlyAspAlaGlyGlyIleGlyAspIysGlyAlaPProGlyArgProGlyArg 60  
DB 187 GGCTCAAGAGGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246  
QY 61 ValGlyProThrArgIleGlyIleGlyAspMetCylAspIysGlyGlyIleGlySerValGly 80

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DB      247  GTCCGCCCCACGGAGAAAAAGAGACATGGGGGCAAGACAGACAGAGTGTGGGT 306
QY      81  ArgHieGlyLysIleGlyProIleGlySerIleGlyGlyLysAspSerGlyAspIle 100
DB      307  CGTCATGGAAAAATGTGCTCCATTTGGCTTAAGGTGAGAAAGAGATTCCGGTGAACATA 366
QY      101  GTPProPProGlyProAsnGlyGluProGlyLysProGlyLysCysSerGlnLeuArgLys 120
DB      367  GGAACCCCTGGTCTTAATGAGAACACAGCCCTCCATGTGAGTGACGACCTGCGCAAG 426
QY      121  AAlaIleGlyLysLeuAspAsnGlnValSerGlnLeuThrSerGlnLeuLysPheIleLys 140
DB      427  GCCATCGGGGAGATGAGACACAGGTCTCTCAGCTGACGACGACGACCTTAATTATCAAG 486
QY      141  AenAlaValAlaGlyValArgGluThrGlnSerLysIleTyrLeuLeuValLysGluGlu 160
DB      487  AATGCTGTGCGCGGTGCGGAGACGAGACGAAAGATCTACCTGCTGTGAGAGAGAG 546
QY      161  LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyArgGlyGlyTyrThrLeuSerMetPro 180
DB      547  AAGGCTTAGCGGAGAGCCAGCTGTCTGCAAGGCGCGGAGGACGCTGAGCATGCGCC 606
QY      181  LysAspGluAlaAlaAsnGlyLeuMetAlaAlaTyrLeuAlaGlnAlaGlyLeuAlaArg 200
DB      607  AAGGACGAGGCTGCCAATGGCTGATGGCCGATACCTGGCGCAAGCGCGCTGGCCCGT 666
QY      201  ValPheIleGlyIleAsnAspLeuGluLysGluGlyAlaPheValTyrSerAspHisSer 220
DB      667  GTCTTCATCGGCATCAACAGCCTGAGAGAGAGGCGCTTCGTGTCTCTGACCACTCC 726
QY      221  ProMetArgThrPheAsnLysTyrPArgSerGlyGlyProAsnAlaAlaTyrAspGluGlu 240
DB      727  CCATGCGGACCTTCAACAGTGGCGGACGCTGAGCCCAACATGCTTACGACGAGAG 786
QY      241  AspCysValGluMetValAlaSerGlyGlyTyrPheAspValAlaCysHisThrThrMet 260
DB      787  GACTGCGGAGATGTGTGGCTCGGGCGGTGAGAACGACGTGGCTGCCACACCACTG 846
QY      261  TyrPheMetCysGluPheAspLysGluAsnMet 271
DB      847  TACTTCATGTGTGAGTTGACAGAGAACATG 879

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## RESULT 3

AACS8385  
ID AACS8385 standard; cDNA; 1238 BP.

AC AACS8385;

DT 29-JAN-2001 (first entry)

DE Human PRO1182 nucleotide sequence SEQ ID NO:50.

XX Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;  
 KW proliferation; tumorigenesis; identification; cancer; cytostatic;  
 KW neurotrophic; neuroprotective; antiinflammatory; immunosuppressive;  
 KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;  
 KW neuronal disorder; glial disorder; astrocytal disorder; angiogenic;  
 KW hypothalamic disorder; glandular disorder; macrophagal disorder;  
 KW epithelial disorder; stromal disorder; blastocoele disorder;  
 KW inflammatory disorder; immunologic disorder; ss.

XX Homo sapiens.

OS WO200053755-A2.

PN 14-SEP-2000.

XX 06-JAN-2000; 2000WO-US000376.

XX 08-MAR-1999; 99WO-US005028.

PR 02-JUN-1999; 99WO-US012252.

PR 23-JUN-1999; 99US-0141037P.

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PR      07-JUN-1999; 99US-0143048P.
PR      26-JUN-1999; 99US-0145698P.
PR      30-NOV-1999; 99WO-US028313.
PR      20-DEC-1999; 99WO-US030911.
PR      05-JAN-2000; 2000WO-US000219.
XX
PA      (GENTH ) GENTTECH INC.
XX
PI      Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;
PI      Watanabe CK, Wood WI;
XX
DR      WPI: 2000-572270/53.
DR      P-PSDB; AAB24075.
XX
PT      Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
PT      treatment, diagnosis and prevention of cancer.
XX
PS      Claim 50; Fig 37; 286pp; English.
XX
CC      The present invention describes an isolated antibody that binds to one of
CC      the human PRO proteins designated PRO212, PRO290, PRO341, PRO355, PRO619,
CC      PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009, PRO1025,
CC      PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184, PRO1187,
CC      PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094, PRO2145 OR
CC      PRO2198. PRO antagonists can be used to inhibit tumour cell growth. The
CC      PRO polypeptides and nucleotides are useful in the treatment, diagnosis
CC      and prevention of cancer. The antibodies and other anti-tumour compounds
CC      maybe used to treat various conditions, including those characterised by
CC      overexpression and/or activation of the amplified PRO genes. Exemplary
CC      conditions or disorders to be treated with such antibodies and other
CC      compounds include benign or malignant tumours (e.g., renal, liver,
CC      kidney, bladder, breast, gastric, ovarian, colorectal, prostate,
CC      pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas, and
CC      glioblastomas), and various head and neck tumours), leukaemias and
CC      lymphoid malignancies, other disorders such as neuronal, glial,
CC      astrocytal, hypothalamic and other glandular, macrophagal, epithelial,
CC      stromal and blastocoele disorders, and inflammatory, angiogenic and
CC      immunologic disorders. AACS8242 to AACS8366 represent PCR primers and
CC      hybridisation probes used in the isolation of the human PRO sequences.
CC      AACS8367 to AACS8386 and AAB24057 to AAB24089 represent human PRO
CC      polynucleotide and protein sequences given in the exemplification of the
CC      present invention
XX
SQ      Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other:

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## Alignment Scores:

Align. No.: 9,91e-263 Length: 1238  
 Pred. No.: 271.00 Matches: 271  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 3 Gaps: 0

US-09-806-277A-6 (1-271) x AACS8385 (1-1238)

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DB      67  ATAGAGGGGAATGTGGCTTGTGGGCTTCTTAATACGCTGCTTCTCTGTACTGCTG 126
QY      21  ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40
DB      127  CCATCTGACATCTCTACGCGGCTGGCGATGACGCTGCTGTGTGACATCTCTGTCCT 186
QY      41  GlyLeuLysGlyAspAlaGlyGlyLysGlyAspLysGlyValaProGlyLysArgProGly 60
DB      187  GGCCTCAAGGGGATCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246
QY      61  ValGlyProThrGlyLysGlyAspMetGlyAspLysGlyGlnLysGlySerValGly 80
DB      247  GTGGGCCCAACGGGAGAAAAAGAGACATGGGGGACAAAGAGACAGAAAGGACATGTGGGT 306
QY      81  ArgHieGlyLysIleGlyProIleGlySerIleGlyGlyLysAspSerGlyAspIle 100

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Db 307 CGTCATGAAAAAATTGGTCCCTTGGCTCTAAAGGTGAGAAAAGGATTCGGGTACATA 366  
 QY 101 G1YProProG1YProAaNG1YGIuProG1YleuProCySG1uCySserG1nleuArylys 120  
 Db 367 GAGACCCCTGGTCTTAATGAGAACCAAGGCTCCCATGTGAGTGCAGCAGCTGGCGAAG 426  
 QY 121 A1a1leG1YGIuMeAaPaaNG1nValSerG1nleuThrSerG1nleuLeuPhe1lelys 140  
 Db 427 GCCATCGGGGAGTGAACCAAGGTCTCTCAGCTGACCAAGGACCTCAAGTTCATCAAG 486  
 QY 141 AaA1aValA1aAG1YValArgG1uThrG1uSerG1uSerG1uSerG1uSerG1uSerG1uSer 160  
 Db 487 AATGCTGTGCGCGGTGTGCGCGAAGCGAGACCAAGATCTTACTCTGTGTGAAGAGAG 546  
 QY 161 LySaArg1YrA1aAaPaa1G1nleuSerCySG1nG1YArg1YGIYThrleuSerMetPro 180  
 Db 547 AAGCGCTACGGCGAGCGCCAGCTGTCTGCGAGGGCCGGGGGGGACCGCTGAGCATGCC 606  
 QY 181 LySaArg1uA1aAaNG1YleuMetA1aA1YrleuA1aG1nA1aG1YleuA1aArg 200  
 Db 607 AAGGACGAGGCTGCAATGCGCTGATGGCCGCTACCTGGCCCAAGCCGGCCCTGGCCCT 666  
 QY 201 ValPhe1leG1Y1leAaAaPaa1G1uYrG1uG1YAlaPheValYrSerAaPaa1Ser 220  
 Db 667 GTCTTCATCGCATCAACGACTCGAGAGAGAGGGCGCTTGTGTACTCTGACCATCTCC 726  
 QY 221 ProMeA1YrThrPheAaNG1YrPaa1SerG1YGIuProAaAaA1aYrAaPaa1G1u 240  
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 ID AAF44230 standard; cDNA; 1238 BP.  
 XX  
 AC AAF44230;  
 XX  
 DT 02-APR-2001 (first entry)  
 XX  
 DE Human PRO1182 (UNQ596) nucleotide sequence SEQ ID NO:356.  
 XX  
 KW Human; secreted and transmembrane protein; PRO; cytosolic; cell death;  
 KW cancer; chromosomal mapping; gene mapping; tissue typing;  
 KW diagnostic assay; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200073454-A1.  
 PD 07-DEC-2000.  
 XX  
 PF 30-MAR-2000; 2000WO-US008439.  
 XX  
 PR 02-JUN-1999; 99WO-US012252.  
 PR 23-JUN-1999; 99US-0141037F.  
 PR 07-JUL-1999; 99US-0143048P.  
 PR 20-JUL-1999; 99US-0144758B.  
 PR 26-JUL-1999; 99US-0145698P.  
 PR 28-JUL-1999; 99US-0146222P.  
 PR 17-AUG-1999; 99US-0149396P.  
 PR 15-SEP-1999; 99WO-US021099.  
 PR 15-SEP-1999; 99WO-US021547.  
 PR 08-OCT-1999; 99US-0158663P.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 16-DEC-1999; 99WO-US030095.

PR 20-DEC-1999; 99WO-US030911.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000376.  
 PR 11-FEB-2000; 2000WO-US003565.  
 PR 18-FEB-2000; 2000WO-US004341.  
 PR 22-FEB-2000; 2000WO-US004414.  
 PR 24-FEB-2000; 2000WO-US004914.  
 PR 02-FEB-2000; 2000WO-US005004.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 15-MAR-2000; 2000WO-US006884.  
 PR 20-MAR-2000; 2000WO-US007377.  
 XX  
 PA (GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,  
 PI Ferrare N, Fong S, Garber H, Gerltzen ME, Goddard A, Godowski PJ,  
 PI Grimaldi CJ, Gurney AL, K1avin ID, Napier MA, Pan J, Paoni NF,  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
 PI Zhang Z;  
 DR WI; 2001-032160/04.  
 DR P-PSDB; AAB65261.  
 XX  
 PT PRO polynucleotides used to produce polypeptides used to target bioactive  
 PT molecules such as toxins, radiolabels or antibodies, to specific cells,  
 PT to cause targeted cell death.  
 XX  
 PS Claim 2; Fig 251; 935pp; English.  
 CC  
 CC The present invention describes human secreted and transmembrane PRO  
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins can  
 CC be used for targeted delivery of bioactive molecules, such as toxins,  
 CC radiolabels or antibodies, that cause cell death. PRO nucleotide  
 CC sequences, and their fragments, can be used as hybridisation probes, in  
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA and  
 CC DNA. They may also be used to produce transgenic animals which are used  
 CC to develop and screen therapeutically useful reagents. The PRO nucleotide  
 CC and protein sequence can be used for tissue typing and in creating  
 CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to  
 CC AAF44470 represent PCR primers and hybridisation probes used in the  
 CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB5154 to  
 CC AAB5300 represent human PRO polynucleotide and protein sequences given  
 CC in the exemplification of the present invention  
 XX  
 SQ Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 9,91e-263 Length: 1238  
 Score: 271.00 Matches: 271  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 5 Gaps: 0  
 US-09-806-277A-6 (1-271) x AAF44230 (1-1238)  
 QY 1 MetArgG1YaaNleuA1aA1euaValG1YValleu1eSer1eua1aPhe1eSer1eua 20  
 Db 67 ATGAGGGGGGAATCTGGCCCTGTGGCGCTTCTAATACAGCCCTGCTCTCACTGCTG 126  
 QY 21 ProSerG1YH1SPROG1nProA1aG1YaaPaaPaa1aCySserValG1n1leuA1Pro 40  
 Db 127 CCATCTGGACATCTCTCAAGCCGCGCTGGCGATACCGCTGTGTCAGATCTCTGCTCCT 186  
 QY 41 G1YleuA1YaaPaa1aG1YGIuYleuG1YaaPaa1aCySserValG1n1leuA1Pro 60  
 Db 187 GGCCTCAAGAGGATCGCGAG 246  
 QY 61 ValG1YProThrG1YGIuYleuG1YaaPaa1aCySserValG1n1leuA1Pro 80  
 Db 247 GTCCGCCCGGAG 306  
 QY 81 ArgH1aG1YH1leG1YPro1leG1YserYerG1YGIuYleuYleuA1aPaa1eG1YaaPaa1le 100

Db 307 CCTCTGAGAAAATTCGTCCTTAAAGGTGAGAAAGGATTCGGTACATA 366  
 Qy 101 GYProProGlyProAsnGlyGluProGlyLeuProGlyCysSerGlnLeuArgLys 120  
 Db 367 GGAACCCCTGGTCTAATGAGAACCAAGGCTCCCATGTGATGACGACGATGGCAAG 426  
 Qy 121 AAlleglyGluMetAspAsnGlnValSerGlnLeuThrSerGlnLeuLysPheIleLys 140  
 Db 427 GGCATCGGGAGATGACCAACAGGCTCTCAAGCTGACGACGACGACCTCAATCTACAG 486  
 Qy 141 AsnAlaValAlaGlyValArgGluThrGluSerLysIleTyrLeuLeuValLysGluLys 160  
 Db 487 AATGCTGTGCGCGGTGCTGCGAGACGAGACCAAGATCTACTCTGTAAGAGAGAG 546  
 Qy 161 LysAlaGlyTyrAlaAspAlaGlnLeuSerCysGlnGlyArgGlyTyrThrLeuSerMetPro 180  
 Db 547 AAGCCCTACGCGGAGCCCAAGCTGTCTGCGAGGCGCGGGGAGCAGCTGAGCATGCC 606  
 Qy 181 LysAspGluAlaAlaAsnGlyLeuMetAlaAlaTyrLeuAlaGlnAlaGlyLeuAlaArg 200  
 Db 607 AAGGACGAGGCTGCGCAATGGCTGATGGCCGCAATCTGGCGCAAGCCGCTGCGCCGT 666  
 Qy 201 ValPheIleGlyLeuAsnAspLeuGluLysGluGlyAlaPheValTyrSerAspHisSer 220  
 Db 667 GTCTTCATCGGCATCAACGACCTGAGAGAGAGGCGCGCTTCTGTACTCTGACCATCCTC 726  
 Qy 221 ProMetAlaGlyThrPheAsnLysTyrArgSerGlyGluProAsnAlaAlaTyrAspGluLys 240  
 Db 727 CCCAAGCGGACCTTCAACAGTGGCGAGCGGTGAGCCCAATGCTTACGACGAGAG 786  
 Qy 241 AspCysValAlaGluMetValAlaSerGlyGlyTyrPheAspValAlaCysHisThrThrMet 260  
 Db 787 GACTCCGCGAGATGCTGCTGCTGCGGCGGCTGGAACGACGTGGCTGACACCAACATG 846  
 Qy 261 TyrPheMetCysGluPheAspLysGluAsnMet 271  
 Db 847 TACTTCATGTGTGAGTTGACAGAGAAACATG 879  
 RESULT 5  
 ABL88155  
 ID ABL88155 standard; cDNA, 1238 BP.  
 XX ABL88155;  
 AC  
 XX 16-MAY-2002 (first entry)  
 DT  
 XX Human PRO1182 cDNA sequence SEQ ID NO:167.  
 DE  
 XX Human, angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;  
 KW gene therapy; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
 KW angiogenic disorder; cardiovascular disorder; endothelial disorder; cancer;  
 KW age-related macular degeneration; arterial restenosis; angina;  
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
 KW wound healing; chromosome mapping; gene mapping; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200200690-A2.  
 XX  
 PD 03-JAN-2002.  
 XX  
 PF 20-JUN-2001; 2001WO-US019692.  
 XX  
 PR 23-JUN-2000; 2000US-0213637P.  
 PR 20-JUL-2000; 2000US-0219556P.  
 PR 25-JUL-2000; 2000US-0220624P.  
 PR 25-JUL-2000; 2000US-0220664P.  
 PR 28-JUL-2000; 2000US-0220710.  
 PR 02-AUG-2000; 2000US-0222695P.  
 PR 17-AUG-2000; 2000US-00643657.

PR 23-AUG-2000; 2000WO-US023522.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 07-SEP-2000; 2000US-0230978P.  
 PR 18-SEP-2000; 2000US-00664610.  
 PR 18-SEP-2000; 2000US-00665350.  
 PR 24-OCT-2000; 2000US-0242922P.  
 PR 08-NOV-2000; 2000US-00709238.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 10-NOV-2000; 2000WO-US030873.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 20-DEC-2000; 2000US-00747259.  
 PR 22-JAN-2001; 2001US-00767609.  
 PR 28-FEB-2001; 2001US-00796498.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-MAR-2001; 2001WO-US006666.  
 PR 09-MAR-2001; 2001US-00802706.  
 PR 14-MAR-2001; 2001US-00808689.  
 PR 22-MAR-2001; 2001US-00816744.  
 PR 05-APR-2001; 2001US-00828366.  
 PR 10-MAY-2001; 2001US-00854208.  
 PR 10-MAY-2001; 2001US-00854280.  
 PR 25-MAY-2001; 2001US-00866028.  
 PR 25-MAY-2001; 2001US-00866034.  
 PR 25-MAY-2001; 2001US-00870992.  
 PR 30-MAY-2001; 2001US-00870574.  
 PR 30-MAY-2001; 2001WO-US017443.  
 PR 01-JUN-2001; 2001WO-US017800.  
 XX  
 PA (GENETH ) GENENTECH INC.  
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Maresca SA, Pan J, Paoni NF, Stephan JF, Watanabe CK, Williams PM, Wood WT, Ye W;  
 DR WPI; 2002-090516/12.  
 DR P-PDB; ABB84900.  
 XX  
 PT One hundred and eighty seven nucleic acid encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal.  
 XX  
 PS Claim 2; Fig 167; 565bp; English.  
 XX  
 CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to  
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,  
 CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic  
 CC activities, and can be used in gene therapy. The PRO polynucleotides,  
 CC proteins, agonists and antagonists are useful for treating or diagnosing  
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.  
 CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,  
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
 CC angina, myocardial infarction, thrombophlebitis, lymphangitis, tumour  
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
 CC healing. The PRO polynucleotides have applications in molecular biology,  
 CC including use as hybridisation probes, and in chromosome and gene  
 CC mapping. ABL88259 to ABL88267 represent primers and probes used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;  
 XX  
 Alignment Scores:  
 Pred. No.: 9, 91e-263  
 Score: 271.00 Length: 1238  
 Percent Similarity: 100.00% Matches: 271  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 0  
 US-09-806-277A-6 (1-271) x ABL88155 (1-1238)  
 Qy 1 MetArgGlyAsnLeuAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeuLeu 20

Db 67 ATGAGGGGAATCTGCGCCCTGCTGCGCTTCTAATCAGCCTGCGCTTCTGCTGCTG 126  
Qy 21 ProSerGIYH1SPROGI1NPRO1AG1YAHPAPALCYSSERVA1G1N11eLeuValPro 40  
Db 127 CCATCTGGAACATCTCTCAGCCGCGCTGCGATGACGCTGCTGCTGCAATCTCTGCTCCCT 186  
Qy 41 G1YLeuLYSG1YAHPALAG1YGL1YLYSG1YAHP1YSG1YA1APROGI1YARGProGI1YARG 60  
Db 187 GGCCTCAAGAGGAGATGCGGAG 246  
Qy 61 ValGIYProTHG1YGL1YLYSG1YAHPMEG1YAHP1YSG1YGL1YLYSG1YSERVA1GIY 80  
Db 247 GTCGCGCCCAAGGAG 306  
Qy 81 ARGH1SG1YLYSG1YLYSG1YLYSG1YLYSG1YLYSG1YLYSG1YLYSG1YLYSG1YLYSG 100  
Db 307 GCGTATGAG 366  
Qy 101 G1YProProGI1YProAHNG1YGL1YLYSG1YLYSG1YLYSG1YLYSG1YLYSG1YLYSG 120  
Db 367 GGAACCCCTGCTGCTAATGAG 426  
Qy 121 Ala1eGIYGL1YGL1YGL1YGL1YGL1YGL1YGL1YGL1YGL1YGL1YGL1YGL1YGL1Y 140  
Db 427 GCCATCGGAGAGATGAG 486  
Qy 141 AsnAlaValAlaGIYValArg1YThrg1YThrg1YThrg1YThrg1YThrg1YThrg1YThrg 160  
Db 487 AATGCTGTCGCGGCTGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546  
Qy 161 LysAArg1YThrg1YThrg1YThrg1YThrg1YThrg1YThrg1YThrg1YThrg1YThrg 180  
Db 547 AAGCGCTAGCGGAG 606  
Qy 181 LysAArg1YThrg1YThrg1YThrg1YThrg1YThrg1YThrg1YThrg1YThrg1YThrg 200  
Db 607 AAGAGCGAGCGCTGAG 666  
Qy 201 ValPhe1eGIY1YAsnAHP1eGIY1YLYSG1YLYSG1YLYSG1YLYSG1YLYSG1YLYSG 220  
Db 667 GTCCTCATGCGCATCAAG 726  
Qy 221 PrometArgThrgPheAsn1YThrgArgSerGIY1YProAHNAla1YThrg1YThrg1YThrg 240  
Db 727 CCCATGCGGAG 786  
Qy 241 AHPCyValAlaMetValAlaSerGIY1YThrgAHPValAlaCySH1eThrgThrgMet 260  
Db 787 GACTGCGTGAAGATGCTGCGCTGCGGCGGCTGGAACGAGCTGCTGCCACACCATG 846  
Qy 261 TyrPheMetCyGluPheAHP1YSG1YLYSG1YLYSG1YLYSG1YLYSG1YLYSG1YLYSG 271  
Db 847 TACTTCATGCTGAGATTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 879  
RESUT 6  
ABL95644  
ID ABL95644 standard; cDNA; 1238 BP.  
XX ABL95644;  
AC  
XX  
XX 19-JUN-2002 (first entry)  
DE Human anglogenesis related cDNA PRO1182 SEQ ID NO: 167.  
XX  
XX Human anglogenesis; PRO protein; cardiovascularisation; wound; cancer;  
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
KW cardiac; cytosolic; antiangiogenic; hypotensive; vulnery;  
KW antiarteriosclerotic; gene; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200208284-A2.  
XX

PD 31-JAN-2002.  
XX  
XX 09-JUN-2001; 2001WO-US021735.  
XX  
XX 20-JUN-2000; 2000US-0219556P.  
PR 25-JUN-2000; 2000US-0220624P.  
PR 25-JUN-2000; 2000US-0220664P.  
PR 28-JUN-2000; 2000US-0220710.  
PR 02-AUG-2000; 2000US-0222695P.  
PR 17-AUG-2000; 2000US-02643657.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 07-SEP-2000; 2000US-0230978P.  
PR 18-SEP-2000; 2000US-02664610.  
PR 18-SEP-2000; 2000US-02665350.  
PR 24-OCT-2000; 2000US-0242922P.  
PR 08-NOV-2000; 2000US-02709238.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-02747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 22-JAN-2001; 2001US-00767609.  
PR 28-FEB-2001; 2001US-00796498.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006686.  
PR 09-MAR-2001; 2001US-00802706.  
PR 14-MAR-2001; 2001US-00808689.  
PR 22-MAR-2001; 2001US-00816744.  
PR 05-APR-2001; 2001US-00828366.  
PR 10-MAY-2001; 2001US-00854288.  
PR 10-MAY-2001; 2001US-00854280.  
PR 25-MAY-2001; 2001US-00866028.  
PR 25-MAY-2001; 2001US-00866034.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 30-MAY-2001; 2001US-00870574.  
PR 30-MAY-2001; 2001WO-US017443.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
XX  
XX (GETH ) GENENTECH INC.  
PA (BAKE ) BAKER K P.  
PA (PERR ) PERRARA N.  
PA (GERB ) GERBER H.  
PA (GERR ) GERRITSEN M E.  
PA (GODD ) GODDARD A.  
PA (GODO ) GODOWSKI P J.  
PA (GURN ) GURNEY A L.  
PA (HILL ) HILLMAN K J.  
PA (HILL ) HILLMAN S A.  
PA (MARS ) MARSTERS S A.  
PA (PANU ) PAN J.  
PA (PAON ) PAONI N P.  
PA (STEP ) STEPHAN J F.  
PA (WATA ) WATANABE C K.  
PA (WILL ) WILLIAMS P M.  
PA (WOOD ) WOOD W I.  
XX  
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,  
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,  
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,  
XX  
XX WPI: 2002-171999/22.  
DR P-PsDB; ABB95506.  
XX  
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
PT infarction), endothelial or angiogenic disorders in a mammal.  
XX  
XX Claim 1; Fig 167; 567pp; English.  
XX  
XX The present invention provides the protein and coding sequences of human  
CC PRO proteins. These are useful for treating or diagnosing a  
CC cardiovascular, endothelial or angiogenic disorder, including cardiac

CC hypertrophy, trauma, cancer, age-related macular degeneration,  
CC atherosclerosis, hypertension, arterial resection, rheumatoid arthritis,  
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
CC healing. The present sequence is a coding sequence of the invention  
XX

Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	9,91e-263	Length:	1238
Score:	271.00	Matches:	271
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-806-277a-6 (1-271) x ABL95644 (1-1238)

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QY 1 MetArgGlyAenLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeu 20
Db 67 ATGAGGGGGAATCTGGCCCTGCTGAGCCTTCTAATCAGCCTGCTCTCTCTGCTG 126
QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40
Db 127 CCATCTGGACATCTCTCAGCCGCGCTGGCCATGACGCTGCTCTGTCAGATCTCTGCTCC 186
QY 41 GlyLeuLysGlyAspAlaGlyGlyLysGlyAspLysGlyValAspProGlyArg 60
Db 187 GGCTCTCAAGGGGATCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246
QY 61 ValGlyProThrGlyGlyLysGlyAspMetGlyAspLysGlyGlnLysSerValGly 80
Db 247 GTCGGCCCAACGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 306
QY 81 ArgHisGlyLysIleGlyProIleGlySerIleGlyLysGlyAspSerGlyAspIle 100
Db 307 CGTATGGAGAAATTTGGTCCATTGGCTCTAAGGTGAGAGAGAGAGAGAGAGAGAGAGATA 366
QY 101 GlyProProGlyProAsnGlyGlyLysProGlyLysProGlyCysSerGlnLeuArgLys 120
Db 367 GGACCCCTGCTCTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 426
QY 121 AlaIleGlyLysMetAspAsnGlnValSerGlnLeuThrSerGlnLeuLysPheIleLys 140
Db 427 GCCATCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 486
QY 141 AsnAlaValAlaGlyValArgGlyThrGlnSerIleIleThrLeuLeuValLysGlyLys 160
Db 487 AATCTGTGCGCGGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546
QY 161 LysArgGlyAlaAspAlaGlnLeuSerCysGlnGlyValArgGlyGlyThrLeuSerMetPro 180
Db 547 AAGCGCTACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 606
QY 181 LysAspGlyAlaAlaAsnGlyLysMetAlaAlaThrLeuAlaGlnAlaGlyLysAlaArg 200
Db 607 AAGGACGAGGCTGCGCAATGCGCTATGCGCCATACCTGGGCGCAAGCGGCTGCGCCGT 666
QY 201 ValPheIleGlyLysLeuAspLeuGlyLysGlyLysValPheValIleThrSerAspHisSer 220
Db 667 GTCTTCATCGGATCAACGAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 726
QY 221 ProMetArgThrPheAsnLysTrpArgSerGlyValProAsnAsnAlaThrAspGluGlu 240
Db 727 CCCATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 786
QY 241 AspCysValGlnMetValAlaSerGlyGlyTrpAsnAspValAlaCysHisIleThrMet 260
Db 787 GACTGCGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 846
QY 261 TyrPheMetCysGlyLysPheAspLysGlyAsnMet 271
Db 847 TACTTCATGTGTGAGTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 879
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RESULT 7
ID ACA64399 standard; cDNA, 1238 BP.
XX
AC ACA64399;
XX
DT 17-JUN-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1182 cDNA.
XX
KW Human; secreted and transmembrane protein; cytosolic; anti-HIV;
KW Viruslike; hepatotropic; antiinflammatory; neuroprotective; gene therapy;
KW PRO; pharmaceutical; diagnostic; biosensor; bioreactor; malignancy;
KW cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; Leukemia;
KW lymphoma; hepatitis B; multiple sclerosis; Crohn's disease;
KW drug screening; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003003531-A1.
XX
PD 02-JAN-2003.
XX
PF 19-NOV-2001; 2001US-0089734.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 25-MAR-1998; 98US-0078810P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.
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PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
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PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
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PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088867P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
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PR 18-JUN-1998; 98US-0089801P.  
PR 18-JUN-1998; 98US-0089907P.  
PR 18-JUN-1998; 98US-0089908P.  
PR 16-SEP-1998; 98MO-US019330.  
PR 17-SEP-1998; 98MO-US019437.  
PR 07-OCT-1998; 98MO-US021141.  
PR 01-DEC-1998; 98MO-US025108.  
PR 05-JAN-1999; 99MO-US000106.  
PR 08-MAR-1999; 99MO-US005028.  
PR 02-JUN-1999; 99MO-US012522.  
PR 15-SEP-1999; 99MO-US021090.  
PR 15-SEP-1999; 99MO-US021547.  
PR 30-NOV-1999; 99MO-US028313.  
PR 01-DEC-1999; 99MO-US028301.  
PR 01-DEC-1999; 99MO-US028634.  
PR 16-DEC-1999; 99MO-US030095.  
PR 20-DEC-1999; 99MO-US030911.  
PR 05-JAN-2000; 2000MO-US000219.  
PR 06-JAN-2000; 2000MO-US000376.  
PR 11-FEB-2000; 2000MO-US003565.  
PR 18-FEB-2000; 2000MO-US004341.  
PR 22-FEB-2000; 2000MO-US004414.  
PR 24-FEB-2000; 2000MO-US004914.  
PR 24-FEB-2000; 2000MO-US005004.  
PR 02-MAR-2000; 2000MO-US005841.  
PR 10-MAR-2000; 2000MO-US006319.  
PR 15-MAR-2000; 2000MO-US006894.  
PR 20-MAR-2000; 2000MO-US007377.  
PR 30-MAR-2000; 2000MO-US008439.  
PR 15-MAY-2000; 2000MO-US013358.  
PR 17-MAY-2000; 2000MO-US013705.  
PR 22-MAY-2000; 2000MO-US014042.  
PR 30-MAY-2000; 2000MO-US014941.  
PR 02-JUN-2000; 2000MO-US015264.  
PR 28-JUN-2000; 2000MO-US020710.  
PR 11-AUG-2000; 2000MO-US022031.  
PR 23-AUG-2000; 2000MO-US023522.  
PR 24-AUG-2000; 2000MO-US023328.  
PR 08-NOV-2000; 2000MO-US030952.  
PR 01-DEC-2000; 2000MO-US032678.  
PR 28-FEB-2001; 2001MO-US006520.  
PR 01-JUN-2001; 2001MO-US017800.  
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PR 29-JUN-2001; 2001MO-US021066.  
PR 09-JUL-2001; 2001MO-US021735.  
PR 28-AUG-2001; 2001US-00941992.  
XX  
XX (GERTH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Fong S, Gerber H, Gertlsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Kijavlin IV, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WT;  
PI Zhang Z;  
XX  
XX WPI; 2003-352829/33.  
XX P-PSDB; AB072552.  
XX  
XX New genes and secreted and transmembrane polypeptides (e.g. PRO183 or  
XX PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's  
XX sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's  
XX disease.  
XX  
XX Claim 1; Fig 251; 663pp; English.  
XX  
XX The invention describes a new isolated nucleic acid molecule comprising  
XX the full length coding sequence of the DNA deposited with the American  
XX Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PHA, 819-PHA,  
XX 209439, 203135, etc.) or a sequence with at least 80% identity to a DNA  
XX encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are  
XX useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These  
XX are particularly useful for detecting or treating e.g. malignancies or  
XX cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma,

CC leukemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's  
CC disease in mammals. The PRO polypeptides are useful in drug screening,  
CC particularly as targets for therapeutic intervention in these diseases,  
CC and in the diagnostic determination of the presence of these diseases.  
CC The PRO polypeptides are also useful as molecular weight markers, or for  
CC chromosome identification. The PRO genes are useful as hybridisation  
CC probes, or for screening libraries of human cDNA, genomic DNA or mRNA.  
CC The PRO genes may also be used in gene therapy, particularly for  
CC replacing a defective gene. This sequence encodes a novel human secreted  
CC and transmembrane PRO polypeptide  
XX

XX Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9,91e-263 Length: 1238  
Score: 271.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 8 Gaps: 0

US-09-806-277A-6 (1-271) x ACA64399 (1-1238)

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DB 127 CCATCTGGACATCTCTCAAGCGGCTGGCGATACCGCTCTCTGTGGCAGATCTCTGCT 186  
QY 41 GILYeuLYSGIYAspAlaGILYGLuLYSGIYAspLYSGIYAlaProGILYARProGILYArg 60  
DB 187 GGCCCTCAAGGGAGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246  
QY 61 ValGILYProThrGILYGLuLYSGIYAspMetGILYAspLYSGIYGLuLYSGIYSerValGILY 80  
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QY 81 ArgHISGILYSLIleGILYProIleGILYSerLYSGIYGLuLYSGIYAspSerGILYAspIle 100  
DB 307 CGTCATGGAAAAATTTGGTCCCATTTGGCTCTAAAGGTGAGAAAGAGATTCGGTGACATA 366  
QY 101 GILYProProGILYProAsnGILYGLuProGILYLeuProCYSGILYCYSerGILuLeuArgLYS 120  
DB 367 GGACCCCTGCTCTTAATGAG 426  
QY 121 AlaIleGILYGLuMetAspAsnGILuValSerGILuLeuThrSerGILuLeuValPheIleLYS 140  
DB 427 GCCATCGGGAGATGAGACACAGAGTCTCTAGCTGACAGAGAGAGAGAGAGAGAGAGAG 486  
QY 141 AsnAlaValAlaGILYValArgGILuThrGILuSerLYSLIleTYrLeuLeuValLYSGILuGLu 160  
DB 487 AATGCTGTGCGCGGTGTGGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546  
QY 161 LYsARGLTYrAlaAspAlaGILuLeuSerCYSGILuGILYArgGILYThrLeuSerMetPro 180  
DB 547 AAGGCTAAGCGGAG 606  
QY 181 LYsAspGILuAlaIleAsnGILuMetValAlaTYrLeuAlaGILuAlaGILYLeuAlaArg 200  
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QY 241 AspCYsValGILuMetValAlaSerGILYGLYrPheAsnAspValAlaCYSHIleThrThMet 260

DB 787 GACTGCGTGGATGATGTCCTCGGGCGGCTGTGAACAGACGTCGCTGCACACACCATG 846  
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DB 847 TACTTCATGTGTGAGTTTGACAGAGAACTG 879

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XX  
AC ABX80858;  
XX  
DT 22-APR-2003 (first entry)  
XX  
DE Human secreted/cranemembrane protein cDNA, #144.  
XX  
KW Human; gene; ss; PRO; secreted; transmembrane; pharmaceutical;  
KW diagnostic; biosensor; bioreactor; tumour; therapeutic; gene therapy;  
KW tumour-associated antigenic target; TAT; ADEPT;  
KW antibody-dependent enzyme mediated prodng therapy; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN US2003027162-A1.  
XX  
PD 06-FEB-2003.  
XX  
PE 15-NOV-2001; 2001US-00997428.  
XX  
PR 16-JUN-1997; 97US-0049787P.  
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PR 28-JUL-2000; 2000US-0020710P.  
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PR 23-AUG-2000; 2000US-0023522P.  
PR 24-AUG-2000; 2000US-0023328P.

## Alignment Scores:

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Score: 271.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
DB: 8  
Gaps: 0

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Db 187 GGCCTCAAGAGGATGCGGAG 246  
QY 61 ValGlyProThrGlyValGlyValGlyValAspMetCysAspIleGlyValGlyValGly 80  
Db 247 GTGGCCCCACGAG 306  
QY 81 ArgHisGlyValIleGlyProIleGlySerIleGlyValGlyValAspSerGlyValIle 100  
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QY 101 GlyProProGlyProAsnGlyValProGlyLeuProCysGluCysSerGlnLeuArgLys 120  
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Db 427 GCCATCGGGAGATGAGACACAGCTCTCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 486  
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XX  
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XX  
XX cDNA encoding human PRO1182 polypeptide.  
XX  
XX Human; PRO polypeptide; secreted protein; transmembrane protein;  
XX genetic disorder; antibacterial; immunosuppressive; transgenic;  
XX gene therapy; gene; ss.  
OS Homo sapiens.  
XX  
XX US2002127576-A1.  
PN

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XX 12-SEP-2002.
XX 14-NOV-2001; 2001US-00991073.
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XX 17-OCT-1997; 97US-0062250P.
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XX 07-OCT-1998; 98WO-US021141.
XX 01-DEC-1998; 98WO-US025108.
XX 05-JAN-1999; 99WO-US000106.
XX 08-MAR-1999; 99WO-US005028.
XX 02-JUN-1999; 99WO-US012252.
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XX 01-DEC-1999; 99WO-US028634.
XX 16-DEC-1999; 99WO-US030095.
XX 20-DEC-1999; 99WO-US030911.
XX 06-JAN-2000; 2000WO-US000219.
XX 06-JAN-2000; 2000WO-US000376.
XX 11-FEB-2000; 2000WO-US003565.
XX 18-FEB-2000; 2000WO-US004341.

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PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
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PR 30-MAY-2000; 2000WO-US015641.
PR 02-JUN-2000; 2000WO-US015694.
PR 28-JUN-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
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PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers J, Eaton DL,
XX Ferrara N, Fong S, Gerber H, Gerltzen ME, Goddard A, Godowski PJ,
XX Grimaldi JC, Gurney AL, Kijavini RJ, Napier MA, Pan J, Paoni NF,
XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,
XX Zhang Z;
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XX WPI; 2003-340824/32.
XX
XX P-PSDB; ABC025998.
XX
XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
XX and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
XX and are therapeutically useful for enhancing immune responses.
XX
XX Claim 2; Fig 251; 661pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
XX polypeptides, and the polynucleotide sequences encoding them. The PRO
XX polypeptides are secreted and transmembrane proteins. The PRO
XX polypeptides are useful for detecting other PRO polypeptides, for linking
XX bioactive molecules to cells expressing PRO polypeptides, for modulating
XX biological activities of cells expressing PRO polypeptides, and for
XX identifying agonists or antagonists. The polynucleotide sequences
XX encoding PRO polypeptides are useful as hybridisation probes, in
XX chromosome and gene mapping, in the generation of antisense RNA and DNA,
XX in the preparation of PRO polypeptides, for generating transgenic animals
XX or knockout animals, to construct hybridisation probes for mapping the
XX gene which encodes the PRO polypeptide, and for the genetic analysis of
XX individuals with genetic disorders, in gene therapy, for chromosome
XX identification, as chromosome markers, and for generating probes for PCR,
XX Northern analysis, Southern analysis and Western analysis. The present
XX sequence encodes a human PRO polypeptide of the invention. Note: The
XX sequence data for this patent was obtained in electronic format directly
XX from the USPTO web site at seqdata.uspto.gov/psipdidentry.html
XX
XX
XX Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 9,91e-263 Length: 1238
XX Score: 271.00 Matches: 271
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 8 Gaps: 0
XX
XX
XX US-09-806-277A-6 (1-271) x ACD44367 (1-1238)

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QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
Db 127 CCATCTTGACATCTCTCAACCGGCTGGCGATACGCTCTCTCTGTCAGATCTCTGCTCT 186  
QY 41 GlyLeuYsgGlyAspAlaGlyValYsgGlyAspYsgGlyValaProGlyYargProGlyYarg 60  
Db 187 GGCCTCAAGAGGGGATGGCGGAGAGAGAGAGCAAAAGCGCGCCCGGAGCGGCTGGAGAG 246  
QY 61 ValGlyProThrGlyValYsgGlyAspMetGlyAspYsgGlyValYsgGlySerValGly 80  
Db 247 GTCCGCCCCACGGGAGAAAAGAGACATGGGGGCAAAAGACAGAAAGGACAGTGGCGT 306  
QY 81 ArgHisGlyValIleGlyProIleGlySerYsgGlyValYsgGlyAspSerGlyAspIle 100  
Db 307 CGTCATGGAAAATTGGTCCCATTTGGCTCTAAAGGTGAAAAGAGATTCCGGTGACATA 366  
QY 101 GlyProProGlyProAsnGlyValProGlyLeuProCysGlyCysSerGlnLeuArgLys 120  
Db 367 GGACCCCTGGTCCATGAAGAGAACCAAGCCCTCCCATGTGAGTGACGACCTGGGCAAG 426  
QY 121 AlaIleGlyGluMetAspAsnGlnValSerGlnLeuThrSerGlnLeuLeuPheIleLys 140  
Db 427 GCCATCGGGGAGATGGACCAACAGGTCTCTCAGCTGACGACGAGCTCAAGTTCATCAAG 486  
QY 141 AsnAlaValAlaGlyValArgGlyValArgGlySerValIleTyrLeuLeuValYsgGlu 160  
Db 487 AATGCTGTCCCGGTGTGTGGGAGACGAGAGCAAGATCTTCTGCTGTAGAGAGAG 546  
QY 161 LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyArgGlyTyrLeuSerMetPro 180  
Db 547 AAGGCTACGGGAGAGCCGACGTCTCTGCCAGGGCCCGGGGGGACGCTGAGCATGCC 606  
QY 181 LysAspGluAlaAlaSerGlyLeuMetAlaAlaTyrLeuAlaGlnAlaGlyLeuAlaArg 200  
Db 607 AAGGACGAGGCTCCAAATGGCTGTATGGCCGATCTCCGCGCAAGCCGGCTGGCCCTG 666  
QY 201 ValPheIleGlyIleAsnAspLeuGluYsgGluGlyAlaPheValTyrSerAspHisSer 220  
Db 667 GTCTTCATGGCATCAACGACTGGAGAAAGAGGGCGCTCTGCTTACTCTGACCATCTCC 726  
QY 221 ProMetArgThrPheAsnLysIleTyrArgSerGlyGluProAsnAsnAlaTyrAspGlu 240  
Db 727 CCCATGGCGGACCTTCAACAGTGGCGGAGCGGTAGCCCAACAAATGCCCTACGAGAGAG 786  
QY 241 AspCysValGluMetValAlaSerGlyGlyTyrAsnAspValAlaCysHisThrThrMet 260  
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QY 261 TyrPheMetCysGluPheAspYsgGluAsnMet 271  
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RESULT 10  
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XX  
AC ABX79538;  
XX  
DT 17-APR-2003 (first entry)  
XX  
DE Human secreted/transmembrane protein cDNA, #144.  
XX  
KW Human; gene; ss; PRO; secreted; transmembrane; signal peptide;  
KW pharmaceutical; diagnostic; biosensor; bioreactor; tumour; therapeutic;  
KW colon cancer; lung cancer; breast cancer; cancer; gene therapy.  
XX  
OS Homo sapiens.  
XX

PN US2002142961-A1.  
XX 03-OCT-2002.  
PD 19-NOV-2001; 2001US-00989721.  
XX 16-JUN-1997; 97US-0049787P.  
XX 17-OCT-1997; 97US-0062250P.  
PR 05-NOV-1997; 97WO-US02006P.  
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PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 02-JUN-1999; 99WO-US012252.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.

PR 18-FEB-2000; 2000WO-US004341.  
 PR 22-FEB-2000; 2000WO-US004414.  
 PR 24-FEB-2000; 2000WO-US004914.  
 PR 24-FEB-2000; 2000WO-US005004.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 10-MAR-2000; 2000WO-US006319.  
 PR 15-MAR-2000; 2000WO-US006884.  
 PR 20-MAR-2000; 2000WO-US007377.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 15-MAY-2000; 2000WO-US013358.  
 PR 17-MAY-2000; 2000WO-US013705.  
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 PR 28-JUL-2000; 2000WO-US020710.  
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 PR 20-JUN-2001; 2001WO-US019692.  
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 PR 09-JUL-2001; 2001WO-US021735.  
 PR 28-AUG-2001; 2001US-00941992.  
 XX  
 PA (GETH ) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Fong S, Garber H, Gertlesen ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NP;  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams FM, Wood WI;  
 PI Zhang Z;  
 XX  
 DR WPI; 2003-155950/15.  
 DR P-PSDB; ABUS9007.  
 XX

PT New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184,  
 PT PRO361 or PRO846) useful as targets for therapeutic intervention in  
 PT cancers (e.g. lung or breast cancers), or for diagnosing these cancers.  
 XX  
 PS Claim 2; Fig 251; 647pp; English.

CC The invention discloses isolated PRO secreted/transmembrane polypeptides  
 CC comprising a sequence without signal peptide and the nucleic acid  
 CC encoding them. The polypeptides can be used to raise antibodies that  
 CC specifically bind to the PRO polypeptide, for linking a bioactive  
 CC molecule to a cell expressing a PRO protein and for modulating at least  
 CC one biological activity of a cell. The PRO polypeptides or  
 CC polynucleotides are also useful as pharmaceuticals, diagnostics,  
 CC biosensors or bioreactors, for detecting or treating e.g. tumors in  
 CC mammals, e.g. humans, dogs, cats, cattle, horses, pigs, goats or  
 CC rabbits as targets for therapeutic intervention in certain cancers (e.g.  
 CC colon, lung or breast cancers) and diagnostic determination of the  
 CC presence of these cancers. The PRO polypeptides are also useful as  
 CC molecular weight markers or for chromosome identification. The PRO genes  
 CC are useful as hybridization probes or for screening libraries of human  
 CC cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene  
 CC therapy, particularly for replacing a defective gene. The sequences  
 CC presented in ABX79290-ABX79675 are the genes encoding, the primers  
 CC amplifying and the probes detecting the PRO polynucleotides of the  
 CC invention. Note: The sequence data for this patent is also available in  
 CC electronic format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)

XX Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 9,91e-263 Length: 1238  
 Score: 271.00 Matches: 271  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0

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 QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuAlaPro 40  
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 Db 367 GAAACCCCTGTGCTTATGAGAACAGAGCCCTCCATGTGATGACAGCCAGCTGGCCAG 426  
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 AC  
 DT 16-JUL-2003 (first entry)  
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 KW PRO943; PRO1133; PRO311; PRO317; PRO363; PRO5723; PRO1114; PRO3301;  
 KW PRO9940; PRO1181; PRO1170; PRO361; PRO846; bioactive molecule; toxin;

KM radiolabel; antibody; cell death; tissue typing; gene therapy;  
KM cytostatic; chromosome mapping; gene mapping; transgenic animal;  
KM knockout animal; immunohistochemical staining; gene; ss.  
XX Homo sapiens.  
XX US2003022187-A1.  
XX  
XX 30-JAN-2003.  
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XX 14-NOV-2001; 2001US-00993667.  
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PR 01-DEC-1998; 98WO-US025108.  
PR 22-DEC-1998; 98US-0113296P.  
PR 05-JAN-1999; 99WO-US000106.  
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PR 08-MAR-1999; 99WO-US005028.  
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PR 15-SEP-1999; 99WO-US021547.  
PR 08-OCT-1999; 99US-0158663P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
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PR 16-DEC-1999; 99WO-US030095.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 15-MAY-2000; 2000WO-US013358.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000US-0215264.  
PR 23-JUN-2000; 2000US-021637P.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.

Alignment Scores:

Pred. No.: 9 91e-263 Length: 1238  
Score: 271.00 Matches: 271  
Percent Similarity: 100.00% Conservaive: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-09-806-277A-6 (1-271) x ACA93559 (1-1238)

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Db 67 ATGAGGGGGAATCGGCGCTGTGGCGCTTCTATCATCGCTCGGCTTCTCTGACGCTG 126  
QY 21 ProSerGlyHisProGlnProCAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
Db 127 CCACTGTGAATCTCTCGCGGCTGTGGGAGCATGCGCTCTGTGCGATCTCTGACCTCC 186  
QY 41 GlyLeuIleGlyAspAlaGlyGlyValGlyAspIleGlyValAlaProGlyValGlyValGly 60  
Db 187 GGCCTCAAGGAGATGCGGAG 246  
QY 61 ValGlyProThrGlyGlyValGlyValGlyValGlyValGlyValGlyValGlyValGly 80  
Db 247 GTCGCGCCCGCGGAG 306  
QY 81 ArgHisGlyValIleGlyValGlyValGlyValGlyValGlyValGlyValGlyValGly 100  
Db 307 CGTCAATGGAATAATGTGCTCCATTTGGCTTAAAGGTGAGAGAGAGAGAGAGAGAGAG 366

QY 101 GlyProProGlyProAunGlyGlyProGlyLeuProCysGlyCysSerGlnLeuArglys 120  
Db 367 GAGACCCCTGTGCTTATGAG 426  
QY 121 AlaIleGlyIleMetAunGlnValSerGlnLeuThrSerGlyLeuIleValPheIleVal 140  
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QY 141 AsnAlaValAlaGlyValArgGlyThrGlySerIleIleTyrLeuLeuValIleGlyGlu 160  
Db 487 AATGCTGTCCCGCGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546  
QY 161 LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyValGlyIleThrLeuSerMetPro 180  
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QY 181 LysAspGlnAlaAlaAunGlyLeuMetAlaAlaTyrLeuAlaGlnAlaGlyLeuAlaArg 200  
Db 607 AAGGACGAGGCTGCGAATGCGCTGATGCGCGATACCTGCGAGAGAGAGAGAGAGAGAG 666  
QY 201 ValPheIleGlyIleAunAunLeuGlyGlyGlyGlyValAlaPheValTyrSerAunPheSer 220  
Db 667 GTCTTCATGCGGATCAACGAG 726  
QY 221 ProMetArgThrPheAunIleTyrPargSerGlyGlyProAunAunAlaTyrAunGlyGlu 240  
Db 727 CCCATCGGAG 786  
QY 241 AspCysValGlyIleMetValAlaSerGlyGlyIleTyrAunAunValAlaCysHisIleThrMet 260  
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QY 261 TyrPheMetCysGlyIleAunAunIleGlyIleMet 271  
Db 847 TACTTCATGTGTGAGTTGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 879

RESULT 12

ID ABX81241 standard; DNA; 1238 BP.

AC ABX81241;

DT 22-APR-2003 (first entry)

XX Novel human secreted or transmembrane protein PRO1155 DNA.

XX Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
XX cardiac insufficiency disorder; cancer; tumour; immune response;  
XX adrenal cortical capillary endothelial growth; c-fos induction;  
XX vascular endothelial growth factor inhibition; VEGF inhibition;  
XX endothelial cell growth inhibitor; T-lymphocytes stimulation;  
XX retinal neurons cell survival; rod photoreceptor cell survival;  
XX retinal disorder; retinitis pigmentosa; kidney disorder;  
XX mammalian kidney mesangial cell proliferation; Berger disease;  
XX dermatitis; hemiplegia; Crohn's disease; chondrocyte proliferation;  
XX chondrocyte redifferentiation; sports injury; arthritis; gene; ds.

OS Homo sapiens.

PN US2003027985-A1.

PD 06-FEB-2003.

PF 14-NOV-2001; 2001US-00990562.

XX 16-JUN-1997; 97US-0049787P.  
XX 17-OCT-1997; 97US-0062250P.  
XX 05-NOV-1997; 97WO-US020069.  
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 PR 22-DEC-1998; 98US-0113296P.  
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 PR 12-MAR-1999; 99US-0144758P.  
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 PR 26-JUL-1999; 99US-0144758P.  
 PR 28-JUL-1999; 99US-0144758P.  
 PR 17-AUG-1999; 99US-0149396P.  
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 PR 08-OCT-1999; 99US-0158663P.  
 PR 30-NOV-1999; 99US-0158663P.  
 PR 30-NOV-1999; 99US-0158663P.

PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 15-MAY-2000; 2000WO-US013358.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.

## Alignment Scores:

Pred. No.:	9,91e-263	Length:	1238
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Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
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US-09-806-277A-6 (1-271) x ABX81241 (1-1238)

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QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
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QY 41 GlyLeuLeuGlyAspAlaGlyGlyLeuGlyAspGlyValAspGlyValProGlyValArg 60  
Db 187 GGCCTCAAGAGGAGATGCGGAG 246  
QY 61 ValGlyProThrGlyGlyLeuGlyAspMetGlyAspGlyValGlyValGlySerValGly 80  
Db 247 GTCCGCCCCCAGGGAG 306  
QY 81 ArgHisGlyValLeuGlyProIleGlySerLeuGlyValGlyValGlyValGlyValGly 100  
Db 307 CGTCAATGAGAAATGCTCCCATTTGGCTCTAAGGTGAGAAAGGAGATTCCGCTGACATA 366  
QY 101 GlyProProGlyProAsnGlyGluProGlyLeuProCysGlyGlyCysSerGlnLeuArgLys 120  
Db 367 GGAACCCCTGGTCTTAATGAGAACACAGGCTCCCATGTGAGTCAAGCCAGCTCGCAAG 426  
QY 121 AlaIleGlyGlyMetAspAsnGlnValSerGlnLeuThrSerGlyLeuLysPheIleLys 140  
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QY 181 LysAspGlyAlaAlaAsnGlyLeuMetAlaAlaTyrLeuAlaGlnAlaGlyLeuAlaArg 200  
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QY 201 ValIleIleGlyIleAsnAspLeuGlyValGlyValAlaPheValTyrSerAspHisSer 220

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Db 727 CCATGCGGACCTTCAACAGAGTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 786  
QY 241 AspCysValGlyMetValAlaSerGlyGlyTyrPheAspValAlaCysHisThrMet 260  
Db 787 GACTGCGTGAAGATGTGTGCGCTCGGCGGCTGGAACGACGTGGCTGCGCACACCACTATG 846  
QY 261 TyrPheMetCysGluPheAspLysGluAsnMet 271  
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AC ACA93057;  
XX 16-JUN-2003 (first entry)  
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XX Novel human secreted and transmembrane protein PRO1182 cDNA.  
DE  
XX Human; secreted and transmembrane protein; PRO; nocrotic;  
KW neuroprotective; antiparkinsonian; cytoskeletal; gene therapy;  
KW chromosome mapping; gene mapping; transgenic animal; knock-out animal;  
KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;  
KW gene; ss.  
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OS Homo sapiens.  
XX  
XX US2003017476-A1.  
XX  
XX 23-JAN-2003.  
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XX 20-NOV-2001; 2001US-00989724.  
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PR 17-OCT-1997; 97US-0062250P.  
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PR 24-NOV-1997; 97US-0066770P.  
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PR 18-AUG-1998; 98US-0096949P.  
PR 18-AUG-1998; 98US-0096950P.  
PR 18-AUG-1998; 98US-0096950P.  
PR 18-AUG-1998; 98US-0096960P.  
PR 18-AUG-1998; 98US-0097022P.  
PR 19-AUG-1998; 98US-0097141P.  
PR 20-AUG-1998; 98US-0097218P.  
PR 24-AUG-1998; 98US-0097661P.  
PR 26-AUG-1998; 98US-0097952P.  
PR 26-AUG-1998; 98US-0097954P.  
PR 26-AUG-1998; 98US-0097955P.  
PR 26-AUG-1998; 98US-0097971P.  
PR 26-AUG-1998; 98US-0097974P.  
PR 26-AUG-1998; 98US-0097978P.  
PR 26-AUG-1998; 98US-0097979P.  
PR 26-AUG-1998; 98US-0097986P.  
PR 26-AUG-1998; 98US-0098014P.  
PR 31-AUG-1998; 98US-0098525P.  
PR 16-SEP-1998; 98US-0100634P.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98US-0100858P.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 01-DEC-1998; 98WO-US025108.  
PR 22-DEC-1998; 98US-0113286P.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 12-MAR-1999; 99US-0123957P.  
PR 02-JUN-1999; 99WO-US012252.  
PR 23-JUN-1999; 99US-0141037P.  
PR 07-JUL-1999; 99US-0143048P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 28-JUL-1999; 99US-0146222P.  
PR 17-AUG-1999; 99US-0149396P.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 08-OCT-1999; 99US-0158663P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028634.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 02-MAR-2000; 2000WO-US005004.  
PR 04-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 15-MAY-2000; 2000WO-US013358.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 23-JUN-2000; 2000US-0213637P.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023582.

Alignment Scores: 9.91e-263  
Pred. No.:  
Length: 1238

Score: 271.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 8 Gaps: 0

US-09-806-277A-6 (1-271) x ACA93057 (1-1238)

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QY 1 MetArgGIYAenLeuAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeuLeu 20
Db 67 ATGAGGGGGAATCTGGCCCTGGTGGCGCTTCTAAACACCTGGCCCTCTCTCACTGCTG 126
QY 21 ProSerGIYHISProGlnProAlaGlyAAspAAspAAspAAspAAspAAspAAspAAsp 40
Db 127 CCATCTGACATCTCTCAACCCGGCTGGCGATGACGCTCTCTCTGTCAGATCTCTGCTCCT 186
QY 41 GILYLeuLYGlyAAspAAGlyGlyLYGlyAAspLYGlyAAspLYGlyAAspLYGlyAAsp 60
Db 187 GGCCCTCAAGGGGAGTGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246
QY 61 ValGlyProThrGlyGlyLYGlyAAspMetGlyAAspLYGlyLYGlyLYGlyLYGlyLYGly 80
Db 247 GTCCGCCCCACGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 306
QY 81 ArgHISGlyLYGlyLYGlyProIleGlySerLYGlyLYGlyLYGlyLYGlyLYGlyLYGly 100
Db 307 CGTCATGAGAAATTTGGTCCCATTTGGCTCTAAAGGTGAGAAAGAGATTCGGTGACATA 366
QY 101 GlyProProGlyProAAspGlyGlyLYGlyLYGlyLYGlyLYGlyLYGlyLYGlyLYGly 120
Db 367 GGAGCCCTGCTGCTCTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 426
QY 121 AlaIleGlyGlyMetAAspAAspGlnValSerGlnLeuThrSerGlyLYGlyLYGlyLYGly 140
Db 427 GCCATCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 486
QY 141 AAspAAspAAspAAspAAspAAspAAspAAspAAspAAspAAspAAspAAspAAspAAsp 160
Db 487 AATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 546
QY 161 LYAAspGlyLYGlyAAspAAspAAspAAspAAspAAspAAspAAspAAspAAspAAsp 180
Db 161 LYAAspGlyLYGlyAAspAAspAAspAAspAAspAAspAAspAAspAAspAAspAAsp 180
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Db 181 LYAAspGlyLYGlyAAspAAspAAspAAspAAspAAspAAspAAspAAspAAspAAsp 200
QY 201 ValPheIleGlyLYGlyAAspAAspAAspAAspAAspAAspAAspAAspAAspAAsp 220
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QY 221 ProMetArgThrPheAAspLYGlyLYGlyLYGlyLYGlyLYGlyLYGlyLYGlyLYGly 240
Db 221 ProMetArgThrPheAAspLYGlyLYGlyLYGlyLYGlyLYGlyLYGlyLYGlyLYGly 240
QY 241 AAspCysValGlyMetValAAspGlyLYGlyLYGlyLYGlyLYGlyLYGlyLYGlyLYGly 260
Db 241 AAspCysValGlyMetValAAspGlyLYGlyLYGlyLYGlyLYGlyLYGlyLYGlyLYGly 260
QY 261 TyrPheMetCysGlyLYGlyLYGlyLYGlyLYGlyLYGlyLYGlyLYGlyLYGlyLYGly 271
Db 261 TyrPheMetCysGlyLYGlyLYGlyLYGlyLYGlyLYGlyLYGlyLYGlyLYGlyLYGly 271
QY 847 TACTTCATGTGTGAGTTTGAACAGAGAAACATG 879
Db 847 TACTTCATGTGTGAGTTTGAACAGAGAAACATG 879
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## RESULT 14

ABX17141  
ID ABX17141 standard; cDNA; 1238 BP.

XX ABX17141;

XX AC 04-FEB-2003 (first entry)

XX DT Human PRO polynucleotide #108.

XX Human; PRO; gene; ss; secreted polypeptide; transmembrane polypeptide;  
KW toxin; radiolabel; cell death; gene mapping; chromosome mapping;  
KW protein electrophoresis; genetic disorder; immunosuppressive; cytostatic;  
KW antibacterial.

XX Homo sapiens.

XX US2002123463-A1.

XX PD 05-SEP-2002.

XX PF 19-NOV-2001; 2001US-00989732.

XX PR 16-JUN-1997; 97US-0049787P.

XX PR 17-OCT-1997; 97US-0062250P.

XX PR 05-NOV-1997; 97WO-US020069.

XX PR 12-NOV-1997; 97US-0065186P.

XX PR 13-NOV-1997; 97US-0065311P.

XX PR 24-NOV-1997; 97US-0066770P.

XX PR 25-FEB-1998; 98US-0075945P.

XX PR 20-MAR-1998; 98US-0078910P.

XX PR 28-APR-1998; 98US-0083322P.

XX PR 07-MAY-1998; 98US-0084600P.

XX PR 28-MAY-1998; 98US-0087106P.

XX PR 02-JUN-1998; 98US-0087607P.

XX PR 02-JUN-1998; 98US-0087609P.

XX PR 02-JUN-1998; 98US-0087759P.

XX PR 03-JUN-1998; 98US-0087827P.

XX PR 04-JUN-1998; 98US-0088021P.

XX PR 04-JUN-1998; 98US-0088025P.

XX PR 04-JUN-1998; 98US-0088026P.

XX PR 04-JUN-1998; 98US-0088028P.

XX PR 04-JUN-1998; 98US-0088029P.

XX PR 04-JUN-1998; 98US-0088030P.

XX PR 04-JUN-1998; 98US-0088033P.

XX PR 04-JUN-1998; 98US-0088326P.

XX PR 05-JUN-1998; 98US-0088167P.

XX PR 05-JUN-1998; 98US-0088202P.

XX PR 05-JUN-1998; 98US-0088212P.

XX PR 05-JUN-1998; 98US-0088217P.

XX PR 09-JUN-1998; 98US-0088655P.

XX PR 10-JUN-1998; 98US-0088734P.

XX PR 10-JUN-1998; 98US-0088738P.

XX PR 10-JUN-1998; 98US-0088742P.

XX PR 10-JUN-1998; 98US-0088810P.

XX PR 10-JUN-1998; 98US-0088824P.

XX PR 10-JUN-1998; 98US-0088826P.

XX PR 11-JUN-1998; 98US-0088858P.

XX PR 11-JUN-1998; 98US-0088861P.

XX PR 11-JUN-1998; 98US-0088876P.

XX PR 12-JUN-1998; 98US-0089105P.

XX PR 16-JUN-1998; 98US-0089440P.

XX PR 16-JUN-1998; 98US-0089512P.

XX PR 16-JUN-1998; 98US-0089514P.

XX PR 17-JUN-1998; 98US-0089532P.

XX PR 17-JUN-1998; 98US-0089538P.

XX PR 17-JUN-1998; 98US-0089588P.

XX PR 17-JUN-1998; 98US-0089599P.

XX PR 17-JUN-1998; 98US-0089600P.

XX PR 17-JUN-1998; 98US-0089630P.

XX PR 18-JUN-1998; 98US-0089801P.

XX PR 18-JUN-1998; 98US-0089907P.

XX PR 18-JUN-1998; 98US-0089908P.

XX PR 15-SEP-1998; 98WO-US019330.

XX PR 17-SEP-1998; 98WO-US019437.

XX PR 07-OCT-1998; 98WO-US021141.

XX PR 01-DEC-1998; 98WO-US025108.

XX PR 05-JAN-1999; 99WO-US000106.

XX PR 08-MAR-1999; 99WO-US000028.

XX PR 02-JUN-1999; 99WO-US012252.

XX PR 15-SEP-1999; 99WO-US021090.

XX PR 15-SEP-1999; 99WO-US021547.



PR 30-NOV-1999; 99MO-US028313.  
PR 01-DEC-1999; 99MO-US028301.  
PR 01-DEC-1999; 99MO-US028634.  
PR 16-DEC-1999; 99MO-US030095.  
PR 20-DEC-1999; 99MO-US030911.  
PR 06-JAN-2000; 2000MO-US000219.  
PR 06-JUN-2000; 2000MO-US000376.  
PR 11-FEB-2000; 2000MO-US003565.  
PR 18-FEB-2000; 2000MO-US004341.  
PR 22-FEB-2000; 2000MO-US004414.  
PR 24-FEB-2000; 2000MO-US004914.  
PR 24-FEB-2000; 2000MO-US005004.  
PR 02-MAR-2000; 2000MO-US005841.  
PR 10-MAR-2000; 2000MO-US006319.  
PR 15-MAR-2000; 2000MO-US006884.  
PR 30-MAR-2000; 2000MO-US007377.  
PR 30-MAR-2000; 2000MO-US008439.  
PR 15-MAY-2000; 2000MO-US013358.  
PR 17-MAY-2000; 2000MO-US013705.  
PR 22-MAY-2000; 2000MO-US014042.  
PR 30-MAY-2000; 2000MO-US014941.  
PR 02-JUN-2000; 2000MO-US015264.  
PR 28-JUL-2000; 2000MO-US020710.  
PR 11-AUG-2000; 2000MO-US022311.  
PR 23-AUG-2000; 2000MO-US023522.  
PR 24-AUG-2000; 2000MO-US02328.  
PR 08-NOV-2000; 2000MO-US030952.  
PR 01-DEC-2000; 2000MO-US032678.  
PR 28-FEB-2001; 2001MO-US006520.  
PR 01-JUN-2001; 2001MO-US017800.  
PR 20-JUN-2001; 2001MO-US019692.  
PR 29-JUN-2001; 2001MO-US021066.  
PR 09-JUL-2001; 2001MO-US021735.  
PR 28-AUG-2001; 2001US-00941992.

XX  
PA (GENTH ) GENENTECH INC.  
PX  
PI Ashkenazi AJ, Baker KP, Botstein D, Desnayers L, Eaton DL;  
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,  
PI Grimaldi JC, Gurney AL, Kijavrin IJ, Napier MA, Pan J, Paoni NF;  
PI Roy M, Stewart TM, Tumas D, Watanabe CK, Williams PM, Wood WI,  
PI Zhang Z;  
DR  
DR WPI; 2003-066810/06.  
DR P-PSDB; ABU10922.  
XX  
PT Novel secreted and transmembrane polypeptide for modulating biological  
PT activity of cell expressing the polypeptide, identifying agonists or  
PT antagonists of polypeptide, and as molecular weight markers.

XX  
PS Claim 2; Fig 25i; 655pp; English.  
XX

CC The invention relates to a secreted and transmembrane polypeptide, termed  
CC PRO polypeptide, and the polynucleotide encoding it. The polypeptide is  
CC useful for detecting PRO polypeptides and for linking a bioactive  
CC molecule to a cell expressing the above polypeptides, where the bioactive  
CC molecule is a toxin, radiolabel or an antibody. The bioactive material  
CC causes the death of the cell. The polypeptide is useful for identifying  
CC agonists or antagonists of the PRO polypeptide, for preparing variants of  
CC PRO, as a molecular weight marker for protein electrophoresis purposes  
CC and the PRO polynucleotide is useful for recombinantly expressing those  
CC markers. The polynucleotide is also useful as a hybridisation probe, in  
CC chromosome and gene mapping, in generation of antisense RNA and DNA, in  
CC the preparation of PRO polypeptide, for generating transgenic animals or  
CC knockout animals which in turn are useful in the development and  
CC screening of therapeutically useful reagents, to construct hybridisation  
CC probes for mapping the gene which encodes PRO and for the genetic  
CC analysis of individuals with genetic disorders, in gene therapy, for  
CC chromosome identification, as a chromosome marker and for generating  
CC probes for PCR, Northern analysis, Southern analysis and Western  
CC analysis. This sequence represents a human PRO polynucleotide of the  
CC invention  
XX

50	Sequence	1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;
Alignment Scores:		
Pred. No.:	9, 91e-263	Length: 1238
Score:	271.00	Matches: 271
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
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DB	67	ATGAGGGGGAAATCGCCCTCGGTGGCGGCTTCTTAAACACCTGGCGCTTCTGTCACTG 128
QY	21	ProSeRcIyHiAProGInProAlaGlyAspAPaIaCySseRValGInIleLeuValPro 40
DB	127	CCATCTGGACATCTCAAGCCGCGCTGCGCANTGACGCTCTCTGTGCAATCTGTCTCT 188
QY	41	GlyLeuLysGlyAspAlaGlyGlyLysGlyAspLysGlyAlaAProGlyArgProGlyArg 60
DB	187	GGCCTCAAGGGGATCGGGAGAGAAAGGAGCAAAAGCGCGCCCGAGCGGCTGGAAGA 248
QY	61	ValGlyProThrGlyGlyLysGlyAspMetGlyAspLysGlyGlyLysGlySerValGly 80
DB	247	GTCGGCGCCCAACGGGAGAAAAGAGCAATGGGGGCAAAAGACAAAGACAGTGGGT 308
QY	81	ArgHiGlyLysIleGlyProIleGlySerLysGlyGlyLysGlyAspSerGlyAspIle 100
DB	307	CGTACAGAAAATATGTGCTCCATGTGCTTAAAGGTGAAAAGAGATTCGGTGACATA 368
QY	101	GlyProProGlyProAsnGlyGlyLysProGlyLeuProCysGlyCysSerGlnLeuArgLys 120
DB	367	GGACCCCTGTGCTCTAATGAGAACCAAGGCTCCCATGTGATGTCAGCAGCTGCGCAG 428
QY	121	AlaIleGlyGlyMetAspAsnGlnValSerGlnLeuThrSerGlyLeuLysPheIleLys 140
DB	427	GCCATCGGGAGATGAGCAACAGGCTCTTCAGCTGACCAAGCGAGCTCAAGTTTCACAG 488
QY	141	AsnAlaValAlaGlyValArgLysLysLysLysLysLysLysLysLysLysLysLysLys 160
DB	487	AATGCTGTGCGCGGTGTGCGAGACGAGAGCAAGATCTACCTGTGTGTGAAGAGAGAG 548
QY	161	LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyArgGlyGlyThrLeuSerMetPro 180
DB	547	AAGCGCTACGGGAGCGCCCAACGCTGTCTGCCAGGGGCGCGGGGGCAGCCTGAGATCCC 608
QY	181	LysAspGlnAlaAlaAsnGlyLeuMetAlaAlaTyrLeuAlaGlnAlaGlyLeuAlaArg 200
DB	607	AAGGACGAGGCTCCCAATGGCTGATGGCGGACATCTGGCGCAAGCGGCGTGGCCGT 668
QY	201	ValPheIleGlyLysAsnAspLeuGlyLysGlyAlaPheValTyrSerAspHisSer 220
DB	667	GTCCTCATCGGCATCAACACCTGAGAAAGAGGGCGGCTTCGTGATCTGACCACTCC 728
QY	221	ProMetArgThrPheAsnLysTrpArgSerGlyGlyProAsnAsnAlaTyrAspGlnGlu 240
DB	727	CCATGCGGACCTTCAACAAAGTGGGCGACGGGTGAGCCCAACAAATGCTTACAGAGAGAG 788
QY	241	AspCysValAlaLysMetValAlaSerGlyGlyTyrPheAspValAlaCysHisThrThMet 260
DB	787	GACGCGGTGAGATGTGTGGCTCTGGGCGGCTGGAAACGATGGGCTGCAACACCATG 848
QY	261	TyrPheMetCysGlyLysPheAspLysGlyLysMet 271
DB	847	TACTTCATGTGTGATTTGACAAAGAGAAACATG 879
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ID	ACA67996	standard; cDNA; 1238 BP.
XX	ACA67996;	

XX 24-JUN-2003 (first entry)  
DT Novel human secreted and transmembrane protein PRO1182 cDNA.  
XX  
XX Human; secreted and transmembrane protein; gene therapy; PRO; PRO943;  
KW PRO183; PRO184; PRO185; PRO131; PRO1133; PRO363; PRO5723; PRO1387;  
KW PRO1114; PRO3301; PRO940; PRO1181; PRO1170; PRO361; PRO846;  
KW bioactive molecule; toxin; radiolabel; antibody; cell death; cancer;  
KW autoimmune disease; chromosome mapping; gene mapping; transgenic animal;  
KW knockout animal; septic shock; gene; ss.  
XX Homo sapiens.  
OS  
XX US2002177164-A1.  
FN  
PD 28-NOV-2002.  
XX  
XX 20-NOV-2001; 2001US-00389233.  
PE  
XX 16-JUN-1997; 97US-0049787P.  
XX 17-OCT-1997; 97US-0062250P.  
XX 05-NOV-1997; 97US-0062250P.  
XX 12-NOV-1997; 97US-0065186P.  
XX 13-NOV-1997; 97US-0065311P.  
XX 24-NOV-1997; 97US-0066770P.  
XX 25-FEB-1998; 98US-0075945P.  
XX 20-MAR-1998; 98US-0078910P.  
XX 28-APR-1998; 98US-0083322P.  
XX 07-MAY-1998; 98US-0084600P.  
XX 28-MAY-1998; 98US-0087106P.  
XX 02-JUN-1998; 98US-0087607P.  
XX 02-JUN-1998; 98US-0087608P.  
XX 03-JUN-1998; 98US-0087759P.  
XX 04-JUN-1998; 98US-0088021P.  
XX 04-JUN-1998; 98US-0088021P.  
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XX 04-JUN-1998; 98US-0088028P.  
XX 04-JUN-1998; 98US-0088029P.  
XX 04-JUN-1998; 98US-0088030P.  
XX 04-JUN-1998; 98US-0088033P.  
XX 04-JUN-1998; 98US-0088326P.  
XX 05-JUN-1998; 98US-0088167P.  
XX 05-JUN-1998; 98US-0088202P.  
XX 05-JUN-1998; 98US-0088212P.  
XX 05-JUN-1998; 98US-0088217P.  
XX 09-JUN-1998; 98US-0088655P.  
XX 10-JUN-1998; 98US-0088734P.  
XX 10-JUN-1998; 98US-0088738P.  
XX 10-JUN-1998; 98US-0088742P.  
XX 10-JUN-1998; 98US-0088810P.  
XX 10-JUN-1998; 98US-0088824P.  
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XX 11-JUN-1998; 98US-0088858P.  
XX 11-JUN-1998; 98US-0088861P.  
XX 11-JUN-1998; 98US-0088876P.  
XX 12-JUN-1998; 98US-0089105P.  
XX 16-JUN-1998; 98US-0089440P.  
XX 16-JUN-1998; 98US-0089512P.  
XX 16-JUN-1998; 98US-0089514P.  
XX 17-JUN-1998; 98US-0089533P.  
XX 17-JUN-1998; 98US-0089538P.  
XX 17-JUN-1998; 98US-0089586P.  
XX 17-JUN-1998; 98US-0089590P.  
XX 17-JUN-1998; 98US-0089600P.  
XX 17-JUN-1998; 98US-0089653P.  
XX 18-JUN-1998; 98US-0089801P.  
XX 18-JUN-1998; 98US-0089907P.  
XX 18-JUN-1998; 98US-0089908P.  
XX 16-SEP-1998; 98WO-US019330.  
XX 17-SEP-1998; 98WO-US019437.  
XX 07-OCT-1998; 98WO-US021141.  
XX

PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 02-JUN-1999; 99WO-US012252.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 02-MAR-2000; 2000WO-US005004.  
PR 10-MAR-2000; 2000WO-US005819.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 15-MAY-2000; 2000WO-US013358.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 28-AUG-2001; 2001US-00941992.  
XX  
XX (GETH ) GENENTECH INC.  
PA  
XX Abkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrera N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Kijavicius J, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;  
XX  
XX WPI; 2003-328481/31.  
DR P-PSDB; AB081674.  
XX  
XX  
XX New secreted and transmembrane polypeptide, useful for modulating  
PT biological activity of cell expressing the polypeptide, for identifying  
PT agonists or antagonists of polypeptide, and as molecular weight markers.  
PS Claim 2; Fig 251; 654pp; English.  
XX  
XX The invention describes an isolated, secreted and transmembrane  
CC polypeptide (I), termed PRO polypeptide. (I) is useful for detecting  
CC PRO943, PRO183, PRO184, PRO185, PRO331, PRO1133, PRO363, PRO5723,  
CC PRO1387, PRO1114, PRO3301, PRO940, PRO1181, PRO1170, PRO361 or PRO846  
CC polypeptide comprising contacting the sample with the polypeptide and  
CC determining formation of a polypeptide conjugate. (I) is also useful for  
CC linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a  
CC cell expressing the above polypeptides to cause cell death. (I) is also  
CC useful as a therapeutic agent e.g. for treating cancer and autoimmune  
CC disease. PRO is useful in assays to identify other proteins or molecules  
CC involved in binding interactions. The polynucleotide (II) encoding (I) is  
CC useful in chromosome and gene mapping, for generating transgenic animals  
CC or knockout animals which in turn are useful in the development and  
CC screening of therapeutically useful reagents, for the genetic analysis of  
CC individuals with genetic disorders, in gene therapy, for chromosome

CC Identification, and as a chromosome marker. An anti-(I)-antibody is  
CC useful in diagnostic assays for PRO, e.g. detecting its expression in  
CC specific cells, tissues or serum, for affinity purification of PRO, and  
CC for treating septic shock. This sequence encodes a novel human secreted  
CC and transmembrane PRO polypeptide

XX  
SQ Sequence 1238 BP: 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	9.91e-263	Length:	1238
Score:	271.00	Matches:	271
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-806-277A-6 (1-271) x ACA67996 (1-1238)

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QY      1 MetAArgGIYAenLEuAAlLeuValGIYValLeuIleSerLEuAAlaPheLeuSerLEu 20
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Db      67 ATGAGGGGGAATCTGGCCCTGGTGCGCTCTTAATCAGCTGGCCCTCTCTCAGCTGCTG 126
QY      21 ProSerGIYHISProGlnProAlaGlyAaPaPaAaCySeraValGlnIleLeuValPro 40
      |||
Db     127 CCATCTGGACATCCTCAACCGCGCTGGCATGACGCTCTCTGTGCAGATCTCTGCTCCCT 186
QY      41 GlyLeuLYSGIYAaPaPaAGIYGIYLYSGIYAaPLYSGIYAlaProGlyAArgProGlyAArg 60
      |||
Db     187 GGCCCTCAAAAGGGGATGCGGAGAGAAAGGAGACAAAGGCGCCCGGAGCGGCTGGAGA 246
QY      61 ValGlyProThrGlyGlnLYSGIYAaPMeGlyYAaPLYSGIYGlnLYSGIYSerValGly 80
      |||
Db     247 GTCCGCCCCACGAGGAAAGGAAAGAGACATGGGGGCAAAAGGACAGAAAGGCAGTGGGT 306
QY      81 ArgHISGlyLYSILEGlyProIleGlySerLYSGIYLYSGIYAaPSeGlyYAaPile 100
      |||
Db     307 CGTCATGGAATAATTGCTCCATTGGCTCTTAAGGTGAAAGAGATTCCGGTGACATA 366
QY     101 GLYProProGlyProAenGlyGlnProGlyLeuProCySGIYCYaSerGlnLeuAArgLYs 120
      |||
Db     367 GGACCCCTGGTCCTAATGAGAACCAAGGCTCCCATGTGATGCAGCCAGCTGGCAAG 426
QY     121 AlaIleGlyGlnMeAaPaPaGlnValSerGlnLeuThrSerGlnLeuLYSPhelIeLYs 140
      |||
Db     427 GCCATCGGGAGATGACCAACCAAGTCTCTCAGCTGACGACGAGCTCAAGTTCATCAAG 486
QY     141 AaPaPaValAlaGlyValAArgGlnThrGlnSerLYSILETYrLeuLeuValLYSGIY 160
      |||
Db     487 AATGCTGTGCGCGGTGCTGCGAGACGAGACCAAGATCTACCTGCTGTGAAGAGSAG 546
QY     161 LYaArgTYrAlaAaPaPaAGlnLeuSerCySGIYArgGlyYrThrLeuSerMePPro 180
      |||
Db     547 AAGCGCTACGCGAGCGCCACGCTGTCTGCCAGGGGCGCGGGGCGACGCTGAGCATGCC 606
QY     181 LYaAaPaPaGlnAlaAaenGlyLeuMeAAlaIaTYrLeuAlaGlnAlaGlyLeuAlaArg 200
      |||
Db     607 AAGGACGAGGCTGCAATGCGCTGATGGCCGATACCTGGCGCAAGCGGCTGGCCCGT 666
QY     201 ValPheIleGlyIleAaPaPaLeuGlnLYSGIYValPheValTYrSerAaPHisSer 220
      |||
Db     667 GTCTTTCATCGGCACTCAAGCATCTGGAGAAAGAGGGCGCTTCTGTACTCTGACCACTCC 726
QY     221 ProMeAArgThrPheAaenLYSTrAArgSerGlyGlnProAaPaPaIaTYrAaPGLY 240
      |||
Db     727 CCCATGCGGACCTTCAACCAAGTGGCGCAGCGGTGAGCCCAATGCTTACGACGAGGAG 786
QY     241 AaPcySeraValGlnMeAValAlaSerGlyGlyrTrPaAaPaPaValAlaCyenIeThrMet 260
      |||
Db     787 GACTGCGTGAAGATGTGGCTCGGGCGGCTGGAAAGAGGTGGCTGCACACCAACCATG 846
QY     261 TyrPheMetCySGIYPhaAaPLYSGIYUaenMet 271
      |||
Db     847 TACTTCATGTGTGAGTTTGACAAAGGAAACATG 879
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Search completed: December 17, 2004, 11:44:16  
Job time : 596 secs

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RESULT 2-  
US-08-340-539A-5  
Sequence 5, Application US/08340539A  
Patent No. 5808025  
GENERAL INFORMATION:  
APPLICANT: Tedder, Thomas F.  
APPLICANT: Kansas, Geoffrey S.  
TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS  
TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION  
NUMBER OF SEQUENCES: 28

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: FISH & NEAVE  
;; STREET: 1251 Avenue of the Americas  
;; CITY: New York  
;; STATE: New York  
;; COUNTRY: USA  
;; ZIP: 10020  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/340.539A  
;; FILING DATE: 16-NOV-1994  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/008,459  
;; FILING DATE: 25-JAN-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Gunnison, Jane  
;; REGISTRATION NUMBER: 38,479  
;; REFERENCE/DOCKET NUMBER: CG-104 CON  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 212-596-9000  
;; TELEFAX: 212-596-9090  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 531 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; US-08-340-539A-5

Query Match 1.5%; Score 19; DB 1; Length 531;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 805 AGGAGGACTGCGTGAGAT 823  
DB 361 AGGAGGACTGCGTGAGAT 379

RESULT 3  
US-08-461-592B-5  
; Sequence 5, Application US/08461592B  
; Patent No. 5834425  
; GENERAL INFORMATION:  
; APPLICANT: Tedder, Thomas F.  
; APPLICANT: Kansas, Geoffrey S.  
; TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS  
; TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes  
; STREET: Ten Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/461,592B  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/340,539  
; FILING DATE: 16-NOV-1994

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/008,459  
;; FILING DATE: 25-JAN-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: James F. Haley, Jr.  
;; REGISTRATION NUMBER: 27,794  
;; REFERENCE/DOCKET NUMBER: CG-104  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 596-9000  
;; TELEFAX: (212) 596-9090  
;; TELEX: 14-8367  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 531 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; US-08-461-592B-5

Query Match 1.5%; Score 19; DB 2; Length 531;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 805 AGGAGGACTGCGTGAGAT 823  
DB 361 AGGAGGACTGCGTGAGAT 379

RESULT 4  
5514582-1  
; Patent No. 5514582  
; APPLICANT: CAPON, DANIEL J.; LASKY, LAURENCE A.  
; TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID  
; IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 43  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/185,670  
; FILING DATE: 21-JAN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 986,931  
; FILING DATE: 08-DEC-1992  
; APPLICATION NUMBER: 808,122  
; FILING DATE: 16-DEC-1991  
; APPLICATION NUMBER: 440,625  
; FILING DATE: 22-NOV-1989  
; APPLICATION NUMBER: 315,015  
; FILING DATE: 23-FEB-1989  
; SEQ ID NO: 1:  
; LENGTH: 1829  
; 5514582-1

Query Match 1.5%; Score 19; DB 6; Length 1829;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 805 AGGAGGACTGCGTGAGAT 823  
DB 502 AGGAGGACTGCGTGAGAT 520

RESULT 5  
US-08-513-278-1  
; Sequence 1, Application US/08513278  
; Patent No. 5840844  
; GENERAL INFORMATION:  
; APPLICANT: LASKY, LAURENCE A.  
; APPLICANT: STACHEL, SCOTT E.  
; APPLICANT: ROSEN, STEVEN D.  
; APPLICANT: SINGER, MARK S.  
; APPLICANT: YEDNOCK, TED A.

TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/513.278  
FILING DATE: 10-AUG-1995  
CLASSIFICATION: 5530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/059027  
FILING DATE: 06-MAY-1993  
APPLICATION NUMBER: 07/786149  
FILING DATE: 31-OCT-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/315015  
FILING DATE: 23-FEB-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Dregar, Ginger R.  
REGISTRATION NUMBER: 33,055  
REFERENCE/DOCKET NUMBER: 565D1C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-3216  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2259 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-513-278-1

Query Match 1.5%; Score 19; DB 2; Length 2259;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 805 AGGAGACTGCGTGGAGAT 823  
|||||  
Db 502 AGGAGACTGCGTGGAGAT 520

RESULT 6  
US-08-481-803-1  
Sequence 1, Application US/08481803  
Patent No. 5679346  
GENERAL INFORMATION:  
APPLICANT: Tedder, Thomas F. and Olivier G. Spretini  
TITLE OF INVENTION: MONOCLONAL ANTIBODY TO LYMPHOCYTE-ASSOCIATED CELL  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/481.803  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215.366  
FILING DATE: 21-MAR-1994  
APPLICATION NUMBER: US 07/720.602  
FILING DATE: 25-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/313.109  
FILING DATE: 21-FEB-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: CG-101 CON  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2330 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 53..1210  
US-08-481-803-1

Query Match 1.5%; Score 19; DB 1; Length 2330;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 805 AGGAGACTGCGTGGAGAT 823  
|||||  
Db 465 AGGAGACTGCGTGGAGAT 483

RESULT 7  
US-08-215-366A-1  
Sequence 1, Application US/08215366A  
Patent No. 5776775  
GENERAL INFORMATION:  
APPLICANT: Tedder, Thomas F. and Olivier G. Spretini  
TITLE OF INVENTION: MONOCLONAL ANTIBODY TO LYMPHOCYTE-ASSOCIATED  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: WHITE & CASE  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/215.366A  
FILING DATE: 21-MAR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/720.602  
FILING DATE: 25-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/313.109  
FILING DATE: 21-FEB-1989

ATTORNEY/AGENT INFORMATION:  
NAME: Nels T. Lippert  
REGISTRATION NUMBER: 25,888  
REFERENCE/DOCKET NUMBER: 110684-0005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 819-8582  
TELEFAX: (212) 354-8113  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2330 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 53..1210  
US-08-215-366A-1

Query Match 1.5%; Score 19; DB 1; Length 2330;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 805 AGGAGACTGCGTGGAGAT 823  
DB 465 AGGAGACTGCGTGGAGAT 483

RESULT 8  
US-08-340-539A-1  
Sequence 1, Application US/08340539A  
Patent No. 5808025  
GENERAL INFORMATION:  
APPLICANT: Tedder, Thomas F.  
APPLICANT: Kansas, Geoffrey S.  
TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS  
TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSER: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/340,539A  
FILING DATE: 16-NOV-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/008,459  
FILING DATE: 25-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Gunnison, Jane  
REGISTRATION NUMBER: 38,479  
REFERENCE/DOCKET NUMBER: CG-104 CON  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2330 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 53..1207  
US-08-340-539A-1

Query Match 1.5%; Score 19; DB 1; Length 2330;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 805 AGGAGACTGCGTGGAGAT 823  
DB 465 AGGAGACTGCGTGGAGAT 483

RESULT 9  
US-08-461-592B-1  
Sequence 1, Application US/08461592B  
Patent No. 5834425  
GENERAL INFORMATION:  
APPLICANT: Tedder, Thomas F.  
APPLICANT: Kansas, Geoffrey S.  
TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS  
TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Weingarten, Schurigin, Gagnebin & Hayes  
STREET: Ten Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,592B  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/340,539  
FILING DATE: 16-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/008,459  
FILING DATE: 25-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: CG-104  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
TELEX: 14-8367  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2330 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 53..1210  
US-08-461-592B-1

Query Match 1.5%; Score 19; DB 2; Length 2330;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Oy 805 AGAGAGACTGCTGGAGAT 823  
Db 465 AGAGAGACTGCTGGAGAT 483

## RESULT 10

US-09-023-655-1154  
; Sequence 1154, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocke, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023,655  
; FILING DATE: HERewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1154:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2354 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: 9187182  
US-09-023-655-1154  
Query Match 1.5%; Score 19; DB 4; Length 2354;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 805 AGAGAGACTGCTGGAGAT 823  
Db 465 AGAGAGACTGCTGGAGAT 507

## RESULT 11

US-08-378-313-26/c  
; Sequence 26, Application US/08378313  
; Patent No. 6207881  
; GENERAL INFORMATION:  
; APPLICANT: THEOLOGIS, ATHANASIOS  
; APPLICANT: SATO, TAKAHITO  
; TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH  
; TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS  
; NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/378,313  
; FILING DATE:  
; CLASSIFICATION: 800

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/862,493

FILING DATE: 02-APR-1992

ATTORNEY/AGENT INFORMATION:  
; NAME: MORASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 29190-20002.20

TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 856-5600

TELEFAX: (415) 494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 7244 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:  
; NAME/KEY: CDS  
; LOCATION: join(3056..3226, 3325..3453, 3539..3700, 4582  
; LOCATION: ..5574)

US-08-378-313-26

Query Match 1.5%; Score 19; DB 3; Length 7244;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1235 TTAAGTCCAAAAA 1253  
Db 645 TTAAGTCCAAAAA 627

## RESULT 12

US-09-621-976-17318  
; Sequence 17318, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 17318  
; LENGTH: 84  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-621-976-17318

Query Match 1.4%; Score 18; DB 4; Length 84;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1236 TTAAGTCCAAAAA 1253

Db 62 TAAGTCCAAAAA 79

RESULT 13

US-09-621-976-7799  
; Sequence 7799, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO: 7799  
; LENGTH: 89  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-621-976-7799

Query Match 1.4%; Score 18; DB 4; Length 89;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1236 TAAGTCCAAAAA 1253  
Db 63 TAAGTCCAAAAA 80

RESULT 14

US-09-401-064-288/c  
; Sequence 288, Application US/09401064  
; Patent No. 6623923  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Secrist, Heather  
; APPLICANT: Benson, Darin R.  
; APPLICANT: Weagner, Madeline Joy  
; APPLICANT: Stolk, John A.  
; APPLICANT: Wang, Tonglong  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE  
; FILE REFERENCE: 210121.471C2  
; CURRENT APPLICATION NUMBER: US/09/401,064  
; CURRENT FILING DATE: 1999-09-22  
; NUMBER OF SEQ ID NOS: 371  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO: 288  
; LENGTH: 290  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-401-064-288

Query Match 1.4%; Score 18; DB 4; Length 290;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 883 AGTTTGACAGAGACA 900  
Db 35 AGTTTGACAGAGACA 18

RESULT 15  
US-09-788-654A-17  
; Sequence 17, Application US/09788654A  
; Patent No. 673392  
; GENERAL INFORMATION:  
; APPLICANT: YE, Jane et al.

; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE  
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF

; FILE REFERENCE: C0001143  
; CURRENT APPLICATION NUMBER: US/09/788,654A  
; CURRENT FILING DATE: 2001-05-21  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO: 17  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-788-654A-17

Query Match 1.4%; Score 18; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1222 AGTAGCAGTAGTTAG 1239  
Db 163 AGTAGCAGTAGTTAG 180

Search completed: December 17, 2004, 03:40:29  
Job time: 157 secs

GenCore version 5.1.6  
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## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 17, 2004, 11:23:35 ; Search time 103 Seconds

(without alignments)  
1870.134 Million cell updates/sec

Title: US-09-806-277A-6

Perfect score: 271  
Sequence: 1 MRGNALVGVLSIAFLSL.....NDVACHTTMYMCERDKENM 271

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Ygapop 60.0	Ygapext 60.0
Fgapop 6.0	Fgapext 7.0
Delop 6.0	Delext 7.0

Searched: 824507 seqs, 355394441 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1643622

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-DB=Issued_Patents_NA -QFMT=fasta -SUFFIX=Oligo.rnt -MINMATCH=0.1 -LOOPTCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
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-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSEBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
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Database: Issued\_Patents\_NA:\*

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2: /cgn2_6/Plodata/1/ina/5B.COMB.seq:*  
3: /cgn2_6/Plodata/1/ina/6A.COMB.seq:*  
4: /cgn2_6/Plodata/1/ina/6B.COMB.seq:*  
5: /cgn2_6/Plodata/1/ina/ECTUS.COMB.seq:*  
6: /cgn2_6/Plodata/1/ina/backfillseq1.seq:*
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	4.1	89	4	US-09-513-999C-36334
2	10	3.7	93	2	US-08-481-658B-32
3	10	3.7	93	2	US-08-477-504A-32
4	10	3.7	93	2	US-08-486-756A-32
5	10	3.7	93	2	US-08-485-862B-32
6	10	3.7	93	3	US-08-787-739-32
7	10	3.7	93	3	US-08-487-077A-32
8	10	3.7	93	3	US-08-485-863A-32
9	10	3.7	93	3	US-08-485-049D-32
10	10	3.7	93	3	US-09-178-115-32
11	10	3.7	93	3	US-09-177-776-32
12	10	3.7	93	4	US-09-772-719B-32

13	10	3.7	1397	1	US-07-964-589-1	Sequence 1, Appli
14	10	3.7	1397	5	PCT-US93-02024-1	Sequence 1, Appli
15	10	3.7	1399	4	US-08-335-469-1	Sequence 1, Appli
16	10	3.7	1399	4	US-08-260-190-1	Sequence 1, Appli
17	10	3.7	1401	2	US-08-481-658B-49	Sequence 49, Appli
18	10	3.7	1401	2	US-08-477-504A-49	Sequence 49, Appli
19	10	3.7	1401	2	US-08-486-756A-49	Sequence 49, Appli
20	10	3.7	1401	2	US-08-485-862B-49	Sequence 49, Appli
21	10	3.7	1401	3	US-08-787-739-49	Sequence 49, Appli
22	10	3.7	1401	3	US-08-487-077A-49	Sequence 49, Appli
23	10	3.7	1401	3	US-08-485-863A-49	Sequence 49, Appli
24	10	3.7	1401	3	US-08-485-049D-49	Sequence 49, Appli
25	10	3.7	1401	3	US-09-178-115-49	Sequence 49, Appli
26	10	3.7	1401	3	US-09-177-776-49	Sequence 49, Appli
27	10	3.7	1401	3	US-09-772-719B-49	Sequence 49, Appli
28	10	3.7	1522	2	US-08-481-658B-1	Sequence 1, Appli
29	10	3.7	1522	2	US-08-477-504A-1	Sequence 1, Appli
30	10	3.7	1522	2	US-08-486-756A-1	Sequence 1, Appli
31	10	3.7	1522	2	US-08-485-862B-1	Sequence 1, Appli
32	10	3.7	1522	3	US-08-787-739-1	Sequence 1, Appli
33	10	3.7	1522	3	US-08-487-077A-1	Sequence 1, Appli
34	10	3.7	1522	3	US-08-485-863A-1	Sequence 1, Appli
35	10	3.7	1522	3	US-08-485-049D-1	Sequence 1, Appli
36	10	3.7	1522	3	US-09-178-115-1	Sequence 1, Appli
37	10	3.7	1522	3	US-09-177-776-1	Sequence 1, Appli
38	10	3.7	1522	4	US-09-772-719B-1	Sequence 1, Appli
39	10	3.7	1522	4	US-08-260-190-5	Sequence 5, Appli
40	10	3.7	1522	4	US-08-260-190-23	Sequence 23, Appli
41	10	3.7	10898	2	US-08-481-658B-5	Sequence 5, Appli
42	10	3.7	10898	2	US-08-477-504A-5	Sequence 5, Appli
43	10	3.7	10898	2	US-08-486-756A-5	Sequence 5, Appli
44	10	3.7	10898	2	US-08-485-862B-5	Sequence 5, Appli
45	10	3.7	10898	3	US-08-787-739-5	Sequence 5, Appli

## ALIGNMENTS

```
RESULT 1  
US-09-513-999C-36334  
Sequence 36334, Application US/09513999C  
Patent No. 6783961  
GENERAL INFORMATION:  
APPLICANT: Dumas Mline Edwards, J.B.  
APPLICANT: Duclerc, A.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
FILE REFERENCE: 59, US2, REG  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO 36334  
LENGTH: 89  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc_feature  
LOCATION: 53  
OTHER INFORMATION: v=a or c or g  
FEATURE:  
NAME/KEY: misc_feature  
LOCATION: 54  
OTHER INFORMATION: v=a or c or g  
US-09-513-999C-36334  
Alignment Scores:  
Pred. No.: 0.0079  
Score: 11.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Length: 89  
Matches: 11  
Conservative: 0  
Mismatches: 0
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Query Match: 4.06% Indels: 0  
DB: 4 Gaps: 0

US-09-806-277A-6 (1-271) x US-09-513-999C-36334 (1-89)

QY 3 GYAAenLauALeuValGlyValLeuIleSer 13  
DB 55 GGGATCTGGCCCTGTGGGCTTCTATACAC 87

RESULT 2

US-08-481-658B-32  
Sequence 32, Application US/08481658B  
Patent No. 5955075

GENERAL INFORMATION:

APPLICANT: Zavada, Jan  
APPLICANT: Pastorekova, Silvia  
APPLICANT: Pastorek, Jaromir  
TITLE OF INVENTION: MN Gene and Protein  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leona L. Lauder  
STREET: 6 Mariposa Court  
CITY: Tiburon  
STATE: California  
COUNTRY: USA  
ZIP: 94920

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/481,658B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/260,190  
FILING DATE: 15-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Lauder, Leona L.  
REGISTRATION NUMBER: 30,863  
REFERENCE/DOCKET NUMBER: D-0021.3E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-435-2034  
TELEFAX: 415-435-0727

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:  
LENGTH: 93 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
DESCRIPTION: 5th MN exon  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-481-658B-32

Alignment Scores:

Pred. No.: 0.0842 Length: 93  
Score: 10.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.69% Indels: 0  
Gaps: 0

US-09-806-277A-6 (1-271) x US-08-481-658B-32 (1-93)

QY 53 GYAAaProGlyAArgProGlyAArgValGly 62  
DB 51 GGGGGCCCGGGAGGAGGCTGGCGTGTGGC 80

RESULT 3

US-08-477-504A-32

Sequence 32, Application US/08477504A  
Patent No. 5972353

GENERAL INFORMATION:

APPLICANT: Zavada, Jan  
APPLICANT: Pastorekova, Silvia  
APPLICANT: Pastorek, Jaromir  
TITLE OF INVENTION: MN Gene and Protein  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leona L. Lauder  
STREET: 6 Mariposa Court  
CITY: Tiburon  
STATE: California  
COUNTRY: USA  
ZIP: 94920

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,504A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/260,190  
FILING DATE: 15-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Lauder, Leona L.  
REGISTRATION NUMBER: 30,863  
REFERENCE/DOCKET NUMBER: D-0021.3D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-435-2034  
TELEFAX: 415-435-0727

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:  
LENGTH: 93 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
DESCRIPTION: 5th MN exon  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-477-504A-32

Alignment Scores:

Pred. No.: 0.0842 Length: 93  
Score: 10.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.69% Indels: 0  
Gaps: 0

US-09-806-277A-6 (1-271) x US-08-477-504A-32 (1-93)

QY 53 GYAAaProGlyAArgProGlyAArgValGly 62  
DB 51 GGGGGCCCGGGAGGAGGCTGGCGTGTGGC 80

RESULT 4

US-08-486-756A-32  
Sequence 32, Application US/08486756A  
Patent No. 5981711

GENERAL INFORMATION:

APPLICANT: Zavada, Jan  
APPLICANT: Pastorekova, Silvia  
APPLICANT: Pastorek, Jaromir  
TITLE OF INVENTION: MN Gene and Protein  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leona L. Lauder  
STREET: 6 Mariposa Court

CITY: Tiburon  
STATE: California  
COUNTRY: USA  
ZIP: 94920  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,756A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/260,190  
FILING DATE: 15-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Lauder, Leona L.  
REGISTRATION NUMBER: 30,863  
REFERENCE/DOCKET NUMBER: D-0021.3C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-435-2034  
TELEFAX: 415-435-0727  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 93 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
DESCRIPTION: 5th MN exon  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-486-756A-32

Alignment Scores:  
Pred. No.: 0.0842 Length: 93  
Score: 10.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.69% Indels: 0  
Gaps: 0

US-09-806-277A-6 (1-271) x US-08-486-756A-32 (1-93)

QY 53 G1YAlaProG1YArProG1YArG1Y 62  
DB 51 GGGGGCCCCGGAGGAGCGCTGGCGCTGTGGC 80

RESULT 5  
US-08-485-862B-32  
Sequence 32, Application US/08/485862B  
Patent No. 5389838  
GENERAL INFORMATION:  
APPLICANT: Zavada, Jan  
APPLICANT: Pastorekova, Silvia  
APPLICANT: Pastorek, Jaromir  
TITLE OF INVENTION: MN Gene and Protein  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leona L. Lauder  
STREET: 6 Mariposa Court  
CITY: Tiburon  
STATE: California  
COUNTRY: USA  
ZIP: 94920  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,862B

FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/477,504  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/260,190  
FILING DATE: 15-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Lauder, Leona L.  
REGISTRATION NUMBER: 30,863  
REFERENCE/DOCKET NUMBER: D-0021.3D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-435-2034  
TELEFAX: 415-435-0727  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 93 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
DESCRIPTION: 5th MN exon  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-485-862B-32

Alignment Scores:  
Pred. No.: 0.0842 Length: 93  
Score: 10.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.69% Indels: 0  
Gaps: 0

US-09-806-277A-6 (1-271) x US-08-485-862B-32 (1-93)

QY 53 G1YAlaProG1YArProG1YArG1Y 62  
DB 51 GGGGGCCCCGGAGGAGCGCTGGCGCTGTGGC 80

RESULT 6  
US-08-787-739-32  
Sequence 32, Application US/08/787739  
Patent No. 6027887  
GENERAL INFORMATION:  
APPLICANT: Zavada, Jan  
APPLICANT: Pastorekova, Silvia  
APPLICANT: Pastorek, Jaromir  
TITLE OF INVENTION: MN Gene and Protein  
NUMBER OF SEQUENCES: 96  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leona L. Lauder  
STREET: 369 Pine Street, Suite 610  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/787,739  
FILING DATE: 24-JAN-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/485,049  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/486,756  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/477,504

FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/481,658  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/485,862  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/485,863  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/487,077  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Lauder, Leona L.  
REGISTRATION NUMBER: 30,863  
REFERENCE/DOCKET NUMBER: D-0021.4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-981-2034  
TELEFAX: 415-981-0332  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 93 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
DESCRIPTION: 5th MN exon  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
US-08-787-739-32

Alignment Scores:  
Pred. No.: 0.0842 Length: 93  
Score: 10.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.69% Indels: 0  
Gaps: 0

US-09-806-277A-6 (1-271) x US-08-787-739-32 (1-93)

QY 53 GYALAPROGLYARGPROGLYARGVALGILY 62  
DB 51 GGGGGCCCCGGAGGCGCTGGCGGTGTGC 80

RESULT 7  
US-08-487-077A-32

Sequence 32, Application US/08487077A

PATENT No. 6069242

GENERAL INFORMATION:  
APPLICANT: Zavada, Jan  
APPLICANT: Pastorekova, Silvia  
APPLICANT: Pastorek, Jaromir  
TITLE OF INVENTION: MN Gene and Protein  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leona L. Lauder  
STREET: 6 Mariposa Court  
CITY: Tiburon  
STATE: California  
COUNTRY: USA  
ZIP: 94920

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,077A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/260,190  
FILING DATE: 15-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Lauder, Leona L.  
REGISTRATION NUMBER: 30,863  
REFERENCE/DOCKET NUMBER: D-0021.3H  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-435-2034  
TELEFAX: 415-435-0727  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 93 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
DESCRIPTION: 5th MN exon  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
US-08-487-077A-32

Alignment Scores:  
Pred. No.: 0.0842 Length: 93  
Score: 10.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.69% Indels: 0  
Gaps: 0

US-09-806-277A-6 (1-271) x US-08-487-077A-32 (1-93)

QY 53 GYALAPROGLYARGPROGLYARGVALGILY 62  
DB 51 GGGGGCCCCGGAGGCGCTGGCGGTGTGC 80

RESULT 8  
US-08-485-863A-32

Sequence 32, Application US/08485863A

PATENT No. 6093548

GENERAL INFORMATION:  
APPLICANT: Zavada, Jan  
APPLICANT: Pastorekova, Silvia  
APPLICANT: Pastorek, Jaromir  
TITLE OF INVENTION: MN Gene and Protein  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leona L. Lauder  
STREET: 6 Mariposa Court  
CITY: Tiburon  
STATE: California  
COUNTRY: USA  
ZIP: 94920

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,863A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/260,190  
FILING DATE: 15-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Lauder, Leona L.  
REGISTRATION NUMBER: 30,863  
REFERENCE/DOCKET NUMBER: D-0021.3G  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-435-2034  
TELEFAX: 415-435-0727  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:

LENGTH: 93 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
DESCRIPTION: 5th MN exon  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-485-863A-32

Alignment Scores:  
Pred. No.: 0.0842 Length: 93  
Score: 10.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.69% Indels: 0  
DB: 3 Gaps: 0

US-09-806-277A-6 (1-271) x US-08-485-863A-32 (1-93)

OY 53 G1YAlAPrOgIYArGPrOgIYArGValG1Y 62  
Db 51 GGGGGCCCCGGAGGCGCTGCGCGTGTGGC 80

RESULT 9  
US-08-485-049D-32.

Sequence 32, Application US/08485049D  
Patent No. 6204370

GENERAL INFORMATION:

APPLICANT: Zavada, Jan  
APPLICANT: Pastorekova, Silvia  
APPLICANT: Pastorek, Jaromir  
TITLE OF INVENTION: MN Gene and Protein  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leona L. Lauder  
STREET: 369 Pine Street  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,049D  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/260,190  
FILING DATE: 15-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Lauder, Leona L.

REGISTRATION NUMBER: 30,863  
REFERENCE/DOCKET NUMBER: D-0021.3E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-981-2034  
TELEFAX: 415-981-0332  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 93 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)  
DESCRIPTION: 5th MN exon  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-485-049D-32

Alignment Scores:

Pred. No.: 0.0842 Length: 93  
Score: 10.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.69% Indels: 0  
DB: 3 Gaps: 0

US-09-806-277A-6 (1-271) x US-08-485-049D-32 (1-93)

OY 53 G1YAlAPrOgIYArGPrOgIYArGValG1Y 62  
Db 51 GGGGGCCCCGGAGGCGCTGCGCGTGTGGC 80

RESULT 10  
US-09-178-115-32

Sequence 32, Application US/09178115  
Patent No. 6297041

GENERAL INFORMATION:

APPLICANT: Zavada, Jan  
APPLICANT: Pastorekova, Silvia  
APPLICANT: Pastorek, Jaromir  
TITLE OF INVENTION: MN Gene and Protein  
FILE REFERENCE: D-0021.5A  
CURRENT APPLICATION NUMBER: US/09/178,115  
EARLIER FILING DATE: 1998-10-23  
EARLIER APPLICATION NUMBER: 09/177,776  
EARLIER FILING DATE: 1998-10-23  
EARLIER APPLICATION NUMBER: 08/787,739  
EARLIER FILING DATE: 1997-01-24  
EARLIER APPLICATION NUMBER: 08/485,049  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/486,756  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/477,504  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/481,658  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/485,862  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/485,863  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/487,077  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/260,190  
EARLIER FILING DATE: 1994-06-15  
EARLIER APPLICATION NUMBER: 08/177,093  
EARLIER FILING DATE: 1993-12-30  
EARLIER APPLICATION NUMBER: 07/964,589  
EARLIER FILING DATE: 1992-10-21  
EARLIER APPLICATION NUMBER: PV-709-92  
EARLIER FILING DATE: 1992-03-11  
NUMBER OF SEQ ID NOS: 116  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 32  
LENGTH: 93  
TYPE: DNA  
ORGANISM: HUMAN  
FEATURE:  
NAME/KEY: exon  
LOCATION: (1)  
OTHER INFORMATION: 5th MN exon  
US-09-178-115-32

Alignment Scores:

Pred. No.: 0.0842 Length: 93  
Score: 10.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.69% Indels: 0  
DB: 3 Gaps: 0

US-09-806-277A-6 (1-271) x US-09-178-115-32 (1-93)

QY 53 G1YAlAPProG1YArGProG1YArGValG1Y 62  
Db 51 GGGGCGCCCGGAGGCGCTGGCGCTGTGGC 80

## RESULT 11

US-09-177-776-32  
Sequence 32, Application US/0917776A  
Patent No. 6297051  
GENERAL INFORMATION:  
APPLICANT: Zavada, Jan  
APPLICANT: Pastorek, Jaromir  
TITLE OF INVENTION: MN Gene and Protein  
FILE REFERENCE: D-0021.5A  
CURRENT APPLICATION NUMBER: US/09/177,776A  
EARLIER FILING DATE: 1998-10-23  
EARLIER APPLICATION NUMBER: 08/787,739  
EARLIER FILING DATE: 1997-01-24  
EARLIER APPLICATION NUMBER: 08/485,049  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/486,756  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/477,504  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/481,658  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/485,862  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/485,863  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/487,077  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/260,190  
EARLIER FILING DATE: 1994-06-15  
EARLIER APPLICATION NUMBER: 08/177,093  
EARLIER FILING DATE: 1993-12-30  
EARLIER APPLICATION NUMBER: 07/964,589  
EARLIER FILING DATE: 1992-10-21  
EARLIER APPLICATION NUMBER: PV-709-92  
EARLIER FILING DATE: 1992-03-11  
NUMBER OF SEQ ID NOS: 116  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 32  
LENGTH: 93  
TYPE: DNA  
ORGANISM: HUMAN  
FEATURE:  
NAME/KEY: exon  
LOCATION: (1)  
OTHER INFORMATION: 5th MN exon  
US-09-177-776-32

## Alignment Scores:

Pred. No.:	0.0842	Length:	93
Score:	10.00	Matches:	10
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.69%	Indels:	0
DB:	3	Gaps:	0

US-09-806-277A-6 (1-271) x US-09-177-776-32 (1-93)

QY 53 G1YAlAPProG1YArGProG1YArGValG1Y 62  
Db 51 GGGGCGCCCGGAGGCGCTGGCGCTGTGGC 80

## RESULT 12

US-09-772-719B-32  
Sequence 32, Application US/09772719B  
Patent No. 6770438  
GENERAL INFORMATION:  
APPLICANT: Zavada, Jan  
APPLICANT: Pastorek, Jaromir

Pastorek, Jaromir  
TITLE OF INVENTION: MN Gene and Protein  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leona L. Lauder  
STREET: 465 California Street, Suite 450  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94104

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/772,719B  
FILING DATE: 30-Jan-2001  
CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/485,049  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Lauder, Leona L.  
REGISTRATION NUMBER: 30,863  
REFERENCE/DOCKET NUMBER: D-0021.3A-2

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-981-2034  
TELEFAX: 415-981-0332  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 93 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)  
DESCRIPTION: 5th MN exon  
HYPOTHETICAL: NO

ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 32:  
US-09-772-719B-32

## Alignment Scores:

Pred. No.:	0.0842	Length:	93
Score:	10.00	Matches:	10
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.69%	Indels:	0
DB:	4	Gaps:	0

US-09-806-277A-6 (1-271) x US-09-772-719B-32 (1-93)

QY 53 G1YAlAPProG1YArGProG1YArGValG1Y 62  
Db 51 GGGGCGCCCGGAGGCGCTGGCGCTGTGGC 80

## RESULT 13

US-07-964-589-1  
Sequence 1, Application US/07964589  
Patent No. 5387676  
GENERAL INFORMATION:  
APPLICANT: Zavada, Jan  
APPLICANT: Pastorek, Jaromir  
APPLICANT: Pastorek, Jaromir  
TITLE OF INVENTION: MN Gene and Protein  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leona L. Lauder  
STREET: Steuart Street Tower, 18th Fl., One Market  
STREET: Plaza  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA



ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/964,589  
FILING DATE: 19921021  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Lauder, Leona L  
REGISTRATION NUMBER: 30,863  
REFERENCE/DOCKET NUMBER: D-0021  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-777-9257  
TELEFAX: 415-543-4219  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1397 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1287  
US-07-964-589-1

Alignment Scores:  
Pred. No.: 1.18 Length: 1397  
Score: 10.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.69% Indels: 0  
DB: 1 Gaps: 0

US-09-806-277A-6 (1-271) x US-07-964-589-1 (1-1397)

Qy 53 G1YAlaProG1YArGProG1YArGValG1Y 62  
Db 684 GGGGGCCCCGGAGGCGCTGGCCGTTGGC 713

RESULT 14  
PCT-US93-02024-1  
Sequence 1, Application PC/TUS9302024  
GENERAL INFORMATION:  
APPLICANT: CIBA Corning Diagnostics Corp.  
TITLE OF INVENTION: Methods to Detect and Quantify MN Protein/Polypeptide  
TITLE OF INVENTION: MN Gene and Protein  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leona L. Lauder  
STREET: Stewart Street Tower, 18th Fl., One Market  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/02024  
FILING DATE: 19930308  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: CS PV-709-92  
FILING DATE: 10-MAR-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/964,589  
FILING DATE: 21-OCT-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Lauder, Leona L  
REGISTRATION NUMBER: 30,863  
REFERENCE/DOCKET NUMBER: D-0021  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-777-9257  
TELEFAX: 415-543-4219  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1397 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1287  
PCT-US93-02024-1

Alignment Scores:  
Pred. No.: 1.18 Length: 1397  
Score: 10.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.69% Indels: 0  
DB: 5 Gaps: 0

US-09-806-277A-6 (1-271) x PCT-US93-02024-1 (1-1397)

Qy 53 G1YAlaProG1YArGProG1YArGValG1Y 62  
Db 684 GGGGGCCCCGGAGGCGCTGGCCGTTGGC 713

RESULT 15  
US-08-335-469-1  
Sequence 1, Application US/08335469A  
Patent No. 6004535  
GENERAL INFORMATION:  
APPLICANT: Zavada, Jan  
APPLICANT: Pastorekova, Silvia  
TITLE OF INVENTION: Methods to Detect and Quantify MN Protein/Polypeptide  
TITLE OF INVENTION: Using MN-Specific Antibodies  
FILE REFERENCE: D-0021A  
CURRENT APPLICATION NUMBER: US/08/335,469A  
CURRENT FILING DATE: 1994-11-07  
EARLIER APPLICATION NUMBER: 07/964,589  
EARLIER FILING DATE: 1992-10-21  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 1399  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(1266)  
US-08-335-469-1

Alignment Scores:  
Pred. No.: 1.18 Length: 1399  
Score: 10.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.69% Indels: 0  
DB: 3 Gaps: 0

US-09-806-277A-6 (1-271) x US-08-335-469-1 (1-1399)

Mon Dec 20 08:22:13 2004

us-09-806-277a-6.Oligo.rn1

**Page 8**

QY 53 GLYALAProGlyArgProGlyArgValGly 62  
 |||||  
 Db 687 GGGGCGCCCGGAGGAGCTGGCCGTGTGGC 716

Search completed: December 17, 2004, 14:21:42  
Job time : 104 secs







PR 02-JUN-1998; 98US-0087759P.  
PR 03-JUN-1998; 98US-0087827P.  
PR 04-JUN-1998; 98US-0088021P.  
PR 04-JUN-1998; 98US-0088025P.  
PR 04-JUN-1998; 98US-0088028P.  
PR 04-JUN-1998; 98US-0088029P.  
PR 04-JUN-1998; 98US-0088030P.  
PR 04-JUN-1998; 98US-0088033P.  
PR 05-JUN-1998; 98US-0088126P.  
PR 05-JUN-1998; 98US-0088167P.  
PR 05-JUN-1998; 98US-0088202P.  
PR 05-JUN-1998; 98US-0088212P.  
PR 09-JUN-1998; 98US-0088217P.  
PR 09-JUN-1998; 98US-0088555P.  
PR 10-JUN-1998; 98US-0088722P.  
PR 10-JUN-1998; 98US-0088730P.  
PR 10-JUN-1998; 98US-0088734P.  
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PR 10-JUN-1998; 98US-0088741P.  
PR 10-JUN-1998; 98US-0088810P.  
PR 10-JUN-1998; 98US-0088811P.  
PR 10-JUN-1998; 98US-0088824P.  
PR 10-JUN-1998; 98US-0088825P.  
PR 10-JUN-1998; 98US-0088826P.  
PR 11-JUN-1998; 98US-0088858P.  
PR 11-JUN-1998; 98US-0088861P.  
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PR 11-JUN-1998; 98US-0088876P.  
PR 12-JUN-1998; 98US-0089090P.  
PR 12-JUN-1998; 98US-0089105P.  
PR 16-JUN-1998; 98US-0089440P.  
PR 16-JUN-1998; 98US-0089512P.  
PR 16-JUN-1998; 98US-0089514P.  
PR 17-JUN-1998; 98US-0089533P.  
PR 17-JUN-1998; 98US-0089538P.  
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PR 17-JUN-1998; 98US-0089600P.  
PR 17-JUN-1998; 98US-0089653P.  
PR 18-JUN-1998; 98US-0089801P.  
PR 18-JUN-1998; 98US-0089907P.  
PR 18-JUN-1998; 98US-0089908P.  
PR 19-JUN-1998; 98US-0089947P.  
PR 19-JUN-1998; 98US-0089948P.  
PR 19-JUN-1998; 98US-0089952P.  
PR 22-JUN-1998; 98US-0090246P.  
PR 22-JUN-1998; 98US-0090252P.  
PR 22-JUN-1998; 98US-0090254P.  
PR 23-JUN-1998; 98US-0090349P.  
PR 23-JUN-1998; 98US-0090355P.  
PR 24-JUN-1998; 98US-0090422P.  
PR 24-JUN-1998; 98US-0090431P.  
PR 24-JUN-1998; 98US-0090435P.  
PR 24-JUN-1998; 98US-0090444P.  
PR 24-JUN-1998; 98US-0090445P.  
PR 24-JUN-1998; 98US-0090461P.  
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PR 24-JUN-1998; 98US-0090535P.  
PR 24-JUN-1998; 98US-0090538P.  
PR 24-JUN-1998; 98US-0090540P.  
PR 25-JUN-1998; 98US-0090557P.  
PR 25-JUN-1998; 98US-0090676P.  
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PR 25-JUN-1998; 98US-0090695P.  
PR 25-JUN-1998; 98US-0090696P.  
PR 26-JUN-1998; 98US-0090862P.  
PR 26-JUN-1998; 98US-0090863P.

PR 01-JUL-1998; 98US-0091358P.  
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PR 02-JUL-1998; 98US-0091478P.  
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PR 02-JUL-1998; 98US-0091519P.  
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PR 02-JUL-1998; 98US-0091628P.  
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PR 02-JUL-1998; 98US-0091646P.  
PR 02-JUL-1998; 98US-0091673P.  
PR 07-JUL-1998; 98US-0091978P.  
PR 07-JUL-1998; 98US-0091982P.  
PR 09-JUL-1998; 98US-0092182P.  
PR 10-JUL-1998; 98US-0092472P.  
PR 20-JUL-1998; 98US-0093339P.  
PR 30-JUL-1998; 98US-0094651P.  
PR 04-AUG-1998; 98US-0095282P.  
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PR 04-AUG-1998; 98US-0095325P.  
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PR 11-AUG-1998; 98US-0096143P.  
PR 11-AUG-1998; 98US-0096146P.  
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PR 17-AUG-1998; 98US-0096766P.  
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PR 17-AUG-1998; 98US-0096773P.  
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PR 17-AUG-1998; 98US-0096867P.  
PR 17-AUG-1998; 98US-0096891P.  
PR 17-AUG-1998; 98US-0096894P.  
PR 17-AUG-1998; 98US-0096895P.  
PR 17-AUG-1998; 98US-0096897P.  
PR 18-AUG-1998; 98US-0096949P.  
PR 18-AUG-1998; 98US-0096950P.  
PR 18-AUG-1998; 98US-0096959P.  
PR 18-AUG-1998; 98US-0096960P.  
PR 18-AUG-1998; 98US-0097022P.  
PR 19-AUG-1998; 98US-0097141P.  
PR 20-AUG-1998; 98US-0097218P.  
PR 24-AUG-1998; 98US-0097661P.  
PR 26-AUG-1998; 98US-0097951P.  
PR 26-AUG-1998; 98US-0097952P.  
PR 26-AUG-1998; 98US-0097954P.  
PR 26-AUG-1998; 98US-0097955P.  
PR 26-AUG-1998; 98US-0097971P.  
PR 26-AUG-1998; 98US-0097974P.  
PR 26-AUG-1998; 98US-0097978P.  
PR 26-AUG-1998; 98US-0097979P.  
PR 26-AUG-1998; 98US-0097986P.  
PR 26-AUG-1998; 98US-0098014P.  
PR 31-AUG-1998; 98US-0098525P.  
PR 16-SEP-1998; 98US-0100634P.  
PR 12-JAN-1999; 99US-0115565P.  
XX  
PA (GETH ) GENENTECH INC.  
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
XX PI Wood WI, Yuan J;  
XX  
XX WPI; 2000-072883/06.  
XX P-PSDB; AAY6738.  
XX  
XX Membrane-bound proteins and related nucleotide sequences.  
XX  
XX Claim 2; Fig 251; 822pp; English.  
PS

XX The invention provides membrane-bound PRO polypeptides and  
CC polynucleotides encoding them. The PRO sequences of the invention were  
CC identified based on extracellular domain homology screening. The PRO  
CC sequences have homology with proteins including LDL receptors, TIR  
CC ligands and various enzymes. The membrane-bound proteins and receptor  
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
CC immunodhesins, for instance, can be used as therapeutic agents to block  
CC receptor-ligand interactions. The membrane-bound proteins can also be  
CC employed for screening of potential peptide or small molecule inhibitors  
CC of the relevant receptor/ligand interaction. The PRO encoding inhibitors  
CC are useful as hybridization probes, in chromosome and gene mapping and in  
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will  
CC also be useful for the preparation of PRO polypeptides, especially by  
CC recombinant techniques  
XX  
SQ Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;  
Query Match 98.2%; Score 1230; DB 3; Length 1238;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 24 GCGACGGGACGAGACGCGCGTTCGCTAGCGCGTCTAGAGATTGCTCTGCTGCG 83  
DB 1 GCGACGGGACGAGACGCGCGTTCGCTAGCGCGTCTAGAGATTGCTCTGCTGCG 60  
OY 84 CTCAGGATGAGGGGGAATCTGGCCCTGCTGAGGCTTCTAATAGCTTGGCTCTGCTCA 143  
DB 61 CTCAGGATGAGGGGGAATCTGGCCCTGCTGAGGCTTCTAATAGCTTGGCTCTGCTCA 120  
OY 144 CTGCTGCATCTGACATCTCAGCGCGGTGAGTGAAGCGCTGCTGTCAGATCTCTC 203  
DB 121 CTGCTGCATCTGACATCTCAGCGCGGTGAGTGAAGCGCTGCTGTCAGATCTCTC 180  
OY 204 GTCCCTGCGCTTAAAGGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 263  
DB 181 GTCCCTGCGCTTAAAGGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
OY 264 GGAAGAGTGGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 323  
DB 241 GGAAGAGTGGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
OY 324 GTGGTGCATGAGAAATTGCTCCATTGGCTCTAAGAGGAGAGAGAGAGAGAGAG 383  
DB 301 GTGGTGCATGAGAAATTGCTCCATTGGCTCTAAGAGGAGAGAGAGAGAGAGAG 360  
OY 384 GACATAGGACCCCTGCTCTAATGAGAGACAGGCTCTCCATGTGAGTGCAGCGCTG 443  
DB 361 GACATAGGACCCCTGCTCTAATGAGAGACAGGCTCTCCATGTGAGTGCAGCGCTG 420  
OY 444 GCGAAGGCGGAG 503  
DB 421 GCGAAGGCGGAG 480  
OY 504 ATCAAGAAATGCTGCGCGGTGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 563  
DB 481 ATCAAGAAATGCTGCGCGGTGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 540  
OY 564 GAGGAGAGCGGCTAGCGGAGCGCCAGCTGCTCTCCAGGCGCGGCGGAGCGCTGAGC 623  
DB 541 GAGGAGAGCGGCTAGCGGAGCGCCAGCTGCTCTCCAGGCGCGGCGGAGCGCTGAGC 600  
OY 624 ATGCCCAAG 683  
DB 601 ATGCCCAAG 660  
OY 684 GCGCGTCTTCTATGCGGATCAACAGACCTGAGAGAGAGAGAGAGAGAGAGAGAG 743  
DB 661 GCGCGTCTTCTATGCGGATCAACAGACCTGAGAGAGAGAGAGAGAGAGAGAGAG 720  
OY 744 CACTCCCCCATGCGGACCTTCAACAAGTGGCGAGCGGTGAGCCCAACAATGCTTACGAC 803  
DB 721 CACTCCCCCATGCGGACCTTCAACAAGTGGCGAGCGGTGAGCCCAACAATGCTTACGAC 780

OY 804 GAGGAGAGCTGCGCTGAGAGATGCTGCGGCGGCTGAGAGAGAGAGAGAGAGAG 863  
DB 781 GAGGAGAGCTGCGCTGAGAGATGCTGCGGCGGCTGAGAGAGAGAGAGAGAGAG 840  
OY 864 ACCATGTACTTCAATGTGAGATTGACACAGAGAGACATGTAGCTCAGGCTGGGGCTGC 923  
DB 841 ACCATGTACTTCAATGTGAGATTGACACAGAGAGACATGTAGCTCAGGCTGGGGCTGC 900  
OY 924 CCATTGGGGGCGCCACATGTCTCTGACAGGCTTGGCAGGAGACAGAGCCAGCATGTGTC 983  
DB 901 CCATTGGGGGCGCCACATGTCTCTGACAGGCTTGGCAGGAGACAGAGCCAGCATGTGTC 960  
OY 984 CAGCAGGAGACCTGCTCTGTAAGAGGCTGAGAGCTCAGTACATGAGAGGCTGTCCT 1043  
DB 961 CAGCAGGAGACCTGCTCTGTAAGAGGCTGAGAGCTCAGTACATGAGAGGCTGTCCT 1020  
OY 1044 AAACCTGAGAAATAGGCTTATGCTTAAAGAGAAATGAAAGTTCCTGGGGTGTCTC 1103  
DB 1021 AAACCTGAGAAATAGGCTTATGCTTAAAGAGAAATGAAAGTTCCTGGGGTGTCTC 1080  
OY 1104 TGAAGAGCAGAGTTTCATTACCTGTATTGAGCCCAATGTCATTATGTAATTATACC 1163  
DB 1081 TGAAGAGCAGAGTTTCATTACCTGTATTGAGCCCAATGTCATTATGTAATTATACC 1140  
OY 1164 CAGAAATGCTCTTCCATTAAGCTTGTGCTTGTCCAAAGCATTAATAAATCTTTAG 1223  
DB 1141 CAGAAATGCTCTTCCATTAAGCTTGTGCTTGTCCAAAGCATTAATAAATCTTTAG 1200  
OY 1224 TAGTGAGTAGTTAAGTCCAAAAA 1253  
DB 1201 TAGTGAGTAGTTAAGTCCAAAAA 1230  
  
RESULT 4  
AAC58385  
ID AAC58385 standard; cDNA; 1238 BP.  
XX  
XX AAC58385;  
XX  
XX 29-JAN-2001 (first entry)  
XX  
DE Human PRO1182 nucleotide sequence SEQ ID NO:50.  
XX  
XX Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;  
XX proliferation; tumorigenesis; identification; cancer; cytostatic;  
XX neotropic; neuroprotective; antiinflammatory; immunosuppressive;  
XX immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;  
XX neuronal disorder; glial disorder; astrocytal disorder; angiogenic;  
XX hypothalamic disorder; glandular disorder; macropylagal disorder;  
XX epithelial disorder; seroma disorder; blastocellular disorder;  
XX inflammatory disorder; immunologic disorder; ss.  
OS  
XX Homo sapiens.  
XX  
XX WO200053755-A2.  
XX  
XX 14-SEP-2000.  
XX  
XX 06-JAN-2000; 2000WO-US000376.  
XX  
XX  
XX 08-MAR-1999; 99WO-US005028.  
XX 02-JUN-1999; 99WO-US012252.  
XX 23-JUN-1999; 99US-0141037P.  
XX 07-JUL-1999; 99US-0143048P.  
XX 26-JUL-1999; 99US-0145698P.  
XX 30-NOV-1999; 99WO-US028313.  
XX 20-DEC-1999; 99WO-US030911.  
XX 05-JAN-2000; 2000WO-US000219.  
XX  
XX (GENTH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;

PI Metanabe CK, Wood WI;  
 XX WPI, 2000-572270/53.  
 DR P-PSDB; AAB24075.  
 XX

XX Thirty PRO polynucleotides encoding PRO polypeptides, useful in the  
 XX treatment, diagnosis and prevention of cancer.  
 PS

PS Claim 50; Fig 37; 286pp; English.

XX The present invention describes an isolated antibody that binds to one of  
 CC the human PRO proteins designated PRO212, PRO290, PRO341, PRO355, PRO619,  
 CC PRO1717, PRO809, PRO830, PRO943, PRO1093, PRO1099, PRO1025,  
 CC PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184, PRO1187,  
 CC PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094, PRO2145 OR  
 CC PRO2198. PRO antagonists can be used to inhibit tumour cell growth. The  
 CC PRO polypeptides and nucleotides are useful in the treatment, diagnosis  
 CC and prevention of cancer. The antibodies and other anti-tumour compounds  
 CC maybe used to treat various conditions, including those characterised by  
 CC overexpression and/or activation of the amplified PRO genes. Exemplary  
 CC conditions or disorders to be treated with such antibodies and other  
 CC compounds include benign or malignant tumours (e.g., renal, liver,  
 CC kidney, bladder, breast, gastric, ovarian, colorectal, prostate,  
 CC pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas,  
 CC glioblastomas, and various head and neck tumours), leukaemias and  
 CC lymphoid malignancies, other disorders such as neuronal, glial,  
 CC astrocytal, hypochalamic and other glandular, macrophagal, epithelial,  
 CC stromal, and blastocoele disorders, and inflammatory, angiogenic and  
 CC immunologic disorders. AAC58242 to AAC58366 represent PCR primers and  
 CC hybridisation probes used in the isolation of the human PRO sequences.  
 CC AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human PRO  
 CC polynucleotide and protein sequences given in the exemplification of the  
 CC present invention  
 XX

XX Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;

XX Query Match 98.2%; Score 1230; DB 3; Length 1238;

XX Best Local Similarity 100.0%; Pred. No. 0;

XX Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GCGAGCGGAGGAGCGCCCGCTTCCGCTGAGCGGCTCTCAAGAGTTGGTCTGCTGCGG 83  
 DB 1 GCGAGCGGAGGAGCGCCCGCTTCCGCTGAGCGGCTCTCAAGAGTTGGTCTGCTGCGG 60  
 QY 84 CTCAGGATGAGGGGGAATCTGGCCCTGAGGGGCTTTCAATCAGGCTGAGCCCTCTGCA 143  
 DB 61 CTCAGGATGAGGGGGAATCTGGCCCTGAGGGGCTTTCAATCAGGCTGAGCCCTCTGCA 120  
 QY 144 CTGCTGCTGATGAGCATCTCAGCGGCTGAGCGGCTGCTGCTGCTGCTGCTGCTGCTG 203  
 DB 121 CTGCTGCTGATGAGCATCTCAGCGGCTGAGCGGCTGCTGCTGCTGCTGCTGCTGCTG 180  
 QY 204 GTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 263  
 DB 181 GTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
 QY 264 GGAAGAGTCGAGCGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 323  
 DB 241 GGAAGAGTCGAGCGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300  
 QY 324 GTGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 383  
 DB 301 GTGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360  
 QY 384 GACATGAGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 443  
 DB 361 GACATGAGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420  
 QY 444 GCGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 503  
 DB 421 GCGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
 QY 504 ATCAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 563

DB 481 ATCAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
 QY 564 GAGGAGAAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 623  
 DB 541 GAGGAGAAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
 QY 624 ATGCCAAGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 683  
 DB 601 ATGCCAAGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
 QY 684 GCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 743  
 DB 661 GCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
 QY 744 CACTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 803  
 DB 721 CACTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
 QY 804 GAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 863  
 DB 781 GAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
 QY 864 ACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 923  
 DB 841 ACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
 QY 924 CCATGCTG 983  
 DB 901 CCATGCTG 960  
 QY 984 CAGCAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1043  
 DB 961 CAGCAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020  
 QY 1044 AAATGAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1103  
 DB 1021 AAATGAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080  
 QY 1104 TGAAGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1163  
 DB 1081 TGAAGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140  
 QY 1164 CAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1223  
 DB 1141 CAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200  
 QY 1224 TAGTGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1283  
 DB 1201 TAGTGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1230

# RESULT 5

AAFA4230

ID AAFA4230 standard; cDNA; 1238 BP.

AC AAFA4230;

DT 02-APR-2001 (first entry)

XX Human PRO1182 (UNQ596) nucleotide sequence SEQ ID NO:356.

XX Human; secreted and transmembrane protein; PRO; cytosolic; cell death;  
 KW cancer; chromosomal mapping; gene mapping; tissue typing;  
 KW diagnostic assay; ss.

XX Homo sapiens.

XX MO200073454-A1.

XX 07-DEC-2000.

XX 30-MAR-2000; 2000MO-UB008439.



XX	02-JUN-1999;	99WO-US01252.	
PR	23-JUN-1999;	99US-0141037P.	
PR	07-JUL-1999;	99US-0143048P.	
PR	20-JUL-1999;	99US-0144758P.	
PR	26-JUL-1999;	99US-0145698P.	
PR	28-JUL-1999;	99US-0146222P.	
PR	17-AUG-1999;	99US-0149396P.	
PR	15-SEP-1999;	99WO-US021090.	
PR	15-SEP-1999;	99WO-US021547.	
PR	08-OCT-1999;	99US-0158663P.	
PR	30-NOV-1999;	99WO-US028313.	
PR	01-DEC-1999;	99WO-US028301.	
PR	16-DEC-1999;	99WO-US030095.	
PR	20-DEC-1999;	99WO-US030911.	
PR	05-JAN-2000;	2000WO-US000219.	
PR	06-JAN-2000;	2000WO-US000376.	
PR	11-FEB-2000;	2000WO-US003565.	
PR	18-FEB-2000;	2000WO-US004341.	
PR	22-FEB-2000;	2000WO-US004414.	
PR	24-FEB-2000;	2000WO-US004914.	
PR	24-FEB-2000;	2000WO-US005094.	
PR	02-MAR-2000;	2000WO-US005841.	
PR	15-MAR-2000;	2000WO-US006884.	
PR	20-MAR-2000;	2000WO-US007377.	
XX			
PA	(GETH ) GENENTECH INC.		
XX			
PI	Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;		
PI	Ferrari N, Fong S, Gebber H, Gerritsen ME, Goddard A, Godowski PJ;		
PI	Grimaldi CJ, Gunney AL, Kijaviri IU, Napier MA, Pan J, Peoni NF;		
PI	Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;		
PI	Zhang Z;		
XX			
DR	WPI, 2001-032160/04.		
DR	P-PSDB; AAB65261.		
XX			
PT	PRO polynucleotides used to produce polypeptides used to target bioactive		
PT	molecules such as toxins, radiolabels or antibodies, to specific cells,		
PT	to cause targeted cell death.		
XX			
PS	Claim 2; Fig 251; 935pp; English.		
XX			
CC	The present invention describes human secreted and transmembrane PRO		
CC	proteins. The PRO proteins have cytostatic activity. The PRO proteins can		
CC	be used for targeted delivery of bioactive molecules, such as toxins,		
CC	radiolabels or antibodies, that cause cell death. PRO nucleotide		
CC	sequences, and their fragments, can be used as hybridisation probes, in		
CC	chromosomal and gene mapping, and in the generation of anti-sense RNA and		
CC	DNM. They may also be used to produce transgenic animals which are used		
CC	to develop and screen therapeutically useful reagents. The PRO nucleotide		
CC	and protein sequence can be used for tissue typing and in treating		
CC	cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to		
CC	AAF44470 represent PCR primers and hybridisation probes used in the		
CC	isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to		
CC	AAB65300 represent human PRO polynucleotide and protein sequences given		
CC	in the exemplification of the present invention		
XX			
XX			
SQ	Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;		
	Query Match	98.2%; Score 1230; DB 5; Length 1238;	
	Best Local Similarity	100.0%; Pred. No. 0;	
	Matches 1230; Conservative	0; Mismatches 0; Indels 0; Gaps	0
OY	24 GCGAGGGGCGAGACCGCCCGTTCCGCTTACCGCGGTGCTCAGAGATTGCTGCTGCTGGG	83	
DB	1 GCGAGGGGCGAGACCGCCCGTTCCGCTTACCGCGGTGCTCAGAGATTGCTGCTGCTGGG	60	
OY	84 CTCAGAGATGAGGGGAGATCTGGCCCTGTGGGGGGGTTCTATCAGACCTGGACCTTCTGTGA	143	
DB	61 CTCAGAGATGAGGGGAGATCTGGCCCTGTGGGGGGGTTCTATCAGACCTGGACCTTCTGTGA	120	
OY	144 CTGCTGCACATCTGGAATCTTCAGCCCGCTGGCGATGAGTACCGCTGCTGTGAGAGATCTTC	203	

D	b	121	CTGCTGCCATCTGGACATCTCAAGCCGGCTGGCGATGACGCTGCTCTGTGACGATCTCTC	180
O	y	204	GTCCCTGGCCTTCAAGGGGAGATGCGGAGAGAGAGCAAAAGCGCCCCCGGACGGCCT	263
D	b	181	GTCCCTGGCCTTCAAGGGGAGATGCGGAGAGAGAGCAAAAGCGCCCCCGGACGGCCT	240
O	y	264	GGAAAGATCGGCCCCCAGGGAGAAAAAGAGACATGGGGGACAAAGGACAAAGAGGCAT	323
D	b	241	GGAAAGATCGGCCCCCAGGGAGAAAAAGAGACATGGGGGACAAAGGACAAAGAGGCAT	300
O	y	324	GTGGGTGCTCATGAAAAATTGGTCCCATTTGGCTCTAAAGGTGAGAAAGAGATTCGGGT	383
D	b	301	GTGGGTGCTCATGAAAAATTGGTCCCATTTGGCTCTAAAGGTGAGAAAGAGATTCGGGT	360
O	y	384	GACATAGGACCCCTGGTCTTAATGAGAACAGGCGTCCATGTTGAGTGACGACGACGTG	443
D	b	361	GACATAGGACCCCTGGTCTTAATGAGAACAGGCGTCCATGTTGAGTGAGCAGCGACGTG	420
O	y	444	CGCAAGCGCATTCGGGGAGATGGAGCAACAGTGTCTCAGCTGACACGAGGACTCAAGTT	503
D	b	421	CGCAAGCGCATTCGGGGAGATGGAGCAACAGTGTCTCAGCTGACACGAGGACTCAAGTT	480
O	y	504	ATCAAGATGCTGTGCGCGGTGTGGCGGAGAGAGAGCAAGATCTACCTGCTGTGGAG	563
D	b	481	ATCAAGATGCTGTGCGCGGTGTGGCGGAGAGAGCAAGATCTACCTGCTGTGGAG	540
O	y	564	GAGAGAAAGCGTATGCGGAGCGCCAGGCTGTCTGCGCAAGGCGCGGGGGGCAAGCTGAG	623
D	b	541	GAGAGAAAGCGTATGCGGAGCGCCAGGCTGTCTGCGCAAGGCGCGGGGGGCAAGCTGAG	600
O	y	624	ATGCCAAGAGAGAGGCTGCCAATGCGCTGATGCGCGATACCTTGCGCAAGCGGCGCTG	683
D	b	601	ATGCCAAGAGAGAGGCTGCCAATGCGCTGATGCGCGCTGATACCTTGCGCAAGCGGCGCTG	660
O	y	684	GCCGTGTCTTCATGCGGATCAACGACCTGGAGAAAGAGAGGGCGCTTGCTGTATCTGTGAC	743
D	b	661	GCCGTGTCTTCATGCGGATCAACGACCTGGAGAAAGAGAGGGCGCTTGCTGTATCTGTGAC	720
O	y	744	CACCTCCCATGCGGAGCCTTCAACAAGTGGCCAGCGGTGAGACCCCAATGCGCTACGAC	803
D	b	721	CACCTCCCATGCGGAGCCTTCAACAAGTGGCCAGCGGTGAGACCCCAATGCGCTACGAC	780
O	y	804	GAGAGAGACTGCGTGGAGATGGTGGCGCTTCGGCGGCTGGAAAGACGCTGGCTTGCAACC	863
D	b	781	GAGAGAGACTGCGTGGAGATGGTGGCGCTTCGGCGGCTGGAAAGACGCTGGCTTGCAACC	840
O	y	864	ACCATGTACTTCATGTGTGAGTTTGACAAAGAGAAATGTGAGCTCAGGCTTGGGGCTGC	923
D	b	841	ACCATGTACTTCATGTGTGAGTTTGACAAAGAGAAATGTGAGCTCAGGCTTGGGGCTGC	900
O	y	924	CCATTGGGGGGCCCAATGTGCCCTGCAGGGGTGGGACGAGGCCAGACCATGTTGTC	983
D	b	901	CCATTGGGGGGCCCAATGTGCCCTGCAGGGGTGGGACGAGGCCAGACCATGTTGTC	960
O	y	984	CAGCCAGGAGGTGTCCCTCTGTGAAAGGTGAGGCTCACTAGTGAAGGCGCTTGTCT	1044
D	b	961	CAGCCAGGAGGTGTCCCTCTGTGAAAGGTGAGGCTCACTAGTGAAGGCGCTTGTCT	1022
O	y	1044	AAACTGAGAAAAATGGCCTTATGTTAAGAGAAAAATGAAGTGTCTCTGGGGTGTGCTC	1104
D	b	1021	AAACTGAGAAAAATGGCCTTATGTTAAGAGAAAAATGAAGTGTCTCTGGGGTGTGCTC	1083
O	y	1104	TGAAGAACAGATTCAATLACNBTATTTGAGCCCAATGTGATATATATATTAAC	1166
D	b	1081	TGAAGAACAGATTCAATLACNBTATTTGAGCCCAATGTGATATATATATTAAC	1144
O	y	1164	CAGAAATGCTCTTCATTAAGCTTGTGCTTGTCCAAGCTATACAAATAATCTTTAAG	1222
D	b	1141	CAGAAATGCTCTTCATTAAGCTTGTGCTTGTCCAAGCTATACAAATAATCTTTAAG	1200
O	y	1224	TATGTCAGTAGTTAAGTCCAAAAAAA	1253

Db 1201 TAGTGCAGTACTAGTCCAAAAA 1230

RESULT 6

ABL8155

ID ABL8155 standard; cDNA, 1238 BP.

XX ABL8155;

AC 16-MAY-2002 (first entry)

XX 16-MAY-2002 (first entry)

DE Human PRO1182 cDNA sequence SEQ ID NO:167.

XX Human; angiogenesis; cardiac; cytosolic; antiangiogenic; hypotensive;

XX vlnery; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;

XX gene therapy; cardiovascular disorder; endothelial disorder; cancer;

XX angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;

XX age-related macular degeneration; arterial restenosis; angina;

XX rheumatoid arthritis; myocardial infarction; thrombophlebitis;

XX lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;

XX wound healing; chromosome mapping; gene mapping; gene; se.

XX Homo sapiens.

XX WO200200690-A2.

XX 03-JAN-2002.

XX 20-JUN-2001; 2001WO-US019692.

XX 23-JUN-2000; 2000US-0213637P.

XX 20-JUL-2000; 2000US-0219556P.

XX 25-JUL-2000; 2000US-0220624P.

XX 28-JUL-2000; 2000US-0220644P.

XX 02-AUG-2000; 2000US-0220671P.

XX 17-AUG-2000; 2000US-0222695P.

XX 23-AUG-2000; 2000WO-US023522.

XX 24-AUG-2000; 2000WO-US023328.

XX 07-SEP-2000; 2000US-0230978P.

XX 18-SEP-2000; 2000US-00664610.

XX 18-SEP-2000; 2000US-00665350.

XX 24-OCT-2000; 2000US-0249222P.

XX 08-NOV-2000; 2000US-00709238.

XX 08-NOV-2000; 2000WO-US030952.

XX 10-NOV-2000; 2000WO-US030873.

XX 01-DEC-2000; 2000WO-US032678.

XX 20-DEC-2000; 2000US-00747259.

XX 20-DEC-2000; 2000WO-US034956.

XX 22-JAN-2001; 2001US-00766498.

XX 28-FEB-2001; 2001US-00766498.

XX 28-FEB-2001; 2001WO-US006520.

XX 01-MAR-2001; 2001WO-US006666.

XX 09-MAR-2001; 2001US-00802706.

XX 14-MAR-2001; 2001US-00808689.

XX 22-MAR-2001; 2001US-00816744.

XX 05-APR-2001; 2001US-00828365.

XX 10-MAY-2001; 2001US-00854208.

XX 10-MAY-2001; 2001US-00854280.

XX 25-MAY-2001; 2001US-00866028.

XX 25-MAY-2001; 2001US-00866034.

XX 25-MAY-2001; 2001WO-US017092.

XX 30-MAY-2001; 2001US-00870574.

XX 30-MAY-2001; 2001WO-US017443.

XX 01-JUN-2001; 2001WO-US017800.

XX (GENTH ) GENENTECH INC.

XX Baker KP, Ferrara N, Gerber H, Gertsen ME, Goddard A,

XX Godowski PJ, Guirey AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,

XX Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,

XX WPI; 2002-090516/12.

DR P-PSDB; ABB84900.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides.

PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial

PT infarction), endothelial or angiogenic disorders in a mammal.

XX Claim 2; Fig 167; 565pp; English.

XX ABL8155 encodes the PRO proteins given in ABB84817 to

CC ABB85003. The PRO proteins and polynucleotides have cardiac, cytosolic,

CC antiangiogenic, hypotensive, vlnery and antiarteriosclerotic

CC activities, and can be used in gene therapy. The PRO polynucleotides

CC proteins, agonists and antagonists are useful for treating or diagnosing

CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.

CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,

CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,

CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour

CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound

CC healing. The PRO polynucleotides have applications in molecular biology,

CC including use as hybridisation probes, and in chromosome and gene

CC mapping. ABL8155 to ABL8267 represent primers and probes used in the

CC exemplification of the present invention

XX Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;

XX

Query Match 98.2%; Score 1230; DB 6; Length 1238;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 84 CTGAGATGAGGGGAGATCGGCTGCTGAGGAGTCTAATCAGCCCTGCTCTCTCA 143

Db 61 CTGAGATGAGGGGAGATCGGCTGCTGAGGAGTCTAATCAGCCCTGCTCTCTCA 120

QY 144 CTGCTGCATCTGAGACATCTCTCAGCGGCTGCGAGTACCGCTGCTGAGATCTC 203

Db 121 CTGCTGCATCTGAGACATCTCTCAGCGGCTGCGAGTACCGCTGCTGAGATCTC 180

QY 204 GTCCCTGCTCAAGGGAGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 263

Db 181 GTCCCTGCTCAAGGGAGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240

QY 264 GGAAGATCGGCCCCAGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 323

Db 241 GGAAGATCGGCCCCAGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300

QY 324 GTGGGTGCTATGAGAGAGATGGTCCCATTTGGCTTAAAGGTGAGAGAGATTCGGT 383

Db 301 GTGGGTGCTATGAGAGAGATGGTCCCATTTGGCTTAAAGGTGAGAGAGATTCGGT 360

QY 384 GACTATGAG 443

Db 361 GACTATGAG 420

QY 444 CGCAAGGCAATCGGGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 503

Db 421 CGCAAGGCAATCGGGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480

QY 504 ATCAAGATGCTGTGCGCGGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 563

Db 481 ATCAAGATGCTGTGCGCGGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540

QY 564 GAG 623

Db 541 GAG 600

QY 624 ATGCCAAG 683

Db 601 ATGCCAAG 660

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QY 864 ACCATGTACTTCATGTGTGAGTTTGAACAAGAGAACATGTGAGCTCAAGGCTGGGGCTGAC 923
DB 841 ACCATGTACTTCATGTGTGAGTTTGAACAAGAGAACATGTGAGCTCAAGGCTGGGGCTGAC 900
QY 924 CCATTGGGGGGCCCAATGTCCTTCGACAGGGTTGGCAGGAGACAGAGCCCAAGCATGTGAC 983
DB 901 CCATTGGGGGGCCCAATGTCCTTCGACAGGGTTGGCAGGAGACAGAGCCCAAGCATGTGAC 960
QY 984 CAGCCAGGAGAGCTGCTCTCTGTGAAAGGTGAGAGGCTCACTGAGTGAAGGGCTGTGTCT 1043
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RESULT 7
ABL95644
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AC ABL95644;
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DT 19-JUL-2002 (first entry)
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DE Human angiogenesis related cDNA P101182 SEQ ID NO: 167.
XX
KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiac; cytosolic; antiangiogenic; hypotensive; vulnerary;
KW antiarteriosclerotic; gene; se.
XX
OS Homo sapiens.
XX
PN W0200208284-A2.
XX
PD 31-JAN-2002.
XX
PF 09-JUL-2001; 2001WO-US021735.
XX
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220624P.
PR 28-JUL-2000; 2000US-0220664P.
PR 02-AUG-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
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PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
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PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006520.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017443.
PR 20-JUN-2001; 2001WO-US017800.
XX
PA (GETH ) GENENTECH INC.
PA (BAKE ) BAKER K P.
PA (FERR ) FERRARA N.
PA (GERB ) GERBER H.
PA (GERR ) GERRITSEN M E.
PA (GODD ) GODDARD A.
PA (GODO ) GODOWSKI P J.
PA (GURN ) GURNEY A L.
PA (HILL ) HILLAN K J.
PA (MARS ) MARSTERS S A.
PA (PANU ) PAN J.
PA (PAON ) PAONI N F.
PA (STEP ) STEPHAN J F.
PA (WATA ) WATANABE C K.
PA (WILL ) WILLIAMS P M.
PA (WOOD ) WOOD W I.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
PI Godowski PJ, Gurney AJ, Hillan KJ, Marsters SA, Pan J,
PI Stephen JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2002-171999/22.
DR P-P8DB; ABB95506.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
PS Claim 1; Fig 167; 567pp; English.
XX
CC The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a coding sequence of the invention
XX
SQ Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;
Query Match 98.2%; Score 1230; DB 6; Length 1238;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 24 GCGAGGCGCAGAGCGCCCGCTTCCGCTTACGCGGCTGAGAGTTGCTGCTGCTGCG 83





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Db 721 CACTCCCCCATGCGGACCTTCAACAATGCGCGAGCGGTGAGCCCAACAATGCTTAGAC 780  
Qy 804 GAGAGGACCTCGTGGAGATGATGGGCTCGGGGCGCTGGAACGAGTGGCTGGCACACC 863  
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Qy 864 ACCATGTACTTCATGTGTGATTTGACAGAGAAACATGTAGCCTCAGGCTGGGCGCTGC 923  
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RESULT 9  
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ID ABX80858 standard; cDNA; 1238 BP.  
XX  
AC ABX80858;  
XX  
DT 22-APR-2003 (first entry)  
XX  
DE Human secreted/transport membrane protein cDNA, #144.  
XX  
KW Human; gene; ss; PRO; secreted; transport membrane; pharmaceutical;  
KW diagnostic; biosensor; bioeffector; tumour; therapeutic; gene therapy;  
KW tumour-associated antigenic target; TAT; ADAPT;  
KW antibody-dependent enzyme mediated prodrug therapy; cytostatic.  
XX  
OS Homo sapiens.  
XX  
FN US2003027162-A1.  
XX  
PD 06-FEB-2003.  
XX  
PF 15-NOV-2001; 2001US-00997428.  
XX  
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PR 17-OCT-1997; 97US-0062250P.  
PR 05-NOV-1997; 97WO-US020069.  
PR 12-NOV-1997; 97US-0065186P.  
PR 13-NOV-1997; 97US-0065311P.  
PR 24-NOV-1997; 97US-0066770P.  
PR 25-FEB-1998; 98US-0075945P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 28-APR-1998; 98US-0083322P.  
PR 07-MAY-1998; 98US-0084600P.  
PR 28-MAY-1998; 98US-0087106P.

PR 02-JUN-1998; 98US-0087607P.  
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Query Match	98.2%;	Score 1230;	DB 8;	Length 1238;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1230;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

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Oy	84	CTCAGGATGAGGGGGGAAATCTGACCTCTGGTGGGCGCTTCAATCAGCCTGACCTTCTGTCA	143
Db	61	CTCAGGATGAGGGGGGAAATCTGACCTCTGGTGGGCGCTTCAATCAGCCTGACCTTCTGTCA	120
Oy	144	CTGCTGCCATCTGGACATCTCAGCGCGCTGGCGATGACGCTGCTCTGTGACAGATCTC	203
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Db	241	GGAAGAGTCGCGCCCCCAGGAGAAAGAGACATGGGGGACAAAGGACAGAAAGGAGT	300
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Db	301	GTCGGTCGTATGAGAAAAATTGTCCTCAATGGCTCTAAAGGTGAGAAAGAGATTCGGT	360
Oy	384	GACATAGGACCCCTGTGCTTAATGAGAACAGAGGCTCCATGTGAGTCAAGCAGCTG	443
Db	361	GACATAGGACCCCTGTGCTTAATGAGAACAGAGGCTCCATGTGAGTCAAGCAGCTG	420
Oy	444	CGAAGGCCATCGGGGAGATGAGCAACAGGCTCTGAGCTGACACAGGAGCTCAAGTTC	503
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Oy	624	ATGCCAAGGACGAGGCTGCAATGAGCTGATGGCGGCAATCTCTGGGCGCAAGCGGCTG	683
Db	601	ATGCCAAGGACGAGGCTGCAATGAGCTGATGGCGGCAATCTCTGGGCGCAAGCGGCTG	660
Oy	684	GCCGTCGTCTCACTGGCATCAACGACCTGAGAAAGAGGGGCGCTTCGTGTACTTGAC	743

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Db 721 CACTCCCCCATGCGGACCTTCAACAAAGTGGCGAGCGGTGAGCCCAATGCTTACGAC 780  
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Qy 864 ACCATGTAATTCATGTGATGATTTGAACAAGAAACATGTAGCCTCAGCTGGGGCTGC 923  
Db 841 ACCATGTAATTCATGTGATGATTTGAACAAGAAACATGTAGCCTCAGCTGGGGCTGC 900  
Qy 924 CCATTGGGGGCCCCCATGTCCTCTGAGGGTGGCAGGAGCAAGGCCAATGCTGC 983  
Db 901 CCATTGGGGGCCCCCATGTCCTCTGAGGGTGGCAGGAGCAAGGCCAATGCTGC 960  
Qy 984 CAGCCAGGAGAGCTGCTCTTGTGTGAAGGGTGGAGGCTCACTGAGTGAAGGGCTGTGCTC 1043  
Db 961 CAGCCAGGAGAGCTGCTCTTGTGTGAAGGGTGGAGGCTCACTGAGTGAAGGGCTGTGCTC 1020  
Qy 1044 AAACAGAGAAATGAGCTATGCTTAAGAGAAATGAAGTGTCTCTGGGGTGTCTC 1103  
Db 1021 AAACAGAGAAATGAGCTATGCTTAAGAGAAATGAAGTGTCTCTGGGGTGTCTC 1080  
Qy 1104 TGAAGAGAGAGTTCATTACCTGTATTGTAGCCCAATGCTATTATTAATTAAC 1163  
Db 1081 TGAAGAGAGAGTTCATTACCTGTATTGTAGCCCAATGCTATTATTAATTAAC 1140  
Qy 1164 CAGATTTGCTCTTCATTAAGCTTGTGCTTGCACAGCTATACATTAATCTTTAAG 1223  
Db 1141 CAGATTTGCTCTTCATTAAGCTTGTGCTTGTCTTGCACAGCTATACATTAATCTTTAAG 1200  
Qy 1224 TAGTCAGTATTGAATGCCAAAAA 1253  
Db 1201 TAGTCAGTATTGAATGCCAAAAA 1230  
RESULT 10  
ACD44367  
ID ACD44367 standard; cDNA, 1238 BP.  
XX  
AC ACD44367;  
XX  
DT 10-SEP-2003 (first entry)  
XX  
DE cDNA encoding human PRO1182 polypeptide.  
XX  
KW Human; PRO polypeptide; secreted protein; transmembrane protein;  
KW genetic disorder; antibacterial; immunosuppressive; transgenic;  
KW gene therapy; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN US2002127576-A1.  
PD 12-SEP-2002.  
XX  
PF 14-NOV-2001; 2001US-00991073.  
XX  
PR 16-JUN-1997; 97US-0049787P.  
PR 17-OCT-1997; 97US-0062250P.  
PR 05-NOV-1997; 97WO-US020065.  
PR 12-NOV-1997; 97US-0065186P.  
PR 13-NOV-1997; 97US-0065311P.  
PR 24-NOV-1997; 97US-0066770P.  
PR 25-FEB-1998; 98US-0075945P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 28-APR-1998; 98US-0083322P.  
PR 07-MAY-1998; 98US-0084600P.  
PR 28-MAY-1998; 98US-0087106P.  
PR 02-JUN-1998; 98US-0087607P.

PR 02-JUN-1998; 98US-0087609P.  
PR 02-JUN-1998; 98US-0087759P.  
PR 03-JUN-1998; 98US-0087827P.  
PR 04-JUN-1998; 98US-0088021P.  
PR 04-JUN-1998; 98US-0088025P.  
PR 04-JUN-1998; 98US-0088026P.  
PR 04-JUN-1998; 98US-0088028P.  
PR 04-JUN-1998; 98US-0088029P.  
PR 04-JUN-1998; 98US-0088030P.  
PR 04-JUN-1998; 98US-0088033P.  
PR 04-JUN-1998; 98US-0088326P.  
PR 05-JUN-1998; 98US-0088167P.  
PR 05-JUN-1998; 98US-0088202P.  
PR 05-JUN-1998; 98US-0088212P.  
PR 05-JUN-1998; 98US-0088217P.  
PR 09-JUN-1998; 98US-0088655P.  
PR 10-JUN-1998; 98US-0088734P.  
PR 10-JUN-1998; 98US-0088738P.  
PR 10-JUN-1998; 98US-0088742P.  
PR 10-JUN-1998; 98US-0088810P.  
PR 10-JUN-1998; 98US-0088824P.  
PR 10-JUN-1998; 98US-0088826P.  
PR 11-JUN-1998; 98US-0088858P.  
PR 11-JUN-1998; 98US-0088861P.  
PR 11-JUN-1998; 98US-0088876P.  
PR 12-JUN-1998; 98US-0089105P.  
PR 16-JUN-1998; 98US-0089440P.  
PR 16-JUN-1998; 98US-0089512P.  
PR 16-JUN-1998; 98US-0089514P.  
PR 17-JUN-1998; 98US-0089512P.  
PR 17-JUN-1998; 98US-0089538P.  
PR 17-JUN-1998; 98US-0089598P.  
PR 17-JUN-1998; 98US-0089599P.  
PR 17-JUN-1998; 98US-0089600P.  
PR 17-JUN-1998; 98US-0089653P.  
PR 18-JUN-1998; 98US-0089801P.  
PR 18-JUN-1998; 98US-0089907P.  
PR 18-JUN-1998; 98US-0089908P.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 02-JUN-1999; 99WO-US012352.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 16-DEC-1999; 99WO-US028634.  
PR 20-DEC-1999; 99WO-US030095.  
PR 06-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005941.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 15-MAY-2000; 2000WO-US013358.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.



PR 08-NOV-2000; 2000MO-US030952.  
PR 01-DEC-2000; 2000MO-US032678.  
PR 28-FEB-2001; 2001MO-US006520.  
PR 01-JUN-2001; 2001MO-US017800.  
PR 20-JUN-2001; 2001MO-US019692.  
PR 29-JUN-2001; 2001MO-US021066.  
PR 09-JUL-2001; 2001MO-US021735.  
PR 28-AUG-2001; 2001US-00941992.  
XX  
XX (GETH ) GENENTECH INC.  
XX Ashkenazi AJ, Baker KP, Botstein D, Desnovers L, Baton DL;  
PI Ferraraz N, Fong S, Gerber H, Gottlieb ME, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Kijavlin IJ, Napier MA, Pan J, Paoni NP;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;  
XX MPI; 2003-340824/32.  
DR P-P9DB; ABO25998.  
XX  
XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
PT and are therapeutically useful for enhancing immune responses.  
XX  
XX Claim 2; Fig 251; 661pp; English.  
XX  
XX The present invention relates to the isolation of novel human PRO  
CC polypeptides, and the polynucleotide sequences encoding them. The PRO  
CC polypeptides are secreted and transmembrane proteins. The PRO  
CC polypeptides are useful for detecting other PRO polypeptides, for linking  
CC biactive molecules to cells expressing PRO polypeptides, for modulating  
CC biological activities of cells expressing PRO polypeptides, and for for  
CC identifying agonists or antagonists. The polynucleotide sequences  
CC encoding PRO polypeptides are useful as hybridisation probes, in  
CC chromosome and gene mapping, in the generation of antisense RNA and DNA,  
CC in the preparation of PRO polypeptides, for generating transgenic animals  
CC or knockout animals, to construct hybridisation probes for mapping the  
CC gene which encodes the PRO polypeptide, and for the genetic analysis of  
CC individuals with genetic disorders, in gene therapy, for chromosome  
CC identification, as chromosome markers, and for generating probes for PCR,  
CC Northern analysis, Southern analysis and Western analysis. The present  
CC sequence encodes a human PRO polypeptide of the invention. Note: The  
CC sequence data for this patent was obtained in electronic format directly  
CC from the USPTO web site at [seqdata.uspto.gov/patseqidntry.html](http://seqdata.uspto.gov/patseqidntry.html)  
XX  
XX Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;  
SQ  
Query Match 98.2%; Score 1230; DB 8; Length 1238;  
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 24 GCGACGGGAGAGACCCCGCTTCCGCTAGCGGCTCTCAGAGTTGGTCTGCTGCTGCG 83  
DB 1 GCGACGGGAGAGACCCCGCTTCCGCTAGCGGCTCTCAGAGTTGGTCTGCTGCTGCG 60  
QY 84 CTCAGAGTAGGGGGAATCTGGCCCTGTGGCGTTCTAATCAGCCTGGCCTTCTGTCA 143  
DB 61 CTCAGAGTAGGGGGAATCTGGCCCTGTGGCGTTCTAATCAGCCTGGCCTTCTGTCA 120  
QY 144 CTGCTGCATCTGGAATCTCAGCGCGGTGGCGATGAGCGCTGCTGTGAGATTCCTC 203  
DB 121 CTGCTGCATCTGGAATCTCAGCGCGGTGGCGATGAGCGCTGCTGTGAGATTCCTC 180  
QY 204 GTCCCTGGCTCAAGAGGGGATCGGAGAGAGAGCAAAAGCGCCCGCCGAGCGCT 263  
DB 181 GTCCCTGGCTCAAGAGGGGATCGGAGAGAGAGCAAAAGCGCCCGCCGAGCGCT 240  
QY 264 GGAAGAGTGGCCCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 323  
DB 241 GGAAGAGTGGCCCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
QY 324 GTGGGTGCTGATGAG 383

DB 301 GTGGGTGCTGATGAG 360  
QY 384 GACATAGAGACCCCTGGTCTCTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 443  
DB 361 GACATAGAGACCCCTGGTCTCTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
QY 444 CGAAGGCTATCGGAG 503  
DB 421 CGAAGGCTATCGGAG 480  
QY 504 ATCAAGAGTGTCTGTCGCGGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 563  
DB 481 ATCAAGAGTGTCTGTCGCGGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540  
QY 564 GAG 623  
DB 541 GAG 600  
QY 624 ATGCGCAAG 683  
DB 601 ATGCGCAAG 660  
QY 684 GCCGTGTCTTCAATCGGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 743  
DB 661 GCCGTGTCTTCAATCGGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720  
QY 744 CACTCCCCATGCGAG 803  
DB 721 CACTCCCCATGCGAG 780  
QY 804 GAG 863  
DB 781 GAG 840  
QY 864 ACCATGTAATTCATGTGATGATTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 923  
DB 841 ACCATGTAATTCATGTGATGATTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900  
QY 924 CCATTGGGGGCGCCCATGATGTCCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 983  
DB 901 CCATTGGGGGCGCCCATGATGTCCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960  
QY 984 CAGCAGGAG 1043  
DB 961 CAGCAGGAG 1020  
QY 1044 AAACCTAG 1103  
DB 1021 AAACCTAG 1080  
QY 1104 TGAAG 1163  
DB 1081 TGAAG 1140  
QY 1164 CAGAAATGCTCTTCCATTAAG 1223  
DB 1141 CAGAAATGCTCTTCCATTAAG 1200  
QY 1224 TAGTCAAGTAAAGTCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1283  
DB 1201 TAGTCAAGTAAAGTCAAAAG 1230  
RESULT 11  
ABX79538  
ID ABX79538 standard; cDNA; 1238 BP.  
XX  
XX ABX79538;  
AC  
XX  
XX 17-APR-2003 (first entry)  
DT  
XX  
XX Human secreted/craniospinal protein cDNA, #144.  
DE

KW Human; gene; ss; PRO; secreted; transmembrane; signal peptide;  
KW pharmaceutical; diagnostic; biosensor; bioreactor; tumour; therapeutic;  
KW colon cancer; lung cancer; breast cancer; cancer; gene therapy.  
OS Homo sapiens.  
PN US2002142961-A1.  
XX 03-OCT-2002.  
PD 19-NOV-2001; 2001US-00989771.  
XX 16-JUN-1997; 97US-0049787P.  
PR 17-OCT-1997; 97US-0062250P.  
PR 05-NOV-1997; 97WO-US020069.  
PR 12-NOV-1997; 97US-0065186P.  
PR 13-NOV-1997; 97US-0065311P.  
PR 24-NOV-1997; 97US-0066770P.  
PR 25-FEB-1998; 98US-0075945P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 28-APR-1998; 98US-0083322P.  
PR 07-MAY-1998; 98US-0084600P.  
PR 28-MAY-1998; 98US-0087106P.  
PR 02-JUN-1998; 98US-0087607P.  
PR 02-JUN-1998; 98US-0087609P.  
PR 03-JUN-1998; 98US-0087827P.  
PR 04-JUN-1998; 98US-0088021P.  
PR 04-JUN-1998; 98US-0088025P.  
PR 04-JUN-1998; 98US-0088026P.  
PR 04-JUN-1998; 98US-0088028P.  
PR 04-JUN-1998; 98US-0088029P.  
PR 04-JUN-1998; 98US-0088030P.  
PR 04-JUN-1998; 98US-0088033P.  
PR 04-JUN-1998; 98US-0088326P.  
PR 05-JUN-1998; 98US-0088167P.  
PR 05-JUN-1998; 98US-0088202P.  
PR 05-JUN-1998; 98US-0088212P.  
PR 05-JUN-1998; 98US-0088217P.  
PR 09-JUN-1998; 98US-0088655P.  
PR 10-JUN-1998; 98US-0088734P.  
PR 10-JUN-1998; 98US-0088738P.  
PR 10-JUN-1998; 98US-0088742P.  
PR 10-JUN-1998; 98US-0088810P.  
PR 10-JUN-1998; 98US-0088824P.  
PR 10-JUN-1998; 98US-0088826P.  
PR 11-JUN-1998; 98US-0088858P.  
PR 11-JUN-1998; 98US-0088861P.  
PR 11-JUN-1998; 98US-0088862P.  
PR 12-JUN-1998; 98US-0089105P.  
PR 16-JUN-1998; 98US-0089440P.  
PR 16-JUN-1998; 98US-0089512P.  
PR 16-JUN-1998; 98US-0089514P.  
PR 17-JUN-1998; 98US-0089533P.  
PR 17-JUN-1998; 98US-0089538P.  
PR 17-JUN-1998; 98US-0089598P.  
PR 17-JUN-1998; 98US-0089599P.  
PR 17-JUN-1998; 98US-0089600P.  
PR 17-JUN-1998; 98US-0089651P.  
PR 18-JUN-1998; 98US-0089801P.  
PR 18-JUN-1998; 98US-0089907P.  
PR 18-JUN-1998; 98US-0089908P.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 02-JUN-1999; 99WO-US012252.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.

PR 01-DEC-1999; 99WO-US028634.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US000365.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 15-MAY-2000; 2000WO-US013358.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUN-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 28-AUG-2001; 2001US-00941992.  
XX (GETH ) GENENTECH INC.  
XX Ashkenazi AV, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Fong S, Gerber H, Gertlisen MB, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;  
XX WPI; 2003-155950/15.  
DR P-PSDB; ABUS9007.  
XX New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184,  
PT PRO361 or PRO846) useful as targets for therapeutic intervention in  
PT cancers (e.g. lung or breast cancers), or for diagnosing these cancers.  
XX Claim 2; Fig 251; 647pp; English.  
XX The invention discloses isolated PRO secreted/transmembrane polypeptides  
CC comprising a sequence without signal peptide and the nucleic acid  
CC encoding them. The polypeptides can be used to raise antibodies that  
CC specifically bind to the PRO polypeptide, for linking a bioactive  
CC molecule to a cell expressing a PRO protein and for modulating at least  
CC one biological activity of a cell. The PRO polypeptides or  
CC polynucleotides are also useful as pharmaceuticals, diagnostics,  
CC biosensors or bioreactors, for detecting or treating e.g. tumours in  
CC mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or  
CC rabbits as targets for therapeutic intervention in certain cancers (e.g.  
CC colon, lung or breast cancer) and diagnostic determination of the  
CC presence of these cancers. The PRO polypeptides are also useful as  
CC molecular weight markers or for chromosome identification. The PRO genes  
CC are useful as hybridisation probes or for screening libraries of human  
CC cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene  
CC therapy, particularly for replacing a defective gene. The sequences  
CC presented in ABX79290-ABX79675 are the genes encoding, the primers  
CC amplifying and the probes detecting the PRO polynucleotides of the  
CC invention. Note: The sequence data for this patent is also available in  
CC electronic format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)  
XX Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;  
SQ

Query Match 98.2%; Score 1230; DB 8; Length 1238;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 GCGACGGGACAGACGCGCTTGCCTAGCGCGTCTCAGAGTTGTGCTCGCTCG 83  
Db 1 GCGACGGGACAGACGCGCTTGCCTAGCGCGTCTCAGAGTTGTGCTCGCTCG 60

Qy 84 CTCAGATGAGGGGAAATCTGGCCCTGTGGCGTTCTAATACGCTTGCTCTGCA 143  
Db 61 CTCAGATGAGGGGAAATCTGGCCCTGTGGCGTTCTAATACGCTTGCTCTGCA 120

Qy 144 CTGCTGCATCTGACATCTCAGCGCGCTGCGATGAGCGCTGTCTGTGAGATCTC 203  
Db 121 CTGCTGCATCTGACATCTCAGCGCGCTGCGATGAGCGCTGTCTGTGAGATCTC 180

Qy 204 GTCCCTGGCTCAAAAGGGATGCGGAGAGAGAGCAAAAGCGCCCGGACGCGCT 263  
Db 181 GTCCCTGGCTCAAAAGGGATGCGGAGAGAGAGCAAAAGCGCCCGGACGCGCT 240

Qy 264 GGAAAGATCGGCCCCACGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 323  
Db 241 GGAAAGATCGGCCCCACGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300

Qy 324 GTGGGTGCTCATGAAAAATTGTGCTCAATGGCTTAAAGTGAGAGAGAGATTCGGGT 383  
Db 301 GTGGGTGCTCATGAAAAATTGTGCTCAATGGCTTAAAGTGAGAGAGAGATTCGGGT 360

Qy 384 GACATAGAGACCCCTGTGCTCTAATGAGAGACGAGGCTCCCATGTAGTGCAGCAGT 443  
Db 361 GACATAGAGACCCCTGTGCTCTAATGAGAGACGAGGCTCCCATGTAGTGCAGCAGT 420

Qy 444 CGCAAGGCCATCGGGGAGATGAGCAACAGTCTCTCAGCTGACGAGCGAGTCAAGTTC 503  
Db 421 CGCAAGGCCATCGGGGAGATGAGCAACAGTCTCTCAGCTGACGAGCGAGTCAAGTTC 480

Qy 504 ATCAAGATGCTGTGCGCGGTGTGCGGAGAGAGAGAGAGAGATCTCCTGTGTGAG 563  
Db 481 ATCAAGATGCTGTGCGCGGTGTGCGGAGAGAGAGAGATCTCCTGTGTGAG 540

Qy 564 GAGGAGAGCGCTACGCGGACGCGAGCTGTCTCCAGGGCGCGGGGAGCGCTGAGC 623  
Db 541 GAGGAGAGCGCTACGCGGACGCGAGCTGTCTCCAGGGCGCGGGGAGCGCTGAGC 600

Qy 624 ATGCCCAAGAGAGAGGCTGCCAATGCTGATGCGCGCATACCTGCGCAAGCGGCTG 683  
Db 601 ATGCCCAAGAGAGAGGCTGCCAATGCTGATGCGCGCATACCTGCGCAAGCGGCTG 660

Qy 684 GCCCGTCTTCAATGGGATCAACGACTGTGAGAGAGGGGCGCTTGTGTACTCTGAC 743  
Db 661 GCCCGTCTTCAATGGGATCAACGACTGTGAGAGAGGGGCGCTTGTGTACTCTGAC 720

Qy 744 CACTCCCCCATGCGGACCTTCAACAAGTGGCGCAGCGGTGAGCCCAACATGCTACAG 803  
Db 721 CACTCCCCCATGCGGACCTTCAACAAGTGGCGCAGCGGTGAGCCCAACATGCTACAG 780

Qy 804 GAGGAGAGCTGCGTGAAGTGTGCTTGGCGGCTGAGAGAGAGAGAGAGAGAGAG 863  
Db 781 GAGGAGAGCTGCGTGAAGTGTGCTTGGCGGCTGAGAGAGAGAGAGAGAGAGAG 840

Qy 864 ACCATGTAATCTTCAATGAGAGTTTGAACAAGAGAGAGAGAGAGAGAGAGAGAG 923  
Db 841 ACCATGTAATCTTCAATGAGAGTTTGAACAAGAGAGAGAGAGAGAGAGAGAGAG 900

Qy 924 CCATTGGGGGGCCCAATGCTCCCTGACAGGTTGGAGGAGAGAGAGAGAGAGAGAG 983  
Db 901 CCATTGGGGGGCCCAATGCTCCCTGACAGGTTGGAGGAGAGAGAGAGAGAGAGAG 960

Qy 984 CAGCCAGGAGAGCTGTCTCTGTGAAGGTTGAGGCTCACTGAGTGAAGAGGCTGTGCT 1043  
Db 961 CAGCCAGGAGAGCTGTCTCTGTGAAGGTTGAGGCTCACTGAGTGAAGAGGCTGTGCT 1020

Qy 1044 AAACGAGAGAAATGCGCTATGCTTAAAGAGAGAAATGAAGTGTCTCTGGGGTCTGCTC 1103

Db 1021 AAACGAGAGAAATGCGCTATGCTTAAAGAGAGAAATGAAGTGTCTCTGGGGTCTGCTC 1080  
Qy 1104 TGAAGAGCAGAGTTTCATTAATCTGTATTTAGAGCCCAATGCTATTAATTAATAC 1163  
Db 1081 TGAAGAGCAGAGTTTCATTAATCTGTATTTAGAGCCCAATGCTATTAATTAATAC 1140

Qy 1164 CAGAAATGCTCTTCTCAATTAAGTGTGCTTTGTCCAAAGCTATTAATTAATCTTTAAG 1223  
Db 1141 CAGAAATGCTCTTCTCAATTAAGTGTGCTTTGTCCAAAGCTATTAATTAATCTTTAAG 1200

Qy 1224 TAGTCAGTACTTAAGTCAAAAAA 1253  
Db 1201 TAGTCAGTACTTAAGTCAAAAAA 1230

RESULT 12  
ACA93559 standard; cDNA; 1238 BP.

AC A93559;  
AC A93559;  
DT 16-JUN-2003 (first entry)  
XX  
DE Novel human secreted and transmembrane protein PRO1182 cDNA.  
XX  
XX Human; secreted and transmembrane protein; PRO; PRO183; PRO184; PRO185;  
KW PRO943; PRO1133; PRO331; PRO1387; PRO563; PRO5723; PRO1114; PRO3301;  
KW PRO9940; PRO1181; PRO170; PRO846; bioactive molecule; toxin;  
KW radiolabel; antibody; cell death; tissue typing; gene therapy;  
KW cyostatic; chromosome mapping; gene mapping; transgenic animal;  
KW knockout animal; immunohistochemical staining; gene; ss.  
OS Homo sapiens.  
XX  
XX US2003022187-A1.  
XX  
XX 30-JAN-2003.  
XX  
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